

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 20:55:30 ; Search time 8502 Seconds

(without alignments)  
1172.999 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

Sequence: 1 MTQVPLRSLVPAALAGSAA.....VRVYISLLPLGDLTLAFKI 262

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cnp2.1/USPTO spool/US10017407/runat\_19042005.142533.29458/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=1500  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10017407 @CNP 1.1 4352 @runat\_19042005.142533.29458 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hgc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1330	99.0	889	4 BM451059
2	1259	93.7	814	4 BM051236
3	1228	91.4	1308	3 CR602194
4	1214	90.4	1006	2 BF663323
5	1188	88.5	921	2 BF664198
6	1186.5	88.3	772	2 BE796570
7	1186.5	88.0	1321	3 CR625911
8	1186.5	87.9	750	6 CB852718
9	1186.5	87.6	779	2 BF663695

10	1163	86.6	934	5 BQ31589
11	1156	86.1	919	3 AK007659
12	1156	86.1	2243	3 AK054334
13	1126	83.8	910	6 BY707694
14	1126	82.7	999	3 BC019467
15	1101	82.0	756	6 CA777547
16	1101	82.0	771	6 CB852030
17	1094	81.5	977	5 BU841828
18	1090	81.2	886	6 CB181160
19	1089	81.1	904	6 CB194568
20	1066.5	79.4	909	6 CB194405
21	1050	78.2	826	5 BP433057
22	1049	78.1	790	4 B1411825
23	1042	77.2	753	5 BP463671
24	1037	77.6	625	4 BM768764
25	1010	75.2	1035	5 BX339546
26	1008	75.1	912	4 BG339399
27	1000	74.5	714	5 BM976177
28	996	74.2	710	5 BQ746381
29	981	73.0	691	2 BE279279
30	981	73.0	1122	4 BG339315
31	975	72.6	688	7 CK464189
32	969.5	72.2	1065	5 BQ072503
33	954	71.0	580	4 BM769685
34	953	71.0	725	7 CN157520
35	953	71.0	725	7 CN159458
36	945	70.4	676	2 BB666437
37	938	69.8	581	5 BP322631
38	930	69.2	614	7 CK622065
39	912	67.9	581	1 AI929359
40	900.5	67.1	998	5 BQ918468
41	882	65.7	587	5 BP272395
42	872	64.9	606	2 AW157329
43	857	63.8	666	7 CK463833
44	855	63.7	710	7 CK771494
45	844	63.6	564	2 AW163385
46	843	62.8	685	7 CN157439
47	843	62.8	685	7 CN159383
48	841	62.6	675	7 CN161942
49	841	62.6	675	7 CN163323
50	841	62.6	681	7 CK938500
51	841	62.6	682	7 CN166896
52	836	61.5	566	2 AW163525
53	823	61.3	549	2 BE014998
54	822	61.2	589	1 AI692198
55	819	61.0	583	5 BP323071
56	818	60.9	714	2 BF341318
57	816	60.8	573	4 B1340505
58	814	60.6	582	2 AW157252
59	800	59.6	639	4 BG910899
60	799	59.5	556	2 BE665755
61	773	57.6	543	2 BE665750
62	773	57.6	546	2 BE237447
63	771	57.4	524	6 CB720369
64	769.5	57.3	1110	4 B1198020
65	769	57.3	550	2 BE684896
66	767.5	57.1	578	2 AW003514
67	767	57.1	579	4 B1341406
68	763	56.8	605	4 BG995491
69	762	56.7	516	6 CB716330
70	760	56.6	622	6 CD674768
71	755	56.2	695	4 BG081244
72	749	55.8	572	1 AI765658
73	745	55.5	513	2 BF193231
74	740	55.1	546	2 AW157459
75	737	54.9	434	4 BM826016
76	735.5	54.8	971	3 BG680071
77	729	54.3	2171	3 AK046931
78	727.5	54.2	1162	2 BE797685
79	726	54.1	456	5 BQ083301
80	724	53.9	517	9 CG851631
81	724	53.9	584	7 CF360100
82	723	53.8	732	2 BE287985

BQ31589	AGENCOURT
AK007659	Mus muscu
AK054334	Mus muscu
BY707694	BY707694
BC019467	Mus muscu
CA777547	ip21G07.x
CB852030	UI-CF-FNO
BU841828	AGENCOURT
CB181160	AGENCOURT
CB194568	AGENCOURT
CB194405	AGENCOURT
BP433057	BP433057
B1411825	602968437
BP463671	BP463671
BM768764	K-EST0051
BX339546	BX339546
BG339399	602437508
BM976177	UI-CF-EN1
BQ746381	UI-M-ERO-
BE279279	601157608
BG339315	602437607
CK464189	935151 MA
BQ072503	AGENCOURT
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BM769685	K-EST0052
CN157520	946232 MA
CN159458	948536 MA
BB666437	BB666437
BP322631	BP322631
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CK622065	ml32b11.y
AI929359	au59803.y
BQ918468	AGENCOURT
BP272395	BP272395
AW157329	au94f01.x
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CK771494	959788 MA
AW163385	au94f01.y
CN157439	946147 MA
CN159383	948451 MA
CN161942	951279 MA
CN163323	952815 MA
CK938500	UI-R-AF1-
CN166896	989978 MA
AW163525	au95h04.y
BE014998	126934 MA
AI692198	wd37h07.x
BP323071	BP323071
BF341318	602013260
B1340505	365795 MA
AW157252	au93601.x
BG910899	602812540
BE665755	154904 MA
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BE237447	146741 MA
CB720369	AMGNNUC:N
B1198020	602762169
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B1341406	368809 MA
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BF193231	244743 MA
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BG680071	602628219
AK046931	Mus muscu
BE797685	601584583
BQ083301	K-EST0145
CG851631	OST413096
CF360100	821402 MA
BE287985	601093725

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580 4 BI680796 459974 MA BI680796 459974 MA 157 571 42.5 453 1 AI969924 wq77f05.x  
485 5 BX524890 BX524890 158 570.5 42.5 1150 3 CR684437 Tetraodon  
446 4 BM825668 K-EST0097 BM825668 K-EST0097 159 570.5 42.5 1162 3 CR683289 Tetraodon  
620 1 AA584408 m81b03.s AA584408 m81b03.s 160 569.5 42.4 1244 3 CR732330 Tetraodon  
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22.6 638 1 BI3339545 BX3339545 BI3339545 BX3339545 162 569 42.4 1208 3 CR700159 Tetraodon  
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52.1 575 1 AI810740 t04a011.x AI810740 t04a011.x 164 568 42.3 582 5 BQ615284 fab24d05.  
52.1 599 4 BG498801 602544450 BG498801 602544450 165 568 42.3 596 4 BM574082 f458h01.y  
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96 670 49.9 481 7 CR749077 CR749077 170 567.5 42.3 1218 3 CR727337 Tetraodon  
97 663 49.4 506 4 BI340371 365618 MA BI340371 365618 MA 171 567.5 42.3 1220 3 CR682032 Tetraodon  
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100 643 47.9 442 7 CK457735 922062 MA CK457735 922062 MA 174 567 42.2 1216 3 CR732881 Tetraodon  
101 643 47.9 442 7 CK458804 923214 MA CK458804 923214 MA 175 566.5 42.2 1161 3 CR682009 Tetraodon  
102 640 47.7 977 4 BI198073 602762269 BI198073 602762269 176 566 42.1 724 6 CA382012 661717 NC  
103 638 47.5 474 4 BM141962 lf24h03.y BM141962 lf24h03.y 177 564 42.0 458 4 BG689814 338070 BA  
104 638 47.5 502 7 CR819655 lf22d02.y CR819655 lf22d02.y 178 563 41.9 1231 3 CR687110 Tetraodon  
105 634 47.2 525 4 BM129725 lf22d02.y BM129725 lf22d02.y 179 562.5 41.9 1074 6 CA490947 AGENCOURT  
106 633.5 47.2 754 5 BP158933 BP158933 180 562 41.8 576 4 AI659582 tt87c02.x  
107 630 46.9 565 4 BM753400 K-EST0030 BM753400 K-EST0030 181 560 41.7 678 6 CA353706 625267 NC  
108 628.5 46.8 664 2 BF181707 601805520 BF181707 601805520 182 560 41.7 1143 3 CR685515 Tetraodon  
109 627 46.7 411 4 BM768965 K-EST0052 BM768965 K-EST0052 183 559 41.6 581 5 BQ450896 fab12d03.  
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111 617.5 46.0 421 1 AJ679437 AJ679437 185 559 41.6 1198 3 CR695082 Tetraodon  
112 612 45.6 519 4 BM141699 9242892 BM141699 9242892 186 553.5 41.2 871 3 CR653669 Tetraodon  
113 611 45.5 1000 5 BX422892 BX422892 187 553.5 41.2 878 3 CR654482 Tetraodon  
114 608 45.3 769 6 CA346219 677059 NC CA346219 677059 NC 188 553 41.2 428 5 BY041621 BY041621  
115 605 45.0 539 2 BF769048 BF769048 189 552.5 41.1 885 3 CR633632 Tetraodon  
116 604 45.0 515 7 CF181537 818378 MA CF181537 818378 MA 190 551.5 41.1 1200 3 CR698066 Tetraodon  
120 593 44.2 414 1 AI892364 mm60d11.y AI892364 mm60d11.y 191 551 41.0 569 5 BQ480163 faa86g07.  
121 592.5 44.1 1235 3 CR721460 Tetraodon CR721460 Tetraodon 192 549.5 40.9 913 3 CR638711 Tetraodon  
122 592 44.1 507 4 BM129438 lf22d02.x BM129438 lf22d02.x 193 547 40.7 1188 3 CR690884 Tetraodon  
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124 590 43.9 1207 3 CR646763 Tetraodon CR646763 Tetraodon 195 546.5 40.7 861 3 CR634105 Tetraodon  
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132 584 43.5 470 6 CA777819 ip21g07.y CA777819 ip21g07.y 203 544.5 40.5 882 3 CR650550 Tetraodon  
133 584 43.5 747 6 CA388383 670627 NC CA388383 670627 NC 204 544.5 40.5 873 3 CR733986 Tetraodon  
134 582.5 43.4 1216 3 CR685301 Tetraodon CR685301 Tetraodon 205 544 40.5 454 5 BU500439 AGENCOURT  
135 581.5 43.3 1238 3 CR682588 Tetraodon CR682588 Tetraodon 206 542.5 40.4 864 3 CR653465 Tetraodon  
136 581 43.3 1229 3 CR701700 Tetraodon CR701700 Tetraodon 207 542.5 40.4 884 3 CR653782 Tetraodon  
137 579.5 43.1 1224 3 CR662508 Tetraodon CR662508 Tetraodon 208 542.5 40.4 904 3 CR639009 Tetraodon  
138 579.5 43.1 1224 3 CR698208 Tetraodon CR698208 Tetraodon 209 542.5 40.4 910 3 CR637674 Tetraodon  
139 577 43.0 413 5 BY094423 BY094423 210 542.5 40.4 910 3 CR637704 Tetraodon  
140 576 43.0 487 7 CR819654 lf22d02.x CR819654 lf22d02.x 211 542.5 40.4 924 3 CR655129 Tetraodon  
141 576 42.9 528 1 AI548694 UI-R-C3-t AI548694 UI-R-C3-t 212 542.5 40.4 1181 3 CR692840 Tetraodon  
142 575.5 42.9 582 4 BM574123 fx59d04.y BM574123 fx59d04.y 213 542 40.4 796 7 CF931709 EST0141.A  
143 575 42.8 1218 3 CR681700 Tetraodon CR681700 Tetraodon 214 542 40.4 905 4 BM439118 f9v8c04.y  
144 575 42.8 1290 3 CR647544 Tetraodon CR647544 Tetraodon 215 542 40.4 1211 3 CR698267 Tetraodon  
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146 574 42.7 459 1 AI929284 au59e03.x AI929284 au59e03.x 217 541.5 40.3 863 3 CR637158 Tetraodon  
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148 572 42.6 458 6 CB739243 AMGNNUC.N CB739243 AMGNNUC.N 219 541 40.3 555 4 BM154433 fv85a10.y  
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152 571.5 42.6 1178 3 CR660388 Tetraodon CR660388 Tetraodon 223 540 40.2 581 5 BQ783563 fab31c01.  
153 571.5 42.6 1201 3 CR633873 Tetraodon CR633873 Tetraodon 224 540 40.1 720 6 CA360096 6331c01.  
154 571.5 42.6 1205 3 CR692309 Tetraodon CR692309 Tetraodon 225 539 40.1 375 2 BE653217 UI-M-AM0-  
155 571.5 42.6 1215 3 CR676419 Tetraodon CR676419 Tetraodon 226 538 40.1 756 4 BJ739050 BJ739050  
c 227 538 40.1 764 4 BJ716953 BJ716953

229	538	40.1	765	6	CA341770	671433 NC	C 302	445	33.1	423	2	AW52701	UI-R-BJO-
230	537	40.0	553	4	BM186049	fv97a10.Y	303	445	33.1	473	6	CA395926	CA395926 c870g11.Y
231	537	40.0	868	7	CK406586	AUF Iflvr	C 304	445	33.1	600	6	C23352	C23352 C23352 Japa
232	537	40.0	869	7	CK409595	AUF Iflvr	305	444	33.1	469	7	BJ010311	BJ010311
233	537	40.0	943	7	CK409493	AUF Iflvr	306	444	33.1	566	7	CK885643	CK885643 SGP166021
234	535	39.8	1215	3	CR726092	Tetraodon	307	444	33.1	781	5	BU296625	BU296625 603733078
235	532	39.6	688	6	CA350955	621897 NC	308	443	33.0	362	5	BY045218	BY045218 BY045218
236	531.5	39.6	583	9	CG567423	621897 NC	309	441	32.8	344	5	BY057551	BY057551 BY057551
237	530	39.5	426	2	BE233897	140418 MA	310	441	32.8	543	6	C23048	C23048 C23048 Japa
238	529	39.4	479	2	AW251950	UI-R-BJO-	C 311	438	32.6	370	1	AI341293	AI341293 qx85d06.x
239	528	39.3	855	7	CK985363	58335 126	312	437.5	32.6	917	7	CK406909	CK406909 AUF Iflvr
240	527	39.2	537	4	BM534699	fx70d07.Y	313	436	32.5	808	7	CK977279	CK977279 27484 125
241	526	39.2	918	7	CK409380	AUF Iflvr	314	434	32.3	336	5	BY048400	BY048400 BY048400
242	525	39.1	921	7	CK406607	AUF Iflvr	315	433	32.2	413	2	AW523346	AW523346 UI-R-BJO-
243	524	39.0	400	5	BY050241	BY050241	C 316	432	32.2	499	1	AL919863	AL919863 AL919863
244	524	39.0	854	3	CR651708	Tetraodon	317	431	32.1	613	7	CK896516	CK896516 SGP159062
245	524	39.0	934	7	CK406893	AUF Iflvr	318	430	32.0	298	2	AW664650	AW664650 h184b01.x
246	522	38.9	422	2	BF593185	7050a03.x	319	427	31.8	610	7	CK896728	CK896728 SGP159280
247	521	38.8	678	7	CK974704	23486 125	C 320	426	31.7	411	2	AW511159	AW511159 UI-R-BJO-
248	520	38.7	869	7	CK985211	57529 127	C 321	423	31.5	627	5	BQ364998	BQ364998 SJ5-0017
249	519	38.6	629	1	AUI79577	AUI79577	322	420	31.3	598	7	CK895980	CK895980 SGP158514
250	518	38.6	460	1	AI340993	Q82809.x	323	420	31.3	847	7	CK175403	CK175403 AGENCOURT
251	518	38.6	614	1	AI180003	AUI180003	324	419	31.2	616	3	CR647326	CR647326 Tetraodon
252	518	38.6	896	7	CK407472	AUF Iflvr	325	419	31.2	937	6	CA458592	CA458592 AGENCOURT
253	512	38.1	421	2	AW299522	x840h01.x	326	416.5	31.0	671	5	EX864474	EX864474 BX864474
254	512	38.1	645	4	BJ705610	BJ705610	C 327	416	31.0	737	2	AW012934	AW012934 Ldt-0102
255	512	38.1	660	4	BJ727162	BJ727162	C 328	413	30.8	635	8	AZ958898	AZ958898 2M026D22
256	511	38.0	902	7	CK409572	AUF Iflvr	329	409.5	30.5	720	5	CK989253	CK989253 55281 125
257	511	38.0	956	7	CK406337	AUF Iflvr	330	408	30.4	416	5	BQ479917	BQ479917 faa8a07.
258	509.5	37.9	691	4	BJ708514	BJ708514	331	408	30.4	439	5	BY447416	BY447416 BX447416
259	509	37.9	448	1	AI349083	Q83909.x	332	407.5	30.3	766	5	BU010720	BU010720 QGJ14E17.
260	509	37.9	643	6	CB512007	sealrgb53	333	407	30.3	539	6	CA333551	CA333551 haa85C09.
261	509	37.9	722	5	BQ208081	UI-R-EP0-	334	406	30.2	526	5	BY468703	BY468703 BX468703
262	509	37.9	837	6	C23373	C23373 Japa	335	404	30.1	351	5	BY085557	BY085557 BY085557
263	508.5	37.9	1205	3	AA652934	Tetraodon	336	404	30.1	808	7	CK991683	CK991683 68533 125
264	507	37.8	384	1	AA068794	mm60d11.x	C 337	403	30.0	406	4	BI288752	BI288752 UI-R-DKO
265	504	37.5	415	2	AW299513	AW299513	338	403	30.0	599	1	AI981881	AI981881 pat.pk006
266	504	37.5	923	3	CK407551	AUF Iflvr	339	403	30.0	635	7	CK984292	CK984292 53247 126
267	503	37.5	612	4	BI304044	UI-R-DR0-	340	401.5	29.9	753	6	CA782445	CA782445 bat28H08.
268	503	37.5	875	7	CK978664	29797 125	341	401	29.9	243	4	BI032844	BI032844 603082670
269	495	36.9	415	1	AI340991	Q82807.x	342	401	29.9	878	7	CK366616	CK366616 RTK1 29.A
270	495	36.9	638	4	BJ711589	BJ711589	C 343	399	29.7	362	2	BF509580	BF509580 UI-H-BJA-
271	494	36.8	905	7	CK407588	AUF Iflvr	344	399	29.7	882	7	CK605765	CK605765 gmrhrw6-
272	492	36.6	670	6	CA355616	627543 NC	C 345	398	29.6	1045	3	CN80A6FG	CN80A6FG gmrhrw6-
273	490	36.5	731	4	BJ722907	BJ722907	C 346	397	29.6	341	1	AI650609	AI650609 w501f04.x
274	490	36.5	866	7	CK175149	AGENCOURT	347	397	29.6	857	7	CK172476	CK172476 AGENCOURT
275	489	36.4	587	7	CK896420	SGP158963	348	396.5	29.5	779	4	BG647257	BG647257 EST508886
276	488	36.3	642	1	AI477552	fx58904.Y	349	396	29.5	759	9	CL975287	CL975287 OBIFFC027
277	486	36.2	401	6	CB698999	AMGNNUC.N	C 350	396	29.5	826	7	CK189143	CK189143 EST778458
278	485.5	36.0	527	5	BQ615750	fab14b01.	351	396	29.5	866	6	CB650869	CB650869 OSJNEB15J
279	484	36.0	371	5	BY048974	BY048974	352	396	29.5	873	7	CK189144	CK189144 EST778459
280	481	35.8	704	2	BF228537	EST00248	C 353	395	29.4	365	6	CB050636	CB050636 NISC GJ18
281	479	35.7	434	2	BB787832	BB787832	354	395	29.4	365	6	CB050637	CB050637 NISC GJ18
282	478	35.6	405	1	AI912836	tx86c05.x	355	395	29.4	635	6	C23181	C23181 C23181 Japa
283	477	35.5	374	5	BY037587	BY037587	C 356	394.5	29.4	720	7	C0532807	C0532807 3530 121
284	477	35.5	579	7	CK995655	SGP158175	357	394	29.3	398	4	BM573972	BM573972 fx57d11.Y
285	477	35.5	874	7	CK169125	AGENCOURT	358	394	29.3	593	7	CK888688	CK888688 SGP160680
286	476	35.4	513	5	BO783421	fab29f02.	359	394	29.3	1064	7	CK163121	CK163121 FCAS01573
287	471.5	35.1	1206	3	CR641100	Tetraodon	C 360	393	29.3	683	2	BB594747	BB594747 BB594747
288	471	35.1	360	5	BY057583	BY057583	361	392.5	29.2	818	7	CF203341	CF203341 RR890915N
289	470	35.0	746	7	CN988270	64067 125	C 362	392	29.2	419	7	CN542838	CN542838 UI-R-EAO-
290	468	34.8	438	2	AW251225	UI-R-BJO-	363	392	29.2	465	4	BJ498661	BJ498661 BJ498661
291	464	34.5	598	7	CK895107	SGP154357	364	392	29.2	499	4	BJ527812	BJ527812 BJ527812
292	463	34.5	661	4	BI468189	EST00596	365	392	29.2	515	4	BJ490344	BJ490344 BJ490344
293	461	34.3	551	7	CK896911	SGP159468	366	392	29.2	562	4	BJ496988	BJ496988 BJ496988
294	459.5	34.2	1211	3	CK863715	Tetraodon	367	391.5	29.2	833	7	CF215293	CF215293 CAST0001
295	458	34.1	372	5	BO442000	BO442000	368	391.5	29.2	924	7	CF652643	CF652643 68-L02013
296	457.5	34.1	812	7	CO804908	AGENCOURT	369	391.5	29.2	942	7	CF516928	CF516928 CAP0004_I
297	454	33.8	292	4	BM856156	K-EST0139	370	391.5	29.2	1003	3	CN80A315	CN80A315 BX828287
298	453.5	33.8	644	6	CA333572	haa85h10.	371	391.5	29.2	1024	3	CN80A355	CN80A355 BX826590
299	453	33.7	503	4	BG669239	DRN1G10.R	372	391	29.1	370	5	BY398556	BY398556 BX826590
300	451	33.6	375	5	BY041991	BY041991	373	390.5	29.1	810	7	CF213611	CF213611 CGF100079
301	451	33.6	963	7	CK409756	AUF Iflvr	374	390	29.0	488	6	CD737778	CD737778 4023355 1





521	356.5	26.5	648	1	AJ560061	AJ560061	594	346.5	25.8	594	2	BE214450	BE214450 HV_CEB000
522	356.5	26.5	685	8	BZ641948	OGAMK72TM	595	346.5	25.8	708	6	CB836411	CB836411 MCV007A06
523	356.5	26.5	683	2	AW030189	EST273444	596	346.5	25.8	804	2	BF624054	BF624054 HVSMER000
524	356.5	26.5	692	7	CF806637	PGHB014xG	597	346	25.8	429	5	BY412806	BY412806
525	356.5	26.5	721	7	CF833360	UCRCS02_0	598	346	25.8	732	6	CD939542	CD939542 OV_113024
526	356.5	26.5	781	8	BH012959	TGQA060TH	599	346	25.8	819	7	CK193277	CK193277 FGAS00169
527	356	26.5	715	6	CD883740	FL114E16	600	346	25.8	836	7	CK195388	CK195388 FGAS00382
528	356	26.5	724	1	AD266351	AU266351	601	345.5	25.7	540	4	BG842718	BG842718 MEST39-C0
529	355.5	26.5	749	2	BF626523	HVSMER001	602	345.5	25.7	595	1	AI857214	AI857214 603008D06
530	355.5	26.5	872	7	CO064791	est_k bre	603	345.5	25.7	622	2	BF005553	BF005553 EST343051
531	355	26.4	782	7	CF669736	RTCNTL_45	604	345.5	25.7	815	7	CO083019	CO083019 GR_Ea470
532	354.5	26.4	745	7	CF470308	RTD1_18	605	345	25.7	682	1	AJ612197	AJ612197
533	354	26.4	802	6	CA158127	SEZRZ305	606	345	25.7	706	2	BF625981	BF625981 HVSMER001
534	353.5	26.3	739	5	BQ986844	QGF10U16.	607	345	25.7	731	5	BQ752847	BQ752847 WHE4119_G
535	353.5	26.3	747	1	AJ614420	AJ614420	608	345	25.7	794	7	CO174177	CO174177 NDL1_42_G
536	353.5	26.3	775	7	CF390634	RTDR2_20	609	344.5	25.7	695	6	CA090038	CA090038 SCSGM207
537	353.5	26.3	781	4	BM407902	EST582225	610	344.5	25.7	709	7	KN825707	KN825707 LJPEST9f3
538	353	26.3	503	6	C23213	C23213 Japa	611	344.5	25.7	814	7	CK300458	CK300458 FGAS00089
539	353	26.3	860	6	CB993812	EST646604	612	344.5	25.7	815	7	CO165535	CO165535 FLD1_55_E
540	352.5	26.2	715	5	BQ23287	EST608863	613	344.5	25.7	817	7	CO364800	CO364800 RTK1_21_H
541	352.5	26.2	864	6	CB823986	BY599654	614	344	25.6	647	2	AW648499	AW648499 EST326953
542	352	26.2	439	6	BY599654	BY599654	615	343.5	25.6	398	1	AA132529	AA132529 z020D02_8
543	352	26.2	686	5	BP184507	BP184507	616	343.5	25.6	563	4	BI308179	BI308179 EST529589
544	352	26.2	774	9	CC694438	OGUJH61TH	617	343.5	25.6	615	6	CA246946	CA246946 SCSGFL5C0
545	352	26.2	783	1	AJ787529	AJ787529	618	343.5	25.6	662	2	AW584279	AW584279 N10278e
546	352	26.2	864	7	CK195971	FGAS00441	619	343.5	25.6	751	6	CD820878	CD820878 BN25_040B
547	351.5	26.1	588	4	BM520677	BAK97B12.	620	343.5	25.6	751	6	CD821098	CD821098 BN25_040N
548	351.5	26.2	693	6	CA153085	SCSBRZ202	621	343.5	25.6	781	7	CF447177	CF447177 EST683522
549	351.5	26.2	714	6	CD864630	AZO2_001G	622	343.5	25.6	792	7	CO363528	CO363528 RTK1_10_G
550	351.5	26.2	752	7	KN012179	WHE3893_E	623	343.5	25.6	810	7	CK197247	CK197247 FGAS00571
551	351.5	26.2	764	5	BQ804819	WHE3559_C	624	343.5	25.6	843	7	CO164960	CO164960 FLD1_51_H
552	351	26.1	665	6	CD860328	TE_002B22	625	343	25.5	658	1	AJ805285	AJ805285 AJ805285
553	350.5	26.1	620	2	AW585897	EST317520	626	343	25.5	694	6	CD937240	CD937240 OV_106G10
554	350.5	26.1	667	2	BF636068	NF069E08D	627	343	25.5	705	2	BE519617	BE519617 HV_CEB001
555	350.5	26.1	697	2	BF634788	NF069G09D	628	343	25.5	807	2	BF065240	BF065240 HV_CEB002
556	350.5	26.1	703	4	BI308339	EST529749	629	343	25.5	930	4	BI956791	BI956791 HVSMER000
557	350.5	26.1	795	5	BQ255166	MTNAR30TK	630	343	25.5	1106	7	CK217545	CK217545 FGAS02954
558	350.5	26.1	877	6	CA755835	BR0300290	631	342.5	25.5	516	1	AJ261400	AJ261400
559	350.5	26.1	1078	4	BG338728	602436489	632	342.5	25.5	571	2	BE803196	BE803196 8x53a11_Y
560	349.5	26.0	590	4	BM660518	952039C01	633	342.5	25.5	649	2	BE216025	BE216025 HV_CEB000
561	349.5	26.0	631	4	BG045213	8a39a10.	634	342.5	25.5	653	7	CO170754	CO170754 NDL1_16_D
562	349.5	26.0	713	6	CD869948	AZO2_113A	635	342.5	25.5	709	7	CO165605	CO165605 FLD1_55_E
563	349.5	26.0	729	6	CD869596	GL18_0010.	636	342.5	25.5	714	7	CF235114	CF235114 PcaJX004_0
564	349.5	26.0	759	2	BF259495	HVSMER001	637	342.5	25.5	772	7	CF235114	CF235114 PcaJX004_0
565	349.5	26.0	789	7	CK119117	214h16.pl	638	342	25.5	352	1	AI712475	AI712475 UT-R-AFL-1
566	349	26.0	553	5	BQ336499	SL5_0018	639	342	25.5	584	1	AJ802385	AJ802385 AJ802385
567	349	26.0	711	6	CD873066	AZO2_122E	640	342	25.5	652	4	BI960399	BI960399 HVSMER002
568	349	26.0	731	6	CD885623	GL18_001P	641	342	25.5	660	6	CA123437	CA123437 SCMLR101
569	349	26.0	762	6	CB649583	OSJNEB13U	642	342	25.5	753	5	BQ518760	BQ518760 EST626175
570	348.5	25.9	605	4	BM660519	952039C01	643	342	25.5	837	3	CSNSOAGFN	CSNSOAGFN
571	348.5	25.9	689	4	BG544230	E2031_Chl	644	341.5	25.4	655	5	BQ838311	BQ838311 WHE2909_A
572	348.5	25.9	693	1	AGU70835	AU270835	645	341.5	25.4	666	4	BG453602	BG453602 NF098F01L
573	348.5	25.9	717	4	BI434036	EST536797	646	341.5	25.4	669	2	BF474987	BF474987 WHE2104_D
574	348.5	25.9	737	2	BE559087	HV_CEB002	647	341.5	25.4	691	1	AJ501241	AJ501241
575	347.5	25.9	619	4	BG045242	8a39a10.	648	341.5	25.4	696	6	CD832570	CD832570 BN40_063N
576	347.5	25.9	622	1	AI637136	603001A11	649	341.5	25.4	740	7	CK1922131	CK1922131 UCRCS06_0
577	347.5	25.9	630	2	AW757356	8132c10_Y	650	341.5	25.4	745	7	CF835276	CF835276 UCRCS02_0
578	347.5	25.9	639	2	BE203346	EST403368	651	341.5	25.4	813	7	CK199240	CK199240 FGAS00773
579	347.5	25.9	657	5	BQ624016	USDA-PP_0	652	341.5	25.4	1141	7	CK210321	CK210321 FGAS02212
580	347.5	25.9	676	2	BF642362	NF05D111	653	341	25.4	746	7	CO520722	CO520722 3530_1_13
581	347.5	25.9	686	2	AW584562	N210630e	654	341	25.4	780	7	CO528134	CO528134 3530_1_18
582	347.5	25.9	728	2	AW775400	EST334465	655	341	25.4	809	7	CK138077	CK138077 OX1_61_CO
583	347.5	25.9	752	6	CA916907	EST641054	656	340.5	25.4	646	6	CD864631	CD864631 AZO2_001G
584	347.5	25.9	803	7	CF395282	RTDS2_10	657	340.5	25.4	655	4	BI270143	BI270143 NF052B07F
585	347	25.8	597	4	BJ505563	BJ505563	658	340.5	25.4	683	5	BO146393	BO146393 NF052B07F
586	347	25.8	697	2	BE216491	HV_CEB001	659	340.5	25.4	689	7	CF233668	CF233668 PcaJX0002
587	347	25.8	700	1	AL503249	AL503249	660	340.5	25.4	728	7	CF418067	CF418067 USDA-PP_1
588	347	25.8	714	2	BE519891	HV_CEB002	661	340.5	25.4	763	7	CK121692	CK121692 202c15.pl
589	347	25.8	723	6	CB653598	OSJNEC04M	662	340.5	25.4	799	7	CF635242	CF635242 zmrw00_0
590	347	25.8	880	4	BI950057	HVSMER1001	663	340.5	25.4	816	3	CSNSOAG6LK	CSNSOAG6LK
591	346.5	25.8	630	4	BI960166	HVSMER002	664	340	25.3	915	6	CA213294	CA213294 SCQGSB113
592	346.5	25.8	673	4	BM370604	EPR008_SQ	665	340	25.3	1080	7	CK213716	CK213716
593	346.5	25.8	692	6	CD866963	AZO2_1040	666	339.5	25.3	627	6	CB910128	CB910128 VVD174D02

667	339.5	25.3	658	7	CK240496	CK240496 VRJ324T7	740	333	24.8	738	7	CK861883	CK861883 33001 In
668	339.5	25.3	676	4	BI263612	BI263612 NF089A09P	c 741	333	24.8	743	4	BJ252414	BJ252414 BJ252414
669	339.5	25.3	721	5	BQ838009	BQ838009 WHE2905 E	742	333	24.8	766	7	CO173178	CO173178 ND11 34 B
c 670	339.5	25.3	802	9	CC615544	CC615544 CGWD123TV	743	333	24.8	882	7	CN201625	CN201625 Tor1590 G
671	339.5	25.3	807	2	BF259949	BF259949 HVSMEn002	744	332.5	24.8	645	2	BF642662	BF642662 NF072H07I
672	339.5	25.3	808	6	CD827397	CD827397 BN25.067F	745	332.5	24.8	671	4	BM063898	BM063898 KS01060G0
673	339.5	25.2	889	6	CA159865	CA159865 SCJFRZ3C0	746	332.5	24.8	725	6	CD823678	CD823678 BN25.049J
674	338.5	25.2	601	2	BE998051	BE998051 EST429774	747	332.5	24.8	726	7	CN190771	CN190771 UCRCS06 0
675	338.5	25.2	662	2	BE610562	BE610562 sq7h11 Y	748	332.5	24.8	739	7	CK932928	CK932928 CGF100434
676	338.5	25.2	666	4	BI265049	BI265049 NF004C10I	749	332.5	24.8	817	7	CK197926	CK197926 FGAS00640
c 677	338.5	25.2	818	6	CD575294	CD575294 UCRPT01 0	750	332	24.7	208	2	BE853865	BE853865 ux22508.0 Y
c 678	338	25.2	797	6	CD868553	CD868553 AZ02.109E	751	332	24.7	867	7	CO102007	CO102007 GR EB002
679	337.5	25.1	548	4	BM527768	BM527768 sal65f09.	752	331.5	24.7	511	4	BG653155	BG653155 sad83f01.
680	337.5	25.1	637	2	BF2520898	BF2520898 EST45837I	753	331.5	24.7	600	7	CO909118	CO909118 BJ0204080
681	337.5	25.1	651	4	BI270050	BI270050 NF003E10F	754	331.5	24.7	649	6	CD879761	CD879761 AZ04.106E
682	337.5	25.1	673	7	CN190619	CN190619 UCRCS06 0	755	331.5	24.7	665	1	AI898029	AI898029 EST267472
683	337.5	25.1	674	2	AW560150	AW560150 EST315198	756	331.5	24.7	681	5	BQ875399	BQ875399 QSI8A03 Y
684	337.5	25.1	683	2	BF520049	BF520049 EST457517	757	331.5	24.7	681	5	BQ987553	BQ987553 QGF12119.
685	337.5	25.1	683	6	CD930335	CD930335 GR45.110P	758	331.5	24.7	683	2	AW030736	AW030736 EST273991
686	337.5	25.1	699	5	BO624767	BO624767 USDA-PP 0	759	331.5	24.7	683	4	BI922821	BI922821 EST542725
687	337.5	25.1	718	6	CD938268	CD938268 OV.109I23	760	331.5	24.7	714	6	CA918225	CA918225 EST642372
c 688	337.5	25.1	746	7	CK215205	CK215205 FGAS02715	761	331.5	24.7	726	5	BQ838107	BQ838107 WHE2806 F
690	337	25.1	629	6	CF438087	CF438087 EST674432	762	331.5	24.7	750	7	CF921444	CF921444 gmrhrwv3-
691	337	25.1	732	7	CF438087	CF438087 eca01-14m	c 763	331	24.6	606	2	BE021597	BE021597 sm0804 Y
692	337	25.1	779	5	BI115361	BI115361 EST600937	764	331	24.6	946	6	CA270677	CA270677 SCRULB206
693	336.5	25.1	543	1	AI939180	AI939180 sc67h02 Y	765	330.5	24.6	519	2	BF636493	BF636493 NF088G06D
694	336.5	25.1	617	2	BE405650	BE405650 WHE1209 G	766	330.5	24.6	596	2	BE403578	BE403578 WHE0434 C
695	336.5	25.1	618	2	BE801899	BE801899 sr20h08 Y	767	330.5	24.6	631	2	BF473218	BF473218 WHE0922 H
696	336.5	25.1	653	4	BI957460	BI957460 HVSMEn000	768	330.5	24.6	648	7	CN192437	CN192437 UCRCS06 0
697	336.5	25.1	704	6	CD817128	CD817128 BN20.040N	769	330.5	24.6	652	7	CF836276	CF836276 UCRCS03 0
698	336.5	25.1	786	7	CN137489	CN137489 OX1 57 D0	770	330.5	24.6	658	7	CN191414	CN191414 UCRCS06 0
699	336.5	25.1	797	7	CK193862	CK193862 FGAS00228	771	330.5	24.6	731	1	AJ803420	AJ803420 AJ803420
c 700	336	25.0	442	7	CN967735	CN967735 14632.100	772	330.5	24.6	772	6	CD839679	CD839679 RFO2.116D
c 701	336	25.0	646	4	BJ466490	BJ466490 BJ466490	773	330.5	24.6	1121	6	CA131093	CA131093 SCBFT106
702	336	25.0	675	4	BM814917	BM814917 EST593011	774	330	24.6	569	7	CK439809	CK439809 GQ0021B.B
703	336	25.0	733	5	BQ838231	BQ838231 WHE2908 A	c 775	330	24.6	706	7	CF517412	CF517412 CAP0005.1
c 704	336	25.0	750	6	CD898674	CD898674 G174.105L	776	330	24.6	712	7	CF389766	CF389766 RTDR2 5 A
c 705	336	25.0	776	5	BO618942	BO618942 RNOSE01F0	777	330	24.6	718	7	CF473897	CF473897 RTW2 19
c 706	335.5	25.0	530	6	CB939523	CB939523 OSTR163G7	778	330	24.6	712	7	CF478998	CF478998 RTW2 21
707	335.5	25.0	559	2	AW102353	AW102353 sd86f04 Y	779	330	24.6	747	7	CF396117	CF396117 RTDS2 13
708	335.5	25.0	623	8	BE641943	BE641943 OGAMK72TC	780	329.5	24.5	562	2	BF484304	BF484304 WHE2321 F
c 709	335.5	25.0	731	7	CK240495	CK240495 VRJ324 V1	781	329.5	24.5	606	2	BE205077	BE205077 EST397753
c 710	335.5	25.0	737	2	AW348485	AW348485 GM210002B	782	329.5	24.5	638	4	BG453560	BG453560 NF096D07L
711	335.5	25.0	747	7	CF474427	CF474427 RTW2 20	783	329.5	24.5	639	4	BI959367	BI959367 HVSMEn001
712	335	24.9	337	2	AW563652	AW563652 38646 MAR	784	329.5	24.5	651	2	AW094365	AW094365 EST287545
713	335	24.9	744	7	CF478537	CF478537 RTW2 20	785	329.5	24.5	666	1	AL504625	AL504625 AL504625
714	334.5	24.9	531	4	BI426741	BI426741 sag06G09.	786	329.5	24.5	672	2	AW442463	AW442463 EST307393
715	334.5	24.9	598	4	BI321639	BI321639 saf15G02.	787	329.5	24.5	684	4	BM110489	BM110489 EST558025
716	334.5	24.9	644	6	CD930761	CD930761 GR45.112E	788	329.5	24.5	693	2	BE208886	BE208886 GF-FV-P3C
717	334.5	24.9	646	5	BO838318	BO838318 WHE2909 A	789	329	24.5	631	4	BM284958	BM284958 kh93a08 Y
718	334.5	24.9	724	7	CF921036	CF921036 gmrhrwv3-	790	329	24.5	672	2	BF473981	BF473981 WHE0839 F
719	334	24.9	646	5	BP176248	BP176248 BP176248	791	328.5	24.5	640	2	AW218547	AW218547 EST303710
720	334	24.9	659	1	AJ615423	AJ615423 AJ615423	792	328.5	24.5	646	2	AW625527	AW625527 EST319434
721	334	24.9	661	4	BJ247474	BJ247474 BJ247474	793	328.5	24.5	649	7	CF227474	CF227474 PtaDEd5D0
722	334	24.9	692	6	CD868552	CD868552 AZ02.109E	794	328.5	24.5	655	4	BI960120	BI960120 HVSMEn002
723	333.5	24.8	630	4	BG449728	BG449728 NF007D11I	c 795	328.5	24.5	762	7	CO171539	CO171539 ND11 22 C
724	333.5	24.8	632	2	BE325133	BE325133 NF087F045	c 796	328.5	24.5	797	7	CF838015	CF838015 UCRCS03 0
725	333.5	24.8	654	6	CA131555	CA131555 SCBGR104	c 797	328.5	24.5	799	7	CF833359	CF833359 UCRCS02 0
726	333.5	24.8	682	2	BF597864	BF597864 su89C03 Y	c 798	328.5	24.5	800	7	CF833320	CF833320 UCRCS02 0
727	333.5	24.8	682	2	BF641947	BF641947 NF011B12I	c 799	328.5	24.5	859	6	CB823461	CB823461 EST 4685
728	333.5	24.8	684	5	BU875316	BU875316 V005C03 P	800	328	24.4	743	6	CA180815	CA180815 SCACST316
729	333.5	24.8	694	1	AJ615461	AJ615461 AJ615461	801	327.5	24.4	621	5	BO743179	BO743179 WHE04101 C
730	333.5	24.8	699	1	BU877332	BU877332 V032G08 P	802	327.5	24.4	623	6	CA821361	CA821361 RSH01H05
731	333.5	24.8	708	7	CN184479	CN184479 UCRCS04 0	803	327.5	24.4	635	1	AJ560090	AJ560090 AJ560090
732	333.5	24.8	709	5	BO752659	BO752659 WHE4117 F	804	327.5	24.4	637	4	BI960118	BI960118 HVSMEn002
733	333.5	24.8	716	5	BU874994	BU874994 V001B12 P	805	327.5	24.4	654	7	CF236064	CF236064 PtaXMT003
734	333.5	24.8	722	5	BO789135	BO789135 WHE4158 A	806	327.5	24.4	721	6	CD839960	CD839960 RFO2.117E
735	333.5	24.8	756	2	BF630744	BF630744 HVSMEn001	807	327	24.3	667	6	CA196132	CA196132 SC8BAD108
c 736	333	24.8	417	1	AI477667	AI477667 fbs5904 X	808	327	24.3	676	7	CV006380	CV006380 CS gil 12
737	333	24.8	650	7	CV093856	CV093856 FAMU USDA	809	327	24.3	762	7	CF472622	CF472622 RTDS1 10
738	333	24.8	664	5	BP184560	BP184560 BP184560	810	326.5	24.3	629	4	BI959561	BI959561 HVSMEn002
739	333	24.8	667	4	BI957447	BI957447 HVSMEn000	811	326.5	24.3	636	6	CA020338	CA020338 HZ36A04 R
							812	326.5	24.3	637	5	BQ623195	BQ623195 USDA-FP_0

813	326.5	24.3	643	5	BU977235	HALLB05r	BU977235	HALLB05r	886	320.5	23.9	681	4	BI959659	HVSMEN002
814	326.5	24.3	648	4	BI959235	HVSMEN001	BI959235	HVSMEN001	887	320.5	23.9	744	4	BM408348	EST502675
815	326.5	24.3	650	7	CK987645	SP7-A3(P1	CK987645	SP7-A3(P1	888	320.5	23.9	904	4	BF972265	602240747
816	326.5	24.3	656	7	CK987647	PI-A3-rev	CK987647	PI-A3-rev	889	320	23.8	712	5	BU672830	NL 6 90 D
817	326.5	24.3	669	7	CV459741	ram01-lme	CV459741	ram01-lme	890	320	23.8	770	3	CNS0AEB3	AX818064 Arabidop
818	326.5	24.3	675	7	CF932162	PI-A4 A s	CF932162	PI-A4 A s	891	320	23.8	835	4	BM407184	EST501511
819	326.5	24.3	712	6	CD841037	RPO2.121J	CD841037	RPO2.121J	892	320	23.8	901	7	CV130539	BSPSP03e08
820	326.5	24.3	719	6	CD840175	RPO2.118E	CD840175	RPO2.118E	893	319.5	23.8	605	1	AI486500	EST244821
821	326.5	24.3	719	7	CF833209	UCRCS02.0	CF833209	UCRCS02.0	894	319.5	23.8	662	6	CA916813	EST640960
822	326.5	24.3	774	6	CA065807	SCBFAID104	CA065807	SCBFAID104	895	319.5	23.8	664	7	CV298172	EST886631
823	326.5	24.3	791	2	BF638077	NF041H0BP	BF638077	NF041H0BP	896	319.5	23.8	666	6	CB869763	HC12G06W
824	326.5	24.3	823	2	BF264389	HV CFa000	BF264389	HV CFa000	897	319.5	23.8	670	4	BG455746	NF066H01P
825	326.5	24.3	1086	7	CK213734	FGAS02564	CK213734	FGAS02564	898	319.5	23.8	740	7	CNO11226	WHE3881 F
826	326	24.3	336	5	BU998227	BY398227	BU998227	BY398227	899	319.5	23.8	748	5	BU635690	004G05 In
827	326	24.3	660	6	CD899633	GI74.113A	CD899633	GI74.113A	900	319.5	23.8	789	5	BU894945	XO17B10 P
828	326	24.3	817	7	CK194117	FGAS00253	CK194117	FGAS00253	901	319	23.8	644	1	AI895091	EST264534
829	325.5	24.2	543	4	BI788369	aag69h09.	BI788369	aag69h09.	902	319	23.8	675	6	CA209393	SCCST3C1
830	325.5	24.2	574	4	BM731352	sal70h05.	BM731352	sal70h05.	903	319	23.8	684	1	AL821924	AL821924
831	325.5	24.2	610	5	BQ467961	HR01H17r	BQ467961	HR01H17r	904	319	23.8	711	4	BU253542	BU253542
832	325.5	24.2	624	6	CA021273	HZ39J21r	CA021273	HZ39J21r	905	319	23.8	756	6	CB680447	OSJNEF05C
833	325.5	24.2	630	7	CNO10185	WHE3867 G	CNO10185	WHE3867 G	906	319	23.8	756	7	CF428636	PH1 9 G09
834	325.5	24.2	647	4	BI960119	HVSMEN002	BI960119	HVSMEN002	907	319	23.8	819	7	CNI27149	RHOH1 21
835	325.5	24.2	660	7	CF418675	USDA-FP 1	CF418675	USDA-FP 1	908	319	23.8	853	2	BF256079	HVSMEN000
836	325.5	24.2	681	1	AV782400	AV782400	AV782400	AV782400	909	318.5	23.7	549	4	BG155028	8ab40b01.
837	325.5	24.2	698	5	BU896211	XO37C08 P	BU896211	XO37C08 P	910	318.5	23.7	570	6	CA279207	SCBFLB209
838	325.5	24.2	714	1	AJ778942	AJ778942	AJ778942	AJ778942	911	318.5	23.7	582	7	CV297680	EST886057
839	325.5	24.2	734	9	CG327759	CGXFO38TH	CG327759	CGXFO38TH	912	318.5	23.7	608	7	CK750439	paM01-6ms
840	325.5	24.2	788	7	CF669731	RTCN1 45	CF669731	RTCN1 45	913	318.5	23.7	609	4	BM065108	K501075A0
841	325	24.2	684	6	CA142702	SCMCHT210	CA142702	SCMCHT210	914	318.5	23.7	623	4	BM111532	EST559068
842	325	24.2	757	7	CF395287	RTDS2.114	CF395287	RTDS2.114	915	318.5	23.7	687	6	CA192398	SCCST3C0
843	324.5	24.2	557	2	BE404145	WHE1201 G	BE404145	WHE1201 G	916	318.5	23.7	694	4	BU261281	BU261281
844	324.5	24.2	591	5	BO753204	WHE4124 C	BO753204	WHE4124 C	917	318.5	23.7	745	6	CA918812	EST636530
845	324.5	24.2	624	5	BO744417	WHE4115 D	BO744417	WHE4115 D	918	318.5	23.7	753	7	CF436915	EST673260
846	324.5	24.2	627	5	BO788936	WHE4155 E	BO788936	WHE4155 E	919	318.5	23.7	856	7	CK202105	FGAS01062
847	324.5	24.2	628	5	BO744183	WHE4112 F	BO744183	WHE4112 F	920	318	23.7	695	5	BA252395	BA252395
848	324.5	24.2	664	6	CD079415	MA3-9999U	CD079415	MA3-9999U	921	318	23.7	720	6	CA221618	SCSGFLA03
849	324.5	24.2	680	4	BI179085	EST520030	BI179085	EST520030	922	318	23.7	787	5	BQ515541	EST622956
850	324.5	24.2	697	4	BG546445	EST508064	BG546445	EST508064	923	317.5	23.6	510	2	AM424002	8H59C10.Y
851	324.5	24.2	704	4	BG587428	EST489200	BG587428	EST489200	924	317.5	23.6	711	5	BQ139680	NF023A10P
852	324.5	24.2	719	7	CNI46340	WOUNDI 39	CNI46340	WOUNDI 39	925	317.5	23.6	720	7	CF921163	gmhrRw3-
853	324	24.1	588	2	BE493950	WHE1276 H	BE493950	WHE1276 H	926	317.5	23.6	756	6	CD849237	DH0AC0172
854	324	24.1	624	5	BP184421	BP184421	BP184421	BP184421	927	317	23.6	468	7	CK895492	SGP158009
855	324	24.1	640	5	BQ743388	WHE4103 D	BQ743388	WHE4103 D	928	317	23.6	605	6	CA155532	SCARFSD101
856	324	24.1	641	4	BM813932	EST592025	BM813932	EST592025	929	317	23.6	663	6	CA280962	SCARFSD101
857	324	24.1	649	6	CA290596	SCUTSDP102	CA290596	SCUTSDP102	930	317	23.6	681	4	BI952091	HVSMEN000
858	324	24.1	791	3	CNS0A0B1	Arabidop	BI952091	Arabidop	931	317	23.6	893	4	BI952091	HVSMEN000
859	323.5	24.1	546	4	BG096397	EST460916	BG096397	EST460916	932	316.5	23.6	515	7	CK864045	35355 In
860	323.5	24.1	664	5	BQ762267	EBR01 SQ	BQ762267	EBR01 SQ	933	316.5	23.6	559	2	BE802841	8r45d12.y
861	323.5	24.1	669	6	CD073690	MA3-0001U	CD073690	MA3-0001U	934	316.5	23.6	566	2	BE942838	EST422417
862	323.5	24.1	669	6	CF507287	USDA-FP 1	CF507287	USDA-FP 1	935	316.5	23.6	571	7	CNO08321	WHE2639 H
863	323.5	24.1	709	6	CA146291	SCVPR207	CA146291	SCVPR207	936	316.5	23.6	578	2	AM695176	NF092D128
864	323.5	24.1	796	2	BE034896	ML05H01 M	BE034896	ML05H01 M	937	316.5	23.6	580	7	CN517425	G00092.B3
865	323.5	24.1	846	7	CK195394	FGAS00393	CK195394	FGAS00393	938	316.5	23.6	590	2	BF006247	EST434745
866	322.5	24.0	633	7	CF418893	USDA-FP 1	CF418893	USDA-FP 1	939	316.5	23.6	595	7	CF092647	QHN12P02.
867	322.5	24.0	674	7	CF739670	USDA-FP 6	CF739670	USDA-FP 6	940	316.5	23.6	598	2	BE124003	EST394128
868	322.5	24.0	840	7	CO234257	WS0261 B2	CO234257	WS0261 B2	941	316.5	23.6	637	5	BQ765794	EBR003 SQ
869	322.5	24.0	840	7	CO234257	WS0261 B2	CO234257	WS0261 B2	942	316.5	23.6	643	7	CF518411	CAP0007 I
870	322	24.0	640	6	CA191213	SCCCHT2C0	CA191213	SCCCHT2C0	943	316	23.5	669	6	CA187131	SCUTST308
871	322	24.0	649	6	CD904272	G356.112P	CD904272	G356.112P	944	316	23.5	691	1	AJ613139	AJ613139
872	322	24.0	716	4	BI960085	HVSMEN001	BI960085	HVSMEN001	945	315.5	23.5	836	9	CG323590	CGWIE57TV
873	322	24.0	736	2	BF630555	HVSMEN002	BF630555	HVSMEN002	946	315.5	23.5	526	6	CF059783	QCS16904.
874	322	24.0	847	7	CF443345	EST679690	CF443345	EST679690	947	315.5	23.5	539	2	AM980337	EST3931490
875	321.5	23.9	607	7	CNO12727	WHE3952 B	CNO12727	WHE3952 B	948	315.5	23.5	561	4	BM732615	sal79d10.
876	321.5	23.9	686	7	CF833210	UCRCS02.0	CF833210	UCRCS02.0	949	315.5	23.5	631	2	AW776700	EST335765
877	321.5	23.9	754	4	BG584701	EST486462	BG584701	EST486462	950	315.5	23.5	668	7	CV299158	EST887617
878	321.5	23.9	770	4	BI967327	GM830001B	BI967327	GM830001B	951	315.5	23.5	702	6	CA179873	SCCST200
879	321	23.9	616	4	BJ259369	BJ259369	BJ259369	BJ259369	952	315	23.5	442	7	CN966263	13760 100
880	321	23.9	678	6	CA071322	SCACAM107	CA071322	SCACAM107	953	315	23.5	660	5	BQ806305	WHE3577 C
881	321	23.9	737	7	CF397756	RTDS3 1 C	CF397756	RTDS3 1 C	954	315	23.5	739	7	CNO13071	WHE3956 D
882	321	23.9	795	7	CV123412	OSTR30010	CV123412	OSTR30010	955	315	23.5	852	9	CG320079	CG320079
883	321	23.9	881	7	CK196097	FGAS00454	CK196097	FGAS00454	956	315	23.5	880	9	CG229531	CG229531
884	320.5	23.9	637	7	CNI89395	UCRCS06 0	CNI89395	UCRCS06 0	957	314.5	23.4	540	4	BG789661	8ae53e08.
885	320.5	23.9	643	2	AW695080	NF091D11S	AW695080	NF091D11S	958	314.5	23.4	562	2	AW683492	NF012H09L

959	314.5	23.4	598	5	BU008292	BU008292 QGH7C13.Y	1032	307.5	22.9	772	7	CF229531	CF229531 PtaXM0026
960	314.5	23.4	616	5	BO788665	BO788665 WHE4152.E	1033	307.5	22.9	775	6	CD839277	CD839277 RFO2.114K
961	314.5	23.4	625	2	AW034347	AW034347 EST279I8	1034	307	22.9	776	6	CD895487	CD895487 G174.001P
962	314.5	23.4	708	7	CF213537	CF213537 CGF100060	1035	306.5	22.8	503	1	AI898952	AI898952 EST268395
963	314.5	23.4	776	7	CN987035	CN987035 62721.125	1036	306.5	22.8	534	2	BE287882	BE287882 N100726e
964	314.5	23.4	684	2	BF627066	BF627066 HVSMB5000	1037	306.5	22.8	535	2	BE574803	BE574803 H20.Triph
965	313.5	23.3	472	5	BQ460884	BQ460884 HB01017r	1038	306.5	22.8	546	1	AL827353	AL827353 AL827353
966	313.5	23.3	573	2	BE998050	BE998050 EST429773	1039	306.5	22.8	580	1	AU261430	AU261430 AU261430
967	313.5	23.3	605	5	BQ970451	BQ970451 QHB42822.	1040	306.5	22.8	618	4	BG453059	BG453059 NF089H11L
968	313.5	23.3	612	5	BQ699842	BQ699842 NXR122.D	1041	306.5	22.8	664	4	BI308484	BI308484 EST529894
969	313.5	23.3	635	5	BQ888753	BQ888753 P012B02.P	1042	306.5	22.8	668	5	BU887057	BU887057 R054A07.P
970	313	23.3	486	3	CR640865	CR640865 Tetracodon	1043	306.5	22.8	694	4	BJ265176	BJ265176 BJ265176
971	313	23.3	679	6	CA262688	CA262688 SCPILB202	1044	306	22.8	626	5	BM895773	BM895773 952065C05
972	313	23.3	702	4	BI073165	BI073165 PIP2A.F04	1045	306	22.8	636	7	CV502501	CV502501 68895.1.M
973	313	23.3	881	7	CK202172	CK202172 FGAS01069	1046	306	22.8	664	1	AJ802646	AJ802646 AJ802646
974	312.5	23.3	539	7	COA15038	COA15038 MgfW2044m	1047	306	22.8	692	6	CA168805	CA168805 SCEQB101
975	312.5	23.3	540	4	BI788174	BI788174 ssg67F01.	1048	306	22.8	698	1	AJ803239	AJ803239 AJ803239
976	312.5	23.3	545	2	AW620537	AW620537 8106G09.Y	1049	306	22.8	727	6	CA219139	CA219139 SCRFAD11L
977	312.5	23.3	577	5	BQ490451	BQ490451 24-E01178	1050	306	22.8	805	8	BZ533265	BZ533265 OGAES43TC
978	312.5	23.3	606	7	CF807049	CF807049 dSHB019xK	1051	306	22.8	884	7	CV270100	CV270100 WS0151.B2
979	312.5	23.3	656	2	BF650456	BF650456 NF097D11E	1052	305.5	22.7	454	4	BM136098	BM136098 WHE2502.F
980	312.5	23.3	670	5	BU816246	BU816246 N062C10.P	1053	305.5	22.7	476	6	CA117774	CA117774 SCBGUR104
981	312.5	23.3	676	6	CD817919	CD817919 EN20.043K	1054	305.5	22.7	544	4	BM527684	BM527684 sal614F09.
982	312.5	23.3	704	5	BU814263	BU814263 N027B09.P	1055	305.5	22.7	561	1	AL819807	AL819807 AL819807
983	312.5	23.3	706	7	CF233163	CF233163 PcaJXO002	1056	305.5	22.7	564	4	BM085705	BM085705 saJ28d08.
984	312.5	23.3	719	7	CV226183	CV226183 WS0163.B2	1057	305.5	22.7	572	5	BQ473426	BQ473426 sap12g01.
985	312.5	23.3	754	1	AJ806917	AJ806917 AJ806917	1058	305.5	22.7	696	6	CA085150	CA085150 SCEZAM206
986	312.5	23.3	815	2	BE642551	BE642551 Cri2.6_F2	1059	305.5	22.7	802	6	CA180913	CA180913 SCACST336
987	312.5	23.3	817	7	CK193931	CK193931 FGAS00235	1060	305.5	22.7	851	7	CK201455	CK201455 FGAS00997
988	312	23.2	817	7	BG935465	BG935465 SL1-0818	1061	305	22.7	646	7	CK860977	CK860977 32005.In
989	312	23.2	647	4	BJ264257	BJ264257 BJ264257	1062	305	22.7	713	6	CA221136	CA221136 SCEZFL404
990	312	23.2	726	6	CA158055	CA158055 SCE2RZ305	1063	304.5	22.7	569	2	AW736350	AW736350 BST332269
991	312	23.2	816	8	BZ541105	BZ541105 OGAET437C	1064	304.5	22.7	594	7	CK319292	CK319292 X9P09b04
992	312	23.2	929	7	CV266697	CV266697 WS0203.B2	1065	304.5	22.7	745	7	CF397680	CF397680 RDS.1.C
993	311.5	23.2	605	6	CA733178	CA733178 wlp1c.pk0	1066	304.5	22.7	768	6	CD839106	CD839106 RFO2.114A
994	311.5	23.2	611	4	BI957501	BI957501 HVSME000	1067	304.5	22.7	831	7	CK201781	CK201781 FGAS01030
995	311.5	23.2	622	7	CF395203	CF395203 RTDS.10	1068	304	22.6	302	2	BF605771	BF605771 272357.MA
996	311	23.2	742	6	CA146092	CA146092 SCVPRFT207	1069	304	22.6	592	4	BM660366	BM660366 952037B06
997	310.5	23.1	559	4	BI894075	BI894075 sai59G06.	1070	304	22.6	622	6	CA182599	CA182599 SCCST314
998	310.5	23.1	608	7	CK318739	CK318739 X9P02911	1071	304	22.6	647	6	CA285613	CA285613 SCEZSD107
999	310.5	23.1	616	5	BQ139156	BQ139156 NF011F12P	1072	304	22.6	661	6	CA107862	CA107862 SCBSHR105
1000	310.5	23.1	624	7	CF417506	CF417506 USDA-FP.1	1073	304	22.6	677	4	BG905724	BG905724 Talr1141H
1001	310.5	23.1	638	4	BI957710	BI957710 HVSME001	1074	304	22.6	685	6	CA121225	CA121225 SCEQR109
1002	310.5	23.1	650	2	BF646063	BF646063 NF066E10E	1075	303.5	22.6	511	7	CF603338	CF603338 BACCA01.0
1003	310.5	23.1	725	5	BU835879	BU835879 T079G08.P	1076	303.5	22.6	618	7	CK010871	CK010871 WHE3877.C
1004	310.5	23.1	756	7	CK215844	CK215844 FGAS02781	1077	303.5	22.6	632	1	AI486948	AI486948 EST245270
1005	310	23.1	447	7	CK879029	CK879029 SGPI43200	1078	303	22.6	609	1	AU263882	AU263882 AU263882
1006	310	23.1	654	6	CA175542	CA175542 SCJLST101	1079	303	22.6	679	6	CD823836	CD823836 BN25.050C
1007	310	23.1	699	5	BX251392	BX251392 BX251392	1080	303	22.6	814	7	CK201094	CK201094 FGAS00961
1008	310	23.1	802	2	BF261040	BF261040 HVSMEf002	1081	302.5	22.5	577	2	AW703717	AW703717 sk23e07.Y
1009	309.5	23.0	505	4	BG835402	BG835402 354322.NA	1082	302.5	22.5	588	1	AL808354	AL808354 AL808354
1010	309.5	23.0	565	2	AW625126	AW625126 EST313943	1083	302.5	22.5	659	6	CA089962	CA089962 SCSGAM207
1011	309.5	23.0	613	4	BI309404	BI309404 EST530814	1084	302	22.5	636	4	BJ259464	BJ259464 BJ259464
1012	309.5	23.0	691	7	CN524624	CN524624 Q0015M16.	1085	302	22.5	670	6	CA151503	CA151503 SCJFRZ201
1013	309.5	23.0	756	6	CD842250	CD842250 RFO2.126L	1086	302	22.5	674	5	BX251216	BX251216 BX251216
1014	309.5	23.0	781	5	BU895241	BU895241 X021B11.P	1087	302	22.5	674	5	BX254999	BX254999 BX254999
1015	309	23.0	489	7	CF931812	CF931812 EST0244.A	1088	302	22.5	689	5	BX250520	BX250520 BX250520
1016	309	23.0	536	2	BF484461	BF484461 WHE2309.A	1089	302	22.5	692	6	CA142664	CA142664 SCMCRT210
1017	309	23.0	638	7	CN975309	CN975309 25032.125	1090	302	22.5	784	6	CD840817	CD840817 RFO2.120M
1018	309	23.0	718	6	CD888511	CD888511 G118.108E	1091	302	22.5	814	7	CK202356	CK202356 FGAS01088
1019	308.5	23.0	507	7	CF972935	CF972935 PSU.2blon	1092	301.5	22.4	548	1	AI899927	AI899927 EST268670
1020	308.5	23.0	685	2	AW690185	AW690185 NF029D09S	1093	301.5	22.4	588	1	AL822798	AL822798 AL822798
1021	308.5	23.0	712	7	CO361980	CO361980 NDL2.8.G1	1094	301.5	22.4	643	5	BU880080	BU880080 UM417B11
1022	308.5	23.0	759	6	CD879592	CD879592 AZO4.105M	1095	301.5	22.4	707	7	CV254061	CV254061 WS0223.B2
1023	308.5	23.0	772	7	CF233249	CF233249 PtaJXO002	1096	301	22.4	600	2	AW306980	AW306980 sf51C05.Y
1024	308.5	23.0	834	7	CO489149	CO489149 Q00258.B7	1097	301	22.4	622	4	BI679740	BI679740 949078E04
1025	308	22.9	520	1	AU164541	AU164541 AU164541	1098	301	22.4	652	6	CD847394	CD847394 DHOAB582H
1026	308	22.9	626	2	BE423372	BE423372 WHE0065.D	1099	301	22.4	666	7	CO532808	CO532808 3530.1.21
1027	307.5	22.9	535	5	BQ624278	BQ624278 USDA-FP.0	1100	301	22.4	702	7	CO230270	CO230270 WS0011.B
1028	307.5	22.9	598	2	AW707192	AW707192 sk2a02.Y	1101	300.5	22.4	560	5	BM885724	BM885724 sam04d08.
1029	307.5	22.9	673	5	BQ991852	BQ991852 QGF24A02.	1102	300.5	22.4	578	4	BM068669	BM068669 WHE3461.D
1030	307.5	22.9	698	7	CV128456	CV128456 Mdftr3088	1103	300.5	22.4	591	1	AA660318	AA660318 00189.MCR
1031	307.5	22.9	765	2	BE705618	BE705618 Sc01_03g1	1104	300.5	22.4	600	4	BI4622587	BI4622587 EST533253

c1105	300.5	22.4	636	7	CK606552	CK606552 gmrhrw6-	c1178	293.5	21.9	630	7	CO174797	CO174797
c1106	300.5	22.4	637	6	CD904273	CD904273 G356.112P	c1179	293.5	21.9	681	7	CF213698	CF213698
c1107	300.5	22.4	661	7	CK987646	CK987646 SP7-B5 (P1	c1180	293.5	21.9	697	7	CK863140	CK863140
c1108	300.5	22.4	690	7	CF233271	CF233271 PcaJXO002	c1181	293.5	21.9	785	4	CG320047	CG320047
c1109	300.5	22.4	720	7	CV272291	CV272291 WS0157.B2	c1182	293	21.8	781	7	CO174891	CO174891
c1110	300.5	22.4	800	5	BQ518761	BQ518761 EST626176	c1183	292.5	21.8	489	2	BE500470	BE500470
c1111	300.5	22.4	850	6	CA107671	CA107671 SCRUHR107	c1184	292.5	21.8	496	2	BE330982	BE330982
c1112	300	22.3	679	6	CA253440	CA253440 SCJLFL410	c1185	292.5	21.8	496	5	BQ247189	BQ247189
c1113	300	22.3	685	5	BUI103556	BUI103556 SCCCHR100	c1186	292.5	21.8	518	4	BG300054	BG300054
c1114	300	22.3	685	6	CA102750	CA102750 SCCCHR100	c1187	292.5	21.8	549	5	BQ080249	BQ080249
c1115	299.5	22.3	516	4	BM402624	BM402624 SLA006D04	c1188	292.5	21.8	573	2	BF065160	BF065160
c1116	299.5	22.3	551	1	AL828595	AL828595 AL828595	c1189	292.5	21.8	573	6	CD877125	CD877125
c1117	299.5	22.3	584	1	AI898101	AI898101 EST267544	c1190	292.5	21.8	588	1	AA660308	AA660308
c1118	299.5	22.3	603	7	CF446610	CF446610 EST682955	c1191	292.5	21.8	590	4	BI779395	BI779395
c1119	299.5	22.3	605	7	CF445936	CF445936 EST682281	c1192	292.5	21.8	617	5	BQ611858	BQ611858
c1120	299.5	22.3	627	4	BG299397	BG299397 HVSMBA001	c1193	292	21.7	628	6	CD909626	CD909626
c1121	299.5	22.3	699	7	CF653377	CF653377 USDA-PP.0	c1194	292	21.7	647	6	CD898525	CD898525
c1122	299	22.2	689	7	CN991252	CN991252 67764.125	c1195	292	21.7	724	6	CD824049	CD824049
c1123	298.5	22.2	531	2	BE124333	BE124333 EST393368	c1196	291.5	21.7	551	6	CA039685	CA039685
c1124	298.5	22.2	534	1	AI443130	AI443130 ea84901.Y	c1197	291.5	21.7	580	4	BM100502	BM100502
c1125	298.5	22.2	590	5	BUS77914	BUS77914 ear94d04.	c1198	291.5	21.7	660	4	BI957746	BI957746
c1126	298.5	22.2	600	9	CR180853	CR180853 Forward.s	c1199	291	21.7	820	7	CO365680	CO365680
c1127	298.5	22.2	617	7	CK745975	CK745975 eca01-12c	c1200	291	21.7	849	7	CO368463	CO368463
c1128	298.5	22.2	637	6	CA835476	CA835476 MCS037E02	c1201	291	21.7	879	7	CO366519	CO366519
c1129	298.5	22.2	640	2	AW684885	AW684885 NF022F07N	c1202	291	21.7	900	7	CO365078	CO365078
c1130	298.5	22.2	766	7	CF236578	CF236578 PtaJXT4E5	c1203	290.5	21.6	483	5	BQ123267	BQ123267
c1131	298.5	22.2	805	2	AW350997	AW350997 GM210010A	c1204	290.5	21.6	525	6	CB395921	CB395921
c1132	298.5	22.2	823	2	BF256995	BF256995 HVSMF001	c1205	290.5	21.6	561	2	BE474577	BE474577
c1133	298.5	22.2	1049	7	CK163799	CK163799 FGAS01643	c1206	290.5	21.6	625	6	CD813970	CD813970
c1134	298	22.2	592	4	BI478930	BI478930 949071A06	c1207	290.5	21.6	654	4	BI957613	BI957613
c1135	298	22.2	673	6	CA234708	CA234708 SCJLSB106	c1208	290.5	21.6	674	2	BF649235	BF649235
c1136	298	22.2	724	4	BJS72947	BJS72947 BJS72947	c1209	290.5	21.6	706	7	CA422211	CA422211
c1137	297.5	22.2	509	4	BJS49094	BJS49094 EST85213	c1210	290.5	21.6	711	6	CA921232	CA921232
c1138	297.5	22.2	515	7	CV296836	CV296836 EST85213	c1211	290.5	21.6	765	7	CO369642	CO369642
c1139	297.5	22.2	561	2	BE450736	BE450736 EST401623	c1212	290.5	21.6	820	7	CF443771	CF443771
c1140	297.5	22.2	636	6	CD934106	CD934106 GR45.123A	c1213	290	21.6	648	5	BQ743293	BQ743293
c1141	297.5	22.2	659	2	BF646182	BF646182 NF068A08E	c1214	290	21.6	655	4	BI960535	BI960535
c1142	297.5	22.2	688	1	AV821843	AV821843 AV821843	c1215	290	21.6	673	6	CA220527	CA220527
c1143	297.5	22.2	713	7	CN146362	CN146362 WOUND1.39	c1216	290	21.6	679	6	CA141617	CA141617
c1144	297.5	22.2	744	6	CD430320	CD430320 ETH1.17.C	c1217	290	21.6	706	2	AW278810	AW278810
c1145	297	22.1	622	6	CA137725	CA137725 SCCRT200	c1218	290	21.6	707	7	CN988152	CN988152
c1146	297	22.1	673	4	BM371957	BM371957 EBma08.SQ	c1219	290	21.6	759	7	CV501184	CV501184
c1147	297	22.1	736	7	CV248404	CV248404 WS01120.B	c1220	289.5	21.6	561	4	BM269671	BM269671
c1148	297	22.1	927	7	CO480346	CO480346 QO018M14.	c1221	289.5	21.6	890	7	CO488997	CO488997
c1149	296.5	22.1	1149	1	AU262139	AU262139 AU262139	c1222	289	21.5	646	7	CO529747	CO529747
c1150	296.5	22.1	537	2	BE490625	BE490625 WHE0370.D	c1223	289	21.5	650	2	BF260414	BF260414
c1151	296.5	22.1	586	7	CF419317	CF419317 USDA-PP.1	c1224	289	21.5	676	7	CF671538	CF671538
c1152	296.5	22.1	664	1	AL820289	AL820289 AL820289	c1225	289	21.5	702	7	CN123933	CN123933
c1153	296.5	22.1	687	6	CD820187	CD820187 BN20.0511	c1226	289	21.5	732	3	CNS0A750	CNS0A750
c1154	296.5	22.1	834	7	CO369560	CO369560 RTK1.48.B	c1227	289	21.5	826	7	CN128942	CN128942
c1155	296	22.0	646	2	AW695899	AW695899 NF100E02S	c1228	288.5	21.5	540	4	BI779178	BI779178
c1156	296	22.0	670	5	BUS98750	BUS98750 H112A22T	c1229	288.5	21.5	559	1	AU263008	AU263008
c1157	296	22.0	691	6	CA182059	CA182059 SCBGS7310	c1230	288.5	21.5	636	6	CD932185	CD932185
c1158	296	22.0	742	5	BQ634193	BQ634193 NKRVO64.H	c1231	288	21.4	690	6	CD918343	CD918343
c1159	296	22.0	1090	7	CK216386	CK216386 FGAS02837	c1232	288	21.4	696	6	CA280310	CA280310
c1160	295.5	22.0	510	7	CV169700	CV169700 remex1.01	c1233	287.5	21.4	510	4	BM357022	BM357022
c1161	295.5	22.0	511	4	BG262486	BG262486 WHE0936.E	c1234	287.5	21.4	550	2	AW278618	AW278618
c1162	295.5	22.0	529	2	BF598865	BF598865 sv23q10.Y	c1235	287.5	21.4	554	5	BX682301	BX682301
c1163	295.5	22.0	564	2	BE398854	BE398854 EST430377	c1236	287.5	21.4	577	4	BM086141	BM086141
c1164	295.5	22.0	589	6	CA018785	CA018785 HV09K09R	c1237	287.5	21.4	634	6	CA136726	CA136726
c1165	295.5	22.0	605	2	AW776435	AW776435 EST335505	c1238	287.5	21.4	634	6	CA823264	CA823264
c1166	295.5	22.0	641	1	AL827928	AL827928 AL827928	c1239	287.5	21.4	643	9	CL561927	CL561927
c1167	295.5	22.0	654	7	CF575000	CF575000 MCSA142A0	c1240	287.5	21.4	655	5	B0750517	B0750517
c1168	295.5	22.0	672	6	CD825507	CD825507 BN25.060P	c1241	287.5	21.4	703	4	BM407958	BM407958
c1169	295	22.0	571	6	CB399845	CB399845 OSTF16367	c1242	287.5	21.4	777	5	BP133915	BP133915
c1170	295	22.0	670	7	CF433879	CF433879 NIT1.30.C	c1243	287	21.4	593	5	BUS79330	BUS79330
c1171	295	22.0	701	4	BI569035	BI569035 HVSMEN000	c1244	287	21.4	630	6	CA191567	CA191567
c1172	294.5	21.9	803	4	BI956671	BI956671 HVSMEN000	c1245	287	21.4	691	5	BQ840928	BQ840928
c1173	294	21.9	571	1	AU246119	AU246119 AU246119	c1246	287	21.4	729	8	BZ635220	BZ635220
c1174	294	21.9	613	6	CD911360	CD911360 G550.110P	c1247	287	21.4	753	7	CF471006	CF471006
c1175	294	21.9	692	4	BI978962	BI978962 2B11.Old	c1248	287	21.4	774	6	CB651301	CB651301
c1176	294	21.9	722	2	BJS76352	BJS76352 EST394300	c1249	287	21.4	795	7	CO176253	CO176253
c1177	293.5	21.9	556	2	BE124175	BE124175 EST394300	c1250	287	21.4	807	7	CF663779	CF663779
c1178	293.5	21.9	630	7	CO174797	CO174797 NDLL.46.G	c1179	293.5	21.9	681	7	CF213698	CF213698
c1179	293.5	21.9	697	7	CK863140	CK863140 34357.In	c1180	293.5	21.9	785	4	CG320047	CG320047
c1180	293.5	21.9	785	4	CG320047	CG320047 Zm03.01c0	c1181	293.5	21.9	781	7	CO174891	CO174891
c1181	293.5	21.9	781	7	CO174891	CO174891 NDLL.46.H	c1182	293	21.8	489	2	BE500470	BE500470
c1182	293	21.8	489	2	BE500470	BE500470 WHE0387.0	c1183	292.5	21.8	496	2	BE330982	BE330982
c1183	292.5	21.8	496	2	BE330982	BE330982 BQ247189	c1184	292.5	21.8	496	5	BQ247189	BQ247189
c1184	292.5	21.8	496	5	BQ247189	BQ247189 TAE15028C	c1185	292.5	21.8	518	4	BG300054	BG300054
c1185	292.5	21.8	518	4	BG300054	BG300054 san30e12.	c1186	292.5	21.8	549	5	BQ080249	BQ080249
c1186	292.5	21.8	549	5	BQ080249	BQ080249 HVCM0002	c1187	292.5	21.8	573	2	BF065160	BF065160
c1187	292.5	21.8	573	2	BF065160	BF065160 HV.CBm002	c1188	292.5	21.8	573	6	CD877125	CD877125
c1188	292.5	21.8	573	6	CD877125	CD877125 AS04.100B	c1189	292.5	21.8	588	1	AA660308	AA660308
c1189	292.5	21.8	588	1	AA660308	AA660308 00178.MLR	c1190	292.5	21.8	590	4	BI779395	BI779395
c1190	292.5	21.8	590	4	BI779395	BI779395 EBRO01.SQ	c1191	292.5	21.8	617	5		

1251	287	21.4	860	7	CO365601	RTK1_18_C	1324	281.5	21.0	569	5	BQ839243	BQ839243	WHE4163_H
1252	287	21.4	919	9	CG235840	QG3AC56TV	1325	281.5	21.0	683	4	BG370011	BG370011	HVSM810D2
1253	286.5	21.3	584	5	BQ623631	USDA_PP_0	1326	281.5	21.0	748	7	CF663501	CF663501	RFCNT1_3
1254	286.5	21.3	595	6	BO075138	IX15902_b	1327	281.5	21.0	749	7	CF671166	CF671166	RFCNT1_55
1255	286.5	21.3	623	6	CAB21671	RSH06A03	1328	281.5	21.0	761	7	CF395084	CF395084	RIDS2_9_C
1256	286	21.3	387	1	AUI179319	AUI179319	1329	281.5	21.0	814	7	CO362000	NDL2_8_BO	
1257	286	21.3	438	6	C23182	C23182_Japa	1330	281	20.9	577	5	BP184433	BP184433	BP184433
1258	286	21.3	568	1	AU267141	AU267141	1331	281	20.9	587	6	CD899632	CD899632	G174_113A
1259	286	21.3	569	1	AU270834	AU270834	1332	281	20.9	711	5	BO533731	BO533731	NXRV060_A
1260	286	21.3	577	1	AU264259	AU264259	1333	280.5	20.9	501	2	BE586643	BE586643	WHE0509_C
1261	286	21.3	582	4	BI432495	EST535256	1334	280.5	20.9	509	7	CA490343	MdW2016F	
1262	286	21.3	609	6	CA139015	SCQRT209	1335	280.5	20.9	519	7	CF439324	EST675669	
1263	286	21.3	649	6	CA120549	SCCCLR107	1336	280.5	20.9	523	1	AV770739	AV770739	
1264	286	21.3	668	4	BI959395	HVSM8001	1337	280.5	20.9	670	6	CA836696	MCU010A09	
1265	286	21.3	866	7	CF667338	RFCNT1_29	1338	280.5	20.9	672	6	CA166266	SCUTR2310	
1266	285.5	21.3	917	4	BI205825	EST523865	1339	280	20.8	509	2	BE050599	za67f09_9	
1267	285.5	21.3	540	6	CD878426	AZ04_102L	1340	280	20.8	580	2	AW686370	NP04UG10N	
1268	285.5	21.3	555	5	BM885163	sa195f06	1341	280	20.8	590	5	BU579089	na65G02	
1269	285.5	21.3	581	6	CB878369	HP08B22T	1342	280	20.8	613	6	CA276256	SCEP8D200	
1270	285.5	21.3	745	7	CF203406	RR80915N	1343	280	20.8	638	6	CA208994	SCEZAD1C0	
1271	285	21.2	566	7	CV511753	kc47C06_Y	1344	280	20.8	656	4	BG836117	Zm06_08E1	
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Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN									
Alignment Scores:									
Pred. No.:	2.98e-125	Length:	889						
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Percent Similarity:	99.62%	Conservative:	0						
Best Local Similarity:	99.62%	Mismatches:	0						
Query Match:	99.03%	Indels:	1						
DB:	4	Gaps:	0						
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Db	73	CTGGCGCGCGCTTTCGACCTGGCCTCTTCTCTGGGAGGCGGTGCCCGCCATGGCGAGGC	132						
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BM051236 814 bp mRNA linear EST 07-NOV-2001									
LOCUS									

RESULT 2  
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LOCUS

DEFINITION 603634191F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:5424766 5', mRNA sequence.

ACCESSION BM051236

VERSION BM051236.1 GI:16780503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 814)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Ingyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LNCM1886 row: e column: 23  
High quality sequence stop: 811.  
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/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4.74e-118 Length: 814

Score: 1259.00 Matches: 259

Percent Similarity: 97.74% Conservative: 0

Best Local Similarity: 97.74% Mismatches: 1

Query Match: 93.75% Indels: 5

DB: 4 Gaps: 0

US-10-017-407A-306 (1-262) x BM051236 (1-814)

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Qy 23 AlaAlaPheAlaThrGlyLeuPheLeuGlyValArgCysProProTrpArgGlyArgArg 42

Db 64 GCCGCTTTCGACCTGGCGCTCTTCTGGGAGCGCGGTGCCCGCCCAITGGGAGCGCGCGA 123

Qy 43 GluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyTrpLeuLeuSerArgSer 62

Db 124 GAGCAGTGCCTGCTTCCCCCGGAGCAGCGCGCTGTGGCAGTATCTTCTGAGCGCTCC 183

Qy 63 MetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGluGlnProGlnGly 82

Db 184 ATCGGAGACACCGCGCGCTGCGAGCCTGAGGCTGTGACCTGGAGCAGCGCGAGGG 243

Qy 83 AspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGln 102

Db 244 GATTCTATGATGACCTGCAGAGGCCCGCAGCTCTTGTGGCCACCTGGCGCGGCTCATCCAG 303



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Db 364 GGCTGCCCGCGGAGCGGGCGGTGTGACTGCGAGTGGACGGCGAGCCCCCGAGCTG 423
QY 143 GlyArgProLeuTyrArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysPro 162
Db 424 GGACGCCCTCTGGAGGCGAGCGGAGCGGAGCACAGATCGACCTCCGGCTGAAGCCC 483
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Db 664 CTCCGAAAGGGAGCTGGCGCGGAGTGTGTGGGAAACCTTAACGAACGCGATCCGGC 723
QY 241 tAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheL 261
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QY 261 ysile 262
Db 784 AGATC 788

RESULT 3
CR602194
LOCUS
DEFINITION
full-length cDNA clone CSODI073YH02 of Placenta Cot 25-normalized
of Homo sapiens (human)
ACCESSION
CR602194
VERSION
CR602194.1 GI:50483001
KEYWORDS
HTC; CNSLT cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1308)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1..1308
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI073YH02"
/tissue_type="Placenta Cot 25-normalized"

FEATURES
source

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/plasmid="pCMVSPORT\_6"

## ORIGIN

## Alignment Scores:

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Pred. No.:      1,36e-114      Length:      1308
Score:          1228.00        Matches:    262
Percent Similarity: 62.23%      Conservative: 0
Best Local Similarity: 62.23%    Mismatches: 0
Query Match:    91.44%         Indels:     159
DB:              3              Gaps:        2

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US-10-017-407A-306 (1-262) x CR602194 (1-1308)

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QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaA 20
Db 6 ATGACCCAGCCGCTGCCCGGCTCTCCGTGCCCGCGCGCTGCCCTGGCGCTCAGCGCA 65
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db 66 CTGGGCGCGCCTTCGCCACTTCCGCTCTTCCTGGGTGAGCAGGACCTGGTCCCGCGCGGC 125
QY 31 ----- 31
Db 126 GGGTGGCGGGCGCAGAGTAGGCGCGCGCTGGCTCAGGTTAATCCAAACACCTCTCCCC 185
QY 32 ----GlyArgArgCysProTyrArgGlyArgArgGluGlnCysLeuLeuProProGl 50
Db 186 GTCAGGAGCGGTGCCCCCATGCGAGCGCGCGAGAGCAGTGCCTCTCCCGCCGA 245
QY 50 uAspSerArgLeuTyrGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeu 70
Db 246 GGACACGCCCTGTGGCAGTATCTTCTGAGCGCTCCATGCGGAGACACCCCGCGCTGGC 305
QY 70 gSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluG 90
Db 306 AGCCTGAGCTGTGACCTCGAGCAGCGCGAGGGGATTCTATGATGACCTGCGAGCA 365
QY 90 nAlaGlnLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysLysAlaLeuAspLeuGl 110
Db 366 GGCCAGCTCTTTGGCCACCTGGCGCGGTCTCATCAGGCGCAAGAGCGCTGACCTGGG 425
QY 110 YThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgVa 130
Db 426 CACCTTCACGGGCTACTCCGCCCTGGCTGCGCTGCGCGCGCGCGCGCGCGCT 485
QY 130 lValThrCysGluValAspAlaGlnProGluLeuGlyArgProLeuTyrArgGlnAl 150
Db 486 GGTGACCTCGGAGGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
QY 150 aGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLe 170
Db 546 CGAGCGGAGCACAAAGATCGACCTCCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCT 605
QY 170 uLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspLysGluAs 190
Db 606 GCTGGCGCGCGGAGCGCGCGACCTTTCACGTGGCGCGTGGTGGTGGTGGTGGTGGT 665
QY 190 nCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyLysLeuAlaVa 210
Db 666 CTGCTCCGCTACTACGAGCGCTGTGCTGAGCTGTGCTGAGCGCGAGGATCTCTCCCGT 725
QY 210 lLeuArg----- 212
Db 726 CCTCAGAGTAAGGATCCACTCGGGGGGAGAGAACACCCCTGTTCGGCGCGGGTCCCCA 785
QY 212 ----- 212
Db 786 TCTTTTTCCTTTCGACTCTCTTTATATACCCCAAGCCCCACCCAGTCCAGTACGTAGGCTAC 845
QY 212 ----- 212
Db 846 ACCCCCTCGGGGCTCCCGGCCCGGTACCCAGGCTTTCTCCGCTTTGTTGTTGTTGTTGTT 905

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QY 212 ----- 212
Db 906 GCTCTGGTCACTCTGCGCGGACCTCCCTCCGAGGCGCGCTCCCGCCAGACACC 965
QY 212 ----- 212
Db 966 TCCCTCCGAGACCCCGCTTCGCTCGTGGCAGCTCCCTCCAGACCCCGCTCCCGCCG 1025
QY 212 ----- 212
Db 1026 GGCACCTCCCTCCAGTCCCGCGCTTCGCGCGGACACCTCCCTCCGAAGCCCGCCTC 1085
QY 213 -----ValLeuTpArgGlyLysValLeuGlnPr 222
Db 1086 CCACGGCCCGTTGGCCCGCCCTCCCGCAGGTCTGTGGCGGGAGAGTGTCTGAACC 1145
QY 222 oProLysGlyAspValAlaAlaGluCysValArgAsnLeuAnGluUArgIleArgAs 242
Db 1146 TCCGAAGGGGACGTGGCGCGGAGTGTGTGCGAAACCTTAACGAACGATCCGCGCGGA 1205
QY 242 pValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheIysI 262
Db 1206 CQTCAGGGTCTACATCAGCTCTCGCCCTGGCGGATGGACTCACCTTGGCCTTCAAGAT 1265
QY 262 e 262
Db 1266 C 1266

RESULT 4
BF663323
LOCUS 602144463F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5',
DEFINITION mRNA sequence.
ACCESSION BF663323
VERSION 1
KEYWORDS NIH-MGC http://mgi.nci.nih.gov/.
SOURCE National Institutes of Health, Mammalian Gene Collection (MGC)
ORGANISM Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1152 row: m column: 16
High quality sequence stop: 745.
FEATURES
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297911"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
Note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

## ORIGIN

Alignment Scores: 2,53e-113 Length: 1006  
 Pred. No.: 1214.00 Matches: 251  
 Score: 96.56% Conservative: 2  
 Percent Similarity: 95.80% Mismatches: 5  
 Best Local Similarity: 90.39% Indels: 5  
 Query Match: 2 Gaps: 0  
 DB:

US-10-017-407A-306 (1-262) x BF663323 (1-1006)

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QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCCGGTGGCCCGGCTCTCCGTGCCCGCGCGCTGGCCCTGGGCTCAGCCGCA 66
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
Db 67 CTGGCGCGCGCTTCGCCACTGGCCCTCTTCTGGGAGGCGGTGCCCCCATGGCGAGGC 126
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlaTyrIleLeuSer 60
Db 127 CGCGCAGAGCAGTGCCTTCCCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC 186
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGluGlnPro 80
Db 187 CGCTCATCGGGAGCACCCGGCGCTGCGAAGCTTGAGGCTGCTGACCTTGAGGAGCGCG 246
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 247 CAGGGGGATTCTATGATGACCTCGCAGCAGGCGCCAGCTCTTGGCCAACTGCGCGGCTC 306
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 307 ATCCAGGCGCAAGCGCTCGACCTGGCGCACTTTCACGGGCTACTCCGCCCTGGCCCTG 366
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 367 GCCCTGGGCGTCCCGCGGACCGGGCGCTGGTGACTCGGAGGTGGACGGCGAGCCCGCG 426
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 427 GAGCTGGGACGCGCCCTGTGGAGGCGGCGGAGGCGGAGCACAGATCGACCTCGCGCTG 486
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaGlyGluAlaGlyThrPheAsp 180
Db 487 AAGCCCGCTTGGAGACCTTGACGAGCTGTCTGGCGGGCGGAGCGCGCACCTTCGAC 546
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 547 GTGGCGGTGGTGGATGCGGACAGAGGAGAACTGCTCCGCTACTACGAGCGCTGTCTGCAG 606
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal-LeuTrpArgGlyLysValLeu 220
Db 607 CTGCTGCGACCGGAGGCGATCTCGCCGCTCTCAGAGTCTTGTGGCGCGGAGAGTGTCT 666
QY 220 uGlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeu-AsnGluArgIle 239
Db 667 GAAACT-CCGAAAGGGGACGTGGCGCGCGAGTGTGTGCGAAACCTAAACAAACGACATC 725
QY 240 ArgArgAspValArgValTyrIleSerLeuLeu-ProLeuGlyAspGlyLeuThrLeu 258
Db 726 CGCGGGAGCGCAGGGTCTATCATCAGGCTTCTGGGCCCTTGGGCGATGAGATCACCTT 783

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RESULT 5  
 BF664198  
 LOCUS 602145812F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309298 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF664198  
 VERSION BF664198.1  
 KEYWORDS GI:11938093  
 SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens	Db	367	GCCTCGCCCTGCCCCGACCGCGCGTGGTACCTGCGAGGTGACGCGCAGCC-CCG	425
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy	141	GUUUGUUGUArgProLeuTyrArgGlnAlaGluAlaGluHisLysIleAspLeuAigLeu	160
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	Db	426	GAGCTGGGACGGCCCTGTGGAGCGAGCGGCGGAGCACAAGATCGACCTCCGGCTG	485
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	Qy	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp	180
JOURNAL	Unpublished (1999)	Db	486	AAGCCCGCCTTGGAGACCTTGGACGAGCTGCTGGCGGCGGAGCGCGGACCTTCGAC	545
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM182 row: h column: 03 High quality sequence stop: 726.	Qy	181	ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln	200
		Db	546	GTGGCGTGGTGGATCCGACAGGAGAACTGCTCCGC-TACTACGAGCGCTCCCTGCAG	604
FEATURES	Location/Qualifiers	Qy	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTyrArgGlyLysValLeu	220
source	1..921 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4309298" /tissue_type="primary B-cells from tonsils (cell line)" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 48" /notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	Db	605	CTGCTCGACCCCGAGGATCTCTCGCCCTCTCAGAGTCTCTGGCGGGAAGGTGCTG	664
		Qy	221	GlnProProGlyGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg	240
		Db	665	CAACCTCCGAAAGGGGACGTCGCGCGGAGTGTGCGACACCT-AACGAAACGATCCGG	723
		Qy	241	ArgAspValArgValTyrIleSerLeuLeuPro 251	
		Db	724	CGGAGCTCAGGCTCTACATCAGCCTCTTCCCT 756	
RESULT 6					
BE796570					
LOCUS	BE796570				
DEFINITION	601592247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946546 5', mRNA linear EST 20-SEP-2000				
ACCESSION	BE796570				
VERSION	BE796570.1 GI:10217768				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 772)				
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabbs-remail.nih.gov Tissue Procurement: DCTD/Drp cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM806 row: m column: 11 High quality sequence stop: 766.				
FEATURES	Location/Qualifiers				
source	1..772 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3946546" /tissue_type="small cell carcinoma" /cell_lines="MGC3" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 7" /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
ORIGIN					
Alignment Scores:					
Pred. No.:	1..02e-110	Length:	921		
Score:	1188.00	Matches:	244		
Percent Similarity:	98.01%	Conservative:	2		
Best Local Similarity:	97.21%	Mismatches:	5		
Query Match:	88.46%	Indels:	3		
DB:	2	Gaps:	0		
US-10-017-407A-306 (1-262) x BF664198 (1-921)					
Qy	1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla	20			
Db	7 ATGACCCAGCCGGTGCCTGCTCTCCGTGCGCGCGCGTGGCGCTGCGGCTCAGCCGCA	66			
Qy	21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGly	40			
Db	67 CTGGGCGCCGCTTCGCCACTGTCCTTCTTGGGAGGCGGTGCCCCCATGCGGAGGC	126			
Qy	41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTyrGlnTyrLeuLeuSer	60			
Db	127 CGCGGAGACAGTCTGCTTCCCCCGGAGGACGCGCTGCGGAGTATCTTCTGAGC	186			
Qy	61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80			
Db	187 CGCTCCATCGGGAGACCCCGCGCTGCGAAGCCTGAGGCTGCTGACCTGGAGCAGCG	246			
Qy	81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100			
Db	247 CAGGGGGATTCATGATGACCTCGGAGCAGGCCAGCTTGGCCCAACCTGGCGGCTC	306			
Qy	101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120			
Db	307 ATCCAGGCCAAGAGGCGCTGACCTGGGACCTTCACGGGTACTTCCGCCCTGGCCCTG	366			
Qy	121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro	140			

ORIGIN

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Alignment Scores:
Pred. No.: 1,13e-110 Length: 772
Score: 1186.50 Matches: 245
Percent Similarity: 94.23% Conservative: 0
Best Local Similarity: 94.23% Mismatches: 12
Query Match: 88.35% Indels: 4
DB: 2 Gaps: 2

US-10-017-407A-306 (1-262) x BE796570 (1-772)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 2 ATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCGCGCTGCGCGCTGAGCGCGA 61
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProThrArgGly 40
Db 62 CTGGGGCGCGCTTCGCCATCGCCCTCTCTCTGGGAGCGGCGGCGCCCATGCGGAGCG 121
QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60
Db 122 CGGCGAGAGCAGTGCCTCTCCCGCGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGC 181
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluPro 80
Db 182 CGCTCCATCGGAGAGCAGCCCGCGCTGCGAAGCCTGAGGCTGTGACCCCTGGAGCAGCG 241
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 242 CAGGGGATTCATGATGACCTGCGAGCAGCGCCAGCTCTTGCGCAACCTGGCGGCGCTC 301
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 302 ATCCAGGCCAACAGAGCGCTGGACCTGGCGACCTTCAAGCGCTACTCCGCCCTGGCGCTG 361
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 362 GGCCTGGCGCTGCGCGGAGCGGCGCTGTGACCTGCGAGTGTGACGCGAGCGCGCGCG 421
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 422 GAGCTGGAGCGGCGCTGTGGAGCGAGCGCGAGCGGAGCGGAGCACAAAGATCGACCTCGGCTG 481
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 482 AAGCCCGCTTGAGACCTTGACGAGCTGTGGCGGCGGCGAGCGGCGAC--TTGAGC 539
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTrpGluArgCysLeuGln 200
Db 540 GTGGCGGTGGTGGTGGAGACAGGAGAACTGTCTCGCCCTACTACGAGCGCTGCCTGCAG 599
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 600 CTGCTGCGACCGGAGGATCTCTCGCGCTCTCAGAGTCTGTGGCGCGGGAAGGTGCTG 659
QY 221 Gln-ProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 660 CAAACCTCGAAGGGAGCTGGCGCGCGAGTGTGCGAACTAAAGAACCGCAT---CG 716
QY 240 gArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAla 259
Db 717 GCGGGACGTGAGC---TCTACATCAGCTCTCTCGCCCTGGGCGATGGAATCACCTGGCT 771

RESULT 7
LOCUS CR625911 1321 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DN002YB07 of Adult brain of Homo sapiens (human).
ACCESSION CR625911
VERSION CR625911.1 GI:50506718
KEYWORDS HTC; CDSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1321)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1321)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1321
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN002YB07"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"
source

ORIGIN
Alignment Scores:
Pred. No.: 7,78e-110 Length: 1321
Score: 1181.50 Matches: 255
Percent Similarity: 65.38% Conservative: 0
Best Local Similarity: 65.38% Mismatches: 0
Query Match: 87.97% Indels: 135
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x CR625911 (1-1321)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 155 ATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCGCGCTGCGCGCTGAGCGCGA 214
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db 215 CTGGCGCGCGCTTTCGCCACTGGCCTCTTCTTGGGTGAGCAGGACCTGTGTCCCGCGGCG 274
QY 31 ----- 31
Db 275 GGGTGGCGGCGCGCAGAGTAGGGCGCGGCTGAGGCTTAATCAACACACCTCTCCCC 334
QY 32 ---GlyArgArgCysProProTrpArgGlyArgGluGlnCysLeuLeuProGln 50
Db 335 GTACGAGGCGGCTGCGCGGCTGCGCGGCGGCGGCGGAGCAGTGTCTTCCCCCGA 394
QY 50 uAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70
Db 395 GGACACGCGCTGTGGCAGTATCTTCTGAGCGGCTCCATGCGGAGACCCCGCGCTGCG 454
QY 70 gSerLeuArgLeu----- 74
Db 455 AAGCCTGAGGTGTGTGTCAGCAGGCGCGGAGCGGAAACGCGGCGTCCCTCTCTGACCCCTGCG 514
QY 74 ----- 74
Db 515 GGTCCACAGTGGCTGTGTGACCTTGGGTGGGCCCTTGGCCCTCCTGGGCTTCCGGCTTC 574
QY 74 ----- 74
Db 575 CTTGGGCGGCTGCGGTGGCGGTTCCGAAGGCGCAGTCCCCCAGGCGCAGCCAGAACCG 634
QY 74 ----- 74
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Db 635 CGCCCCCTGGGGCTTGGGAGCCCCAGCGGCGAAGTGGGTGACCTGCATGCTGTGTGCCACC 694
QY 75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGI 89
Db 695 CTCTCTTTTCACGACGCTGACCTGGAGCAGCGCGAGGGGGATTTCTATGATGACCTGCCA 754
QY 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysAlaLeuAspLe 109
Db 755 GCAGGCCACAGCTCTTGGCCAACTGGCGCGGTCTATCCAGGCCCAAGAGCGCTGGACCT 814
QY 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 815 GGGCACCTTCACGGGTACTTCGGCCCTGCGCCCTGGCGCTGGCGCTGCCCGGACGGCG 874
QY 129 gValValThrCysGluValAspAlaGlnProGluLeuGluGlyArgProLeuTyrArg-- 148
Db 875 CGTGTGACTTGGAGTGGAGCGCGAGCCCCCGGAGCTGGGACGCCCTTGTGGAGGCA 934
QY 148 ----- 148
Db 935 GGTGAGCGCCCGCCCTAGCTCTGCAGCCCCAGCGCGGGCGCGCAACGGCTGACCCGCTCC 994
QY 149 -----GlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrL 167
Db 995 CTCGCGAGCGCGAGCGGAGCACAAGATCGACTCCGGCTGAAGCCCGCTTGGAGACCC 1054
QY 167 euAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaA 187
Db 1055 TGGACGAGCTGTGGCGGGCGGCGAGCGGCACCTTCACGTGGCGGTGTGGATCGCG 1114
QY 187 sPlysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyI 207
Db 1115 ACAAGAGAACTGCTCCGCTACTACGAGCGCTGCTGCAGCTGTCTGCACCGGAGGCA 1174
QY 207 leuAlaValLeuArgValLeuTyrArgLysValLeuGlnProProLysGlyAspV 227
Db 1175 TCCTGCCCTCTCAGAGTCTGTGGCGGGGAAGGTGTGCACACTCCGAAGGGGAGC 1234
QY 227 alAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrI 247
Db 1235 TGGCGGCCGAGTGTGTGCAGAACCTTAACGACGCATCCGGCGGACGTACAGGTCTACA 1294
QY 247 leSerLeuLeuProLeuGlyAspGly 255
Db 1295 TCAGCCTCTGCCCTGGCGGTGA 1320

RESULT 8
CB852718 750 bp mRNA linear EST 22-APR-2003
LOCUS UI-CF-FN0-afl-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-afl-p-08-0-UI 3', mRNA sequence.
ACCESSION CB852718
VERSION CB852718.1 GI:30047716
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
79044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
```

```
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
Genetics (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=No.

FEATURES
            Location/Qualifiers
    source          1..750
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-CF-FN0-afl-p-08-0-UI"
                    /tissue_type="Human Lung Epithelial cells"
                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                    /clone_lib="UI-CF-FN0"
                    /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
                    modified polylinker; Site 1: EcoR I; Site 2: Not I;
                    UI-CF-FN0 is a subtracted cDNA library derived from two
                    normalized Human lung epithelial cell libraries (EN1 and
                    DUI). The library was subtracted according to according to
                    Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
                    1996. For additional information, contact:
                    bento-soares@uiowa.edu
                    TAG_SEQ=None found"

ORIGIN
Alignment Scores:
Pred. No.:      5e-110      Length:      750
Score:          1180.00     Matches:    228
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      87.86%     Indels:     0
DB:               6         Gaps:        0

US-10-017-407A-306 (1-262) x CB852718 (1-750)

QY 32 GlyArgArgCysProProTyrArgGlyArgArgGluGlnCysLeuLeuProGluAsp 51
Db 30 GGGAGGGGGTGGCCCCCATGGCGAGCGCGCGAGAGCAGTGTCTTCCCCCGAGGAC 89
QY 52 SerArgLeuTyrGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuArgSer 71
Db 90 AGCGCGCTGTGGCAGTATCTTCTGAGCGCTCATGCGGGAGCACCGCGCTGCCAAGC 149
QY 72 LeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAla 91
Db 150 CTGAGGCTGCTGACCTGGAGCAGCGCGAGGGGGATTCTATGATGACCTGCCGAGGAGCC 209
QY 92 GlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysLysAlaLeuAspLeuGlyThr 111
Db 210 CAGCTCTTGGCCAACTGGCGGGCTCATCCAGGCCAAGAGCGCTGACCTGGGCACC 269
QY 112 PheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValVal 131
Db 270 TTTCACGGGCTACTCCGCCCTGGCCCTGGCGCTGCGCGCTGCCCGAGCGCGCTGGTG 329
QY 132 ThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTyrArgGlnAlaGlu 151
Db 330 ACCTCGAGGTGGAGCGCGCGCGCGCGAGCTGGGACCGCGCTGTGGAGGCGAGGCCGAG 389
QY 152 AlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeu 171
Db 390 GGGGAGCACACAGATCGACCTCGGGTGAAGCCCGCTTGGAGACCTTGGAGCGTGTG 449
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCys 191
Db 450 GCGCGGGCGAGCGCGGACCTTCGACGTGGCGCTGGTGGATCGCGACAAGAGAACTGC 509
QY 192 SerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleAlaValLeu 211
Db 510 TCCGCTACTACGAGCGCTGCCTGCAGCTGTGCGACCGCGAGGCATCTCCCGCTCTC 569
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CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.reagen.com) or from Open Biosystems  
Genetics (www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=No.

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QY 212 ArgValLeuTIPArgGlyLysValLeuGlnProProLysGlyAspValAlaAlaGluCys 231
Db 570 AGAGTCCTGTGGCGGGAGGTGTGCAACCTCCGAAAGGGAGCGTGGCGGGAGTGT 629

QY 232 ValArgAsnLeuAsnGluArgLeuArgAspValArgValTyrIleSerLeuLeuPro 251
Db 630 GTGCGAAACCTTAAACGAACGATCCGCGGGAGCGTCAGGGTCTTACATCAGCCTCCTGCC 689

QY 252 LeuGlyAspGlyLeuThrLeuAla 259
Db 690 CTGGCGATGGACTACCTTGGCT 713

RESULT 9
BF663695 779 bp mRNA linear EST 21-DEC-2000
LOCUS 602145414F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4309010 5',
DEFINITION mRNA sequence.
ACCESSION BF663695
VERSION BF663695.1 GI:11937590
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 779)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM181 row: 1 column: 03
High quality sequence stop: 761.
Location/Qualifiers
1. 779
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4309010"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1,07e-109 Length: 779
Score: 1177.00 Matches: 249
Percent Similarity: 95.08% Conservative: 1
Best local Similarity: 94.68% Mismatches: 5
Query Match: 87.64% Indels: 8
DB: 2 Gaps: 0

US-10-017-407A-306 (1-262) x BF663695 (1-779)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCGGTGCCCGGCTCTCCGTGTCGCCGCGCGCTGGCCCTGGGCTCAGCCGCA 66

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QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTIPArgGly 40
Db 67 CTGGGGCGCGCTTCGCCACTTCTTCTCTGGGGAGCGGTGCCCCCATGGCGAGCG 126

QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTIPdlnTyrLeuLeuSer 60
Db 127 CGGCGAGAGCAGTGCCTTCTCCCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC 186

QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGlnPro 80
Db 187 CGCTCCATCGGGAGCACCGCGCTGCGAAGCCCTGAGCTGCTGACCTGGAGCAGCG 246

QY 81 GlnGlyAspSerMetThrCysGlu-GlnAlaGlnLeuAlaAsnLeuAla-ArgL 100
Db 247 CAGGGGGATTCATATGATGACCTGGCAGCATGCCCGAGCTCTTGGCAACCTGGCTGGCG 306

QY 100 euileGlnAlaLysAlaLeuAspLeuGlyThrPheThr-GlyTyr-SerAlaLeuAla 119
Db 307 TCATCCAGCCCAAGAGCGCTGGACCTGGGCACCTTCACTGGGCTACTCCGCGCTGGCC 366

QY 120 LeuAlaLeuAla-LeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPr 139
Db 367 CTGGCCCTGGCTGTGCGCGGACGGCGGTGTGACCTGCGAGGTGGACGCGCAGCGC 426

QY 139 oProGlnLeuGlyArgProLeuTIPArgGlnAlaGluAlaGluHisLysIleAspLeuAr 159
Db 427 CCGGAGCTGGAGCGGCCCTGTGTGAGCAGCGCGGAGGACAAAGATCGACCTCG 486

QY 159 gLeuLysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPh 179
Db 487 GCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGTGCGCGCGGAGCGCGCACCTT 546

QY 179 eaSpValAlaValVal-AspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysL 199
Db 547 CGACGTGGCGCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 606

QY 199 euGlnLeuLeuArgProGlyGlyIle-LeuAlaValLeuArgValLeuTIPArgGlyLys 218
Db 607 TGCAGCTCTGGACCGCGAGGCATCTCTGCGCGCTCTCAGAGTCTGTGGCGCGGGAG 666

QY 219 ValLeuGlnProProLysGlyAsp-ValAlaAlaGluCysValArgAsnLeuAsnGluAr 238
Db 667 GTGCTGCAACCTCCGAAAGGGAGCGGTGGCGCGCGAGTGTGTGCGAAAACTAAACGACG 726

QY 238 gileArgArgAsp-ValArgValTyrIleSerLeuLeuProLeuGlyAspGly 255
Db 727 CATCCGCGCGGACCGCTCAGGGTCTACATCAGCTTCTTGGCCCTTGGCCGATGCG 779

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RESULT 10
BQ931589 934 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT_8795361 NTH_MGC_101 Homo sapiens cDNA clone IMAGE:642775
DEFINITION 5', mRNA sequence.
ACCESSION BQ931589
VERSION BQ931589.1 GI:22346620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LfCM2613 row: e column: 24
High quality sequence stop: 532.
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/mol_type="mRNA"
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/clone="IMAGE:6427775"
/issue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 101"
/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 3 71e-108 Length: 934
Score: 1163.00 Matches: 246
Percent Similarity: 94.36% Conservative: 5
Best Local Similarity: 92.48% Mismatches: 8
Query Match: 86.60% Indels: 8
DB: 5 Gaps: 2
US-10-017-407A-306 (1-262) x BQ931589 (1-934)
QY 2 ThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAlaLeu 21
Db 1 ACCGAGCGGTGCCTTCTCCGTGCGCGCGCGCTGGCCCTGGGCTCAGCGCACTG 60
QY 22 GlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGlyArg 41
Db 61 GCGCGCGCTTCGCCACTCGCCCTCTTCCTGGGAGCGCGTGGCCCATGGGAGCGCG 120
QY 42 ArgGluGlnCysLeuLeuProGluAaspSerArgLeuTrpGlnTyrLeuLeuSerArg 61
Db 121 CGAGAGCAGTGCTGCTTCCCCCGAGGACGCCGCTGTGGCAGTATCTTCTGAGCGCG 180
QY 62 SerMetArgGluHiPProAlaLeuArgSerLeuArgLeuThrLeuGluGlnProGln 81
Db 181 TCCATGCGGAGCAGCCCGCGCTGCGAGCCTGAG---CTGACCTCGGAGCGCGCAG 236
QY 82 GlyAaspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 101
Db 237 GGGGATTCTATGATGACCTCGCAGCAGCGCCAGCTCTTGGCCCAACCTGGCGGGCTCATC 296
QY 102 GlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 121
Db 297 CAGGCCAAGAGCGCTGAGCCTTGGCACCTTACAGGGCTACTCGCGCCCTGGCCCTGGCC 356
QY 122 LeuAlaLeuProAlaAaspGlyArgValValThrCysGluValAspAlaGlnProGlu 141
Db 357 CTGGCGCTGCCCGGAGCGGCGCTGTGTGACTCGGAGTGGAGCGCGAGCCCGCGAG 416
QY 142 LeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysPheAspLeuArgLeu 161
Db 417 CTGGGAGCGCCCTGTGGAGGAGCGCGGAGGCGGAGCACAAGATCGACCTCGGCTGAAG 476
QY 162 ProAlaLeuGluThrLeuAspGluLeuLeuAlaGlyGluAlaGlyThrPheAspVal 181
Db 477 CCGCGCTTGGAGACCTTGGACGAGTGTCTGGCGGCGGCGGAGCGCGGAGCTTCACGCTG 536
QY 182 AlaValAspAlaAaspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeu 201
Db 537 GCGGTGTGGATCGGAGCAGGAGAGACTGCTCCGCTACTACAGCGCTGCTGAGCTG 596
QY 202 LeuArgProGlyGlyLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGln 221

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|||||
597 CTGCGACCGGAGGCATCTCGCGCTCTGAGATCTCTGCGCGGAGGTGCTGCA 656
QY |||||||
222 ProProLysGlyAspValAlaAlaGluCysVal---ArgAsnLeuAsnGluArg-1leAr 240
|||||
657 CTCCCAAGGGGAAGTCTGGCGCGCGATGTGTGCAAAACCTAAACGACCCATCCG 716
QY |||||||
240 gArg-AspValArg-ValTyrIleSerLeu-LeuProLeuGlyAsp-GlyLeuThrLeuA 259
|||||
717 GCGGGGAGCTCAGGGGTCTACATCAGCCTCCCGGCCCTGGGCGAAGGAGTACCTTGG 776
QY |||||||
259 laPheLys 261
|||
777 CCTTCAA 784
Db |||

RESULT 11
AK007659
LOCUS
DEFINITION
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
enriched library, clone:1810030M08 product:weakly similar to
PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) (Rhodothermus marinus),
full insert sequence.
ACCESSION AK007659
VERSION AK007659.1 GI:12841341
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
3
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
4
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
5
REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12011111
6 (bases 1 to 919)
ADACHI, J., AIZAWA, K., AKAHIRA, S., AKIMURA, T., ARAI, A., AONO, H.,
ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y.,
FURUKAWA, M., HANAGAKI, T., HARA, A., HAYATSU, N., HIRAMOTO, K.,
HIRAOKA, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., IZAWA, M.,
KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONNO, H., KOUDA, M.,

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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGCGCCGAATTAATTCGAGTTAATTAATATCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

#### FEATURES

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/dev\_stage="10 day old"  
1..919  
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ORIGIN

Alignment Scores:  
Pred. No.: 1,88e-107 Length: 919  
Score: 1156.00 Matches: 224  
Percent Similarity: 92.37% Conservative: 18  
Best Local Similarity: 85.50% Mismatches: 20  
Query Match: 86.08% Indels: 0  
DB: 3 Gaps: 0

US-10-017-407A-306 (1-262) x AK007659 (1-919)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 37 ATGGCTCAGCCGCTCCCTCGGTATCTATCCAGCGGCACGTGGCTCGGCGCGG 96  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40  
DB 97 CTGGGCGCGCTCGTCTCTCTTCTTCTGGGAAACGCTGGCTCCATGGGGGTCC 156  
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpArgLeuSer 60  
DB 157 AGCGGCGAGAGCGCTGTGTCACCTGAGACATCCCTGTGGCAGTATCTGTGAGC 216  
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGluGlnPro 80  
DB 217 CGCTCCATGAGAGAGACCGCGCGCTGCGAGCGCTGCGAGCTGCTGACCTGAGCAGCG 276

QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
DB 277 CAGGGGATTCATGATGACCTGTGACAGGCCAGCTTCTGGCCAACTGGCGGCTC 336  
QY 101 IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyzSerAlaLeuAlaLeu 120  
DB 337 ATTAAGGCCAAGAAAGCTCTGGATCTGGGTACTTTTCAGGGGTACTTCGGCCCTT 396  
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValValAspAlaGlnProPro 140  
DB 397 GCCTTTGGCGCTTCCCGAGGCTGGCGCGTGGTGACCTGCGAGGTTGACGACAGAGCCCG 456  
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysAlaAspLeuArgLeu 160  
DB 457 AAGCTGGGACGCCCATGTGGAAGCAGGAGGAGTGGAGCAGAGATCGACCTTGGCTG 516  
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
DB 517 CAGCCCGCTTCACAGCATTTGGATGAGCTCTAGCGGGCGGAGCGCGAACCTTCGAC 576  
QY 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyzTyzGluArgCysLeuGln 200  
DB 577 ATAGCGGTGGTGGACCGCGACAAAGAGAACTGTACCGCTTACTAGAGCGCTGTCTGCAG 636  
QY 201 LeuLeuArgProGlyGlyLysLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
DB 637 CTCCTACGTCCCGAGGCGTCTCTGCTACTCAGAGCTCTGTGGCGGAGAGTGCTG 696  
QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLeuArg 240  
DB 697 CAGCCTCAGCCAGGACCAAGACTGTTGAATGTGTGGGAACCTGAACGACATCCCTG 756  
QY 241 ArgAspValArgValTyzIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
DB 757 AGGGAGCGCAGGGTCTACATCAGCTCTCTGCGCCCTGGATGATGGCTCTCTCTGGCTTT 816  
QY 261 LysIle 262  
DB 817 AAGATC 822  
RESULT 12  
AK054334  
LOCUS  
DEFINITION  
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:B330016L21 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.  
ACCESSION  
AK054334  
VERSION  
AK054334.1 GI:26344156  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1  
AUTHORS  
Carninci,P. and Hayashizaki,Y.  
TITLE  
High-efficiency full-length cDNA cloning  
JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636  
REFERENCE  
2  
AUTHORS  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20499374  
PUBMED  
11042159  
REFERENCE  
3  
AUTHORS  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,



Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2243)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sagaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tegawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
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QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
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QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
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QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
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QY 261 LysIle 262  
DB 820 AAGATC 825



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 ACCESSION BC019467.1 GI:18043387  
 VERSION BC019467.1  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932

TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

REMARK  
 COMMENT

2 (bases 1 to 999)  
 Strausberg, R.  
 Direct Submission  
 Submitted (19-DEC-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulèsed, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 37 Row: a Column: 14

This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
 identity to protein  
 This clone has the following problem: frame shifted.

## FEATURES

## source

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## ORIGIN

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 Query Match: 82.73% Indels: 26  
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US-10-017-407A-306 (1-262) x BC019467 (1-999)

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QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100

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QY 141 GluLeuGlyArgProLeuTrpArg-----148

Db 443 AGCTGGGAGCGCCCATGTGGAA-CGAGGTGAGAGCCCCACACCTGCGGCGCTCGGGCT 501

QY 149 -----GlnAlaGluAlaGluHisLys 155

Db 502 CCGGCTCGGGGCGTGGCGCGCTGACCGGCTCTTCCGCGAGCAGAGTGGAGCAGAAAG 561

QY 156 IleAspLeuArgLeuLysProAlaLeuThrLeuAspGluLeuLeuAlaGlyGlu 175

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DEFINITION  
ip21q07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6217933 3',  
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CA777547  
CA777547.1 GI:26015422

EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 756)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
Schmitt,A., Theising,B., Richter,E., Ronko,I., Bennett,J.,  
Cardenas,M., Gibbons,Y., McCann,R., Cole,R., Tsagarishevili,R.,  
Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 462.

Location/Qualifiers

FEATURES

source

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XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

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ORIGIN

Alignment Scores:

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US-10-017-407A-306 (1-262) x CA777547 (1-756)

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Job time : 8586 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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2555.431 Million cell updates/sec

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Searched: 5622541 seqs, 303335566 residues

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Maximum Match 100%  
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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40	1343	100.0	989	16	US-10-013-909A-305
63	1343	100.0	989	17	US-10-211-858-21
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70	1343	100.0	989	17	US-10-307-817-125
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82	413	30.8	1159	17	US-10-425-114-2777
83	413	30.8	1218	16	US-10-361-460-77
84	411	30.6	86941	17	US-10-461-194-2
85	409.5	30.5	85692	17	US-10-461-194-1
86	407	30.3	901	17	US-10-425-114-27082
87	407	30.3	2381	18	US-10-425-115-138013
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90	405.5	30.2	1508	17	US-10-424-599-18320
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131	383.5	28.6	1089	17	US-10-425-114-2526
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137	378	28.1	944	16	US-10-361-460-32	Sequence 32, Appl	210	173.5	12.9	584	18	US-10-425-115-53810	Sequence 53810, A
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140	377	28.0	1233	9	US-09-452-239-7	Sequence 7, Appl	213	172	12.8	2256646	18	US-10-470-565-1	Sequence 53, Appl
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142	376	28.0	1106	17	US-10-425-114-27818	Sequence 27818, A	215	170	12.7	447	11	US-09-732-627A-4334	Sequence 4334, Ap
143	374	27.8	1146	18	US-10-425-115-53825	Sequence 53825, A	216	170	12.7	75216	15	US-10-080-170-646	Sequence 646, App
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146	369	27.5	966	18	US-10-739-930-382	Sequence 382, App	219	169	12.6	1289	17	US-10-398-221-1713	Sequence 1713, Ap
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172	311.5	23.2	699	11	US-09-938-842A-1739	Sequence 1739, Ap	245	121.5	9.0	11309	17	US-10-158-844-108	Sequence 4979, Ap
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185	249.5	18.6	786	18	US-10-425-115-53809	Sequence 53809, A	258	112	8.3	2086	9	US-09-935-757-5	Sequence 5, Appl
186	231.5	17.2	1159	18	US-10-425-115-53828	Sequence 53828, A	259	111.5	8.3	602	18	US-10-425-115-172234	Sequence 172234, A
187	224.5	16.7	760	15	US-10-174-693-25	Sequence 25, Appl	260	111	8.3	13715	8	US-08-781-986A-195	Sequence 195, App
188	224	16.7	534	9	US-09-452-239-47	Sequence 47, Appl	261	111	8.3	13715	17	US-10-329-624-195	Sequence 195, App
189	220	16.4	575	18	US-10-425-115-140243	Sequence 140243, A	262	110	8.2	236	15	US-10-174-693-175	Sequence 175, App
190	219	16.3	481	18	US-10-425-115-155678	Sequence 155678, A	263	110	8.2	919	17	US-10-425-114-3232	Sequence 3232, Ap
191	216.5	16.1	578	18	US-10-767-701-26345	Sequence 26345, A	264	109	8.1	521	17	US-10-424-599-35115	Sequence 35115, A
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198	200.5	14.9	632	13	US-10-194-163-655	Sequence 655, App	271	107	8.0	253	9	US-09-923-876-4875	Sequence 4875, Ap
199	194.5	14.5	525	18	US-10-021-323-10926	Sequence 10926, A	272	107	8.0	253	10	US-09-923-876-4875	Sequence 4875, Ap
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202	183	13.6	594	15	US-10-174-693-105	Sequence 105, App	275	106	7.9	1350	9	US-09-925-301-266	Sequence 266, App
203	181.5	13.5	505	9	US-09-452-239-29	Sequence 29, Appl	276	105.5	7.9	374	18	US-10-425-115-148943	Sequence 148943, A
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205	176.5	13.1	510	9	US-09-452-239-9	Sequence 9, Appl	278	105	7.8	356	14	US-10-062-727-156	Sequence 156, App
206	176.5	13.1	600	9	US-09-452-239-39	Sequence 39, Appl	279	105	7.8	457	9	US-09-935-757-3	Sequence 3, Appl
207	176	13.1	451	14	US-10-062-727-457	Sequence 457, App	280	104.5	7.8	1593	18	US-10-437-963-40777	Sequence 40777, A
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283	103	7.7	64322	17	US-10-378-083-1	Sequence 1, Appli	356	93	6.9	1524	18	US-10-425-115-114038	Sequence 114038,
284	102	7.6	328	17	US-10-425-114-6556	Sequence 6556, Ap	357	93	6.9	1308	17	US-10-369-493-33780	Sequence 33780, A
285	101.5	7.6	2505	17	US-10-303-110A-1	Sequence 1, Appli	358	93	6.9	2176	8	US-08-808-031A-1	Sequence 1, Appli
286	101.5	7.6	2505	17	US-10-303-110A-4	Sequence 4, Appli	359	93	6.9	3744	17	US-10-302-172-585	Sequence 585, App
287	101	7.5	1602	18	US-10-437-963-102014	Sequence 102014,	360	93	6.9	4018	17	US-10-172-118-308	Sequence 308, App
288	101	7.5	1786	17	US-10-302-172-657	Sequence 657, App	361	93	6.9	4018	17	US-10-342-887-308	Sequence 308, App
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291	100.5	7.5	1815	18	US-10-717-049-3	Sequence 3, Appli	364	93	6.9	7788	16	US-10-329-079-8	Sequence 8, Appli
292	100	7.4	8460	14	US-10-237-271-2	Sequence 2, Appli	365	93	6.9	37360	16	US-10-329-079-6	Sequence 6, Appli
293	100	7.4	8460	17	US-10-191-997-115	Sequence 115, App	366	92.5	6.9	1107	15	US-10-156-761-6131	Sequence 6131, Ap
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295	100	7.4	8460	18	US-10-171-597-192	Sequence 192, App	368	92.5	6.9	2433	11	US-09-864-426A-587	Sequence 587, App
296	100	7.4	8460	19	US-10-278-698-161	Sequence 161, App	369	92.5	6.9	2433	16	US-10-084-839-587	Sequence 587, App
297	100	7.4	8460	19	US-10-278-698-677	Sequence 677, App	370	92.5	6.9	2445	10	US-09-864-636A-575	Sequence 575, App
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300	99	7.4	2010	18	US-10-641-935-7	Sequence 7, Appli	373	92.5	6.9	2445	10	US-09-864-636A-581	Sequence 581, App
301	99	7.4	2010	18	US-10-437-963-10627	Sequence 10627, A	374	92.5	6.9	2445	11	US-09-864-426A-571	Sequence 571, App
302	99	7.4	2685	17	US-10-401-403-147	Sequence 147, App	375	92.5	6.9	2445	11	US-09-864-426A-575	Sequence 575, App
303	99	7.4	2685	17	US-10-401-403-171	Sequence 171, App	376	92.5	6.9	2445	11	US-09-864-426A-579	Sequence 579, App
304	98.5	7.3	1338	15	US-10-156-761-3240	Sequence 3240, Ap	377	92.5	6.9	2445	11	US-09-864-426A-581	Sequence 581, App
305	98.5	7.3	2384	17	US-10-104-047-567	Sequence 567, App	378	92.5	6.9	2445	16	US-10-084-839-571	Sequence 571, App
306	98.5	7.3	3147	9	US-09-741-669-216	Sequence 216, App	379	92.5	6.9	2445	16	US-10-084-839-575	Sequence 575, App
307	98.5	7.3	3147	9	US-09-815-243-5965	Sequence 5965, Ap	380	92.5	6.9	2445	16	US-10-084-839-579	Sequence 579, App
308	98.5	7.3	3147	15	US-10-301-997-84	Sequence 84, Appl	381	92.5	6.9	2445	16	US-10-084-839-581	Sequence 581, App
309	98.5	7.3	3147	17	US-10-282-122A-20260	Sequence 20260, A	382	92.5	6.9	2445	16	US-10-084-839-2818	Sequence 2818, Ap
310	98.5	7.3	3147	18	US-10-818-509-84	Sequence 84, Appl	383	92.5	6.9	2445	16	US-10-084-839-2822	Sequence 2822, Ap
311	98.5	7.3	77536	10	US-09-940-316B-1	Sequence 1, Appli	384	92.5	6.9	2445	16	US-10-084-839-2826	Sequence 2826, Ap
312	98	7.3	828	17	US-10-282-122A-31998	Sequence 31998, A	385	92.5	6.9	2445	16	US-10-084-839-2828	Sequence 2828, Ap
313	98	7.3	77294	19	US-10-729-802-1	Sequence 1, Appli	386	92.5	6.9	2493	10	US-09-864-636A-589	Sequence 589, App
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318	97.5	7.3	2505	17	US-10-303-110A-7	Sequence 7, Appli	391	92.5	6.9	2493	11	US-09-864-426A-585	Sequence 585, App
319	97.5	7.3	2505	17	US-10-303-110A-10	Sequence 10, Appl	392	92.5	6.9	2493	16	US-10-084-839-585	Sequence 585, App
320	97.5	7.3	5208	18	US-10-437-963-69592	Sequence 69592, A	393	92.5	6.9	2508	10	US-09-864-636A-401	Sequence 401, App
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322	97	7.2	1104	17	US-10-282-122A-33573	Sequence 33573, A	395	92.5	6.9	2508	10	US-09-864-636A-407	Sequence 407, App
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325	96.5	7.2	2227	18	US-10-425-115-3967	Sequence 3967, Ap	398	92.5	6.9	2508	10	US-09-864-636A-415	Sequence 415, App
326	96.5	7.2	5397	18	US-10-437-963-69644	Sequence 69644, A	399	92.5	6.9	2508	10	US-09-864-636A-417	Sequence 417, App
327	96	7.1	1322	18	US-10-425-115-122270	Sequence 122270,	400	92.5	6.9	2508	10	US-09-864-636A-419	Sequence 419, App
328	96	7.1	15952	14	US-10-171-311-51	Sequence 51, Appl	401	92.5	6.9	2508	10	US-09-864-636A-423	Sequence 423, App
329	95.5	7.1	348	17	US-10-424-599-30454	Sequence 30454, A	402	92.5	6.9	2508	10	US-09-864-636A-426	Sequence 426, App
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334	95.5	7.1	2553	17	US-10-282-122A-29994	Sequence 29994, A	407	92.5	6.9	2508	11	US-09-864-426A-407	Sequence 407, App
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336	95	7.1	1717	15	US-10-156-761-4336	Sequence 4336, Ap	409	92.5	6.9	2508	11	US-09-864-426A-411	Sequence 411, App
337	95	7.1	1062	18	US-10-739-930-1766	Sequence 1766, Ap	410	92.5	6.9	2508	11	US-09-864-426A-415	Sequence 415, App
338	95	7.1	1948	17	US-10-282-122A-15101	Sequence 15101, A	411	92.5	6.9	2508	11	US-09-864-426A-417	Sequence 417, App
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340	95	7.1	4184	10	US-09-927-827-42	Sequence 42, Appl	413	92.5	6.9	2508	11	US-09-864-426A-423	Sequence 423, App
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342	94.5	7.0	1243	18	US-10-739-930-2839	Sequence 2839, Ap	415	92.5	6.9	2508	11	US-09-864-426A-431	Sequence 431, App
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344	94	7.0	717	17	US-10-282-122A-31785	Sequence 31785, A	417	92.5	6.9	2508	16	US-10-084-839-401	Sequence 401, App
345	94	7.0	4618	18	US-10-723-860-4935	Sequence 4935, Ap	418	92.5	6.9	2508	16	US-10-084-839-405	Sequence 405, App
346	94	7.0	14101	17	US-10-197-824-6	Sequence 6, Appli	419	92.5	6.9	2508	16	US-10-084-839-407	Sequence 407, App
347	94	7.0	17589	17	US-10-197-824-3	Sequence 3, Appli	420	92.5	6.9	2508	16	US-10-084-839-409	Sequence 409, App
348	93.5	7.0	840	15	US-10-156-761-1969	Sequence 1969, Ap	421	92.5	6.9	2508	16	US-10-084-839-411	Sequence 411, App
349	93.5	7.0	1107	15	US-10-156-761-4441	Sequence 4441, Ap	422	92.5	6.9	2508	16	US-10-084-839-415	Sequence 415, App
350	93.5	7.0	2505	17	US-10-303-110A-8	Sequence 8, Appli	423	92.5	6.9	2508	16	US-10-084-839-417	Sequence 417, App
351	93.5	7.0	2505	17	US-10-303-110A-9	Sequence 9, Appli	424	92.5	6.9	2508	16	US-10-084-839-419	Sequence 419, App
352	93.5	7.0	2505	17	US-10-303-110A-11	Sequence 11, Appl	425	92.5	6.9	2508	16	US-10-084-839-423	Sequence 423, App
353	93.5	7.0	2505	17	US-10-303-110A-12	Sequence 12, Appl	426	92.5	6.9	2508	16	US-10-084-839-426	Sequence 426, App
354	93.5	7.0	125746	15	US-10-156-761-15102	Sequence 15102, A	427	92.5	6.9	2508	16	US-10-084-839-431	Sequence 431, App



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C 429	92.5	6.9	2508	16	US-10-084-839-2737	Sequence 2737, App	C 502	92.5	6.9	2517	16	US-10-084-839-495	Sequence 495, App
C 430	92.5	6.9	2508	16	US-10-084-839-2739	Sequence 2739, App	C 503	92.5	6.9	2517	16	US-10-084-839-501	Sequence 501, App
C 431	92.5	6.9	2508	16	US-10-084-839-2741	Sequence 2741, App	C 504	92.5	6.9	2517	16	US-10-084-839-509	Sequence 509, App
C 432	92.5	6.9	2508	16	US-10-084-839-2743	Sequence 2743, App	C 505	92.5	6.9	2517	16	US-10-084-839-513	Sequence 513, App
C 433	92.5	6.9	2508	16	US-10-084-839-2745	Sequence 2745, App	C 506	92.5	6.9	2517	16	US-10-084-839-517	Sequence 517, App
C 434	92.5	6.9	2508	16	US-10-084-839-2747	Sequence 2747, App	C 507	92.5	6.9	2517	16	US-10-084-839-521	Sequence 521, App
C 435	92.5	6.9	2508	16	US-10-084-839-2749	Sequence 2749, App	C 508	92.5	6.9	2517	16	US-10-084-839-525	Sequence 525, App
C 436	92.5	6.9	2508	16	US-10-084-839-2751	Sequence 2751, App	C 509	92.5	6.9	2517	16	US-10-084-839-529	Sequence 529, App
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C 442	92.5	6.9	2511	10	US-09-940-244-258	Sequence 258, App	C 515	92.5	6.9	2517	16	US-10-084-839-2779	Sequence 2779, App
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C 444	92.5	6.9	2511	10	US-09-758-282-59	Sequence 59, Appl	C 517	92.5	6.9	2517	16	US-10-084-839-2790	Sequence 2790, App
C 445	92.5	6.9	2511	11	US-09-864-426A-262	Sequence 262, App	C 518	92.5	6.9	2517	16	US-10-084-839-2794	Sequence 2794, App
C 446	92.5	6.9	2511	16	US-10-084-839-262	Sequence 262, App	C 519	92.5	6.9	2517	16	US-10-084-839-2796	Sequence 2796, App
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C 448	92.5	6.9	2511	16	US-10-084-839-2834	Sequence 2834, App	C 521	92.5	6.9	2517	16	US-10-084-839-2800	Sequence 2800, App
C 449	92.5	6.9	2511	18	US-10-309-584-258	Sequence 258, App	C 522	92.5	6.9	2517	16	US-10-084-839-2802	Sequence 2802, App
C 450	92.5	6.9	2511	19	US-10-783-557-259	Sequence 259, App	C 523	92.5	6.9	2517	16	US-10-084-839-2804	Sequence 2804, App
C 451	92.5	6.9	2514	10	US-09-864-636A-133	Sequence 133, App	C 524	92.5	6.9	2517	16	US-10-084-839-2808	Sequence 2808, App
C 452	92.5	6.9	2514	10	US-09-864-636A-454	Sequence 454, App	C 525	92.5	6.9	2517	16	US-10-084-839-2856	Sequence 2856, App
C 453	92.5	6.9	2514	10	US-09-864-636A-475	Sequence 475, App	C 526	92.5	6.9	2520	10	US-09-864-636A-222	Sequence 222, App
C 454	92.5	6.9	2514	10	US-09-864-636A-499	Sequence 499, App	C 527	92.5	6.9	2520	10	US-09-864-636A-505	Sequence 505, App
C 455	92.5	6.9	2514	10	US-09-758-282-260	Sequence 260, App	C 528	92.5	6.9	2520	10	US-09-864-636A-541	Sequence 541, App
C 456	92.5	6.9	2514	11	US-09-864-426A-133	Sequence 133, App	C 529	92.5	6.9	2520	10	US-09-864-636A-543	Sequence 543, App
C 457	92.5	6.9	2514	11	US-09-864-426A-454	Sequence 454, App	C 530	92.5	6.9	2520	10	US-09-864-636A-573	Sequence 573, App
C 458	92.5	6.9	2514	11	US-09-864-426A-475	Sequence 475, App	C 531	92.5	6.9	2520	10	US-09-864-636A-577	Sequence 577, App
C 459	92.5	6.9	2514	11	US-09-864-426A-499	Sequence 499, App	C 532	92.5	6.9	2520	10	US-09-864-636A-583	Sequence 583, App
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C 461	92.5	6.9	2514	16	US-10-084-839-454	Sequence 454, App	C 534	92.5	6.9	2520	11	US-09-864-426A-222	Sequence 222, App
C 462	92.5	6.9	2514	16	US-10-084-839-475	Sequence 475, App	C 535	92.5	6.9	2520	11	US-09-864-426A-505	Sequence 505, App
C 463	92.5	6.9	2514	16	US-10-084-839-499	Sequence 499, App	C 536	92.5	6.9	2520	11	US-09-864-426A-541	Sequence 541, App
C 464	92.5	6.9	2514	16	US-10-084-839-2708	Sequence 2708, App	C 537	92.5	6.9	2520	11	US-09-864-426A-543	Sequence 543, App
C 465	92.5	6.9	2514	16	US-10-084-839-2764	Sequence 2764, App	C 538	92.5	6.9	2520	11	US-09-864-426A-573	Sequence 573, App
C 466	92.5	6.9	2514	16	US-10-084-839-2775	Sequence 2775, App	C 539	92.5	6.9	2520	11	US-09-864-426A-577	Sequence 577, App
C 467	92.5	6.9	2514	16	US-10-084-839-2788	Sequence 2788, App	C 540	92.5	6.9	2520	11	US-09-864-426A-583	Sequence 583, App
C 468	92.5	6.9	2514	16	US-10-084-839-2850	Sequence 2850, App	C 541	92.5	6.9	2520	16	US-10-084-839-222	Sequence 222, App
C 469	92.5	6.9	2514	16	US-10-084-839-2852	Sequence 2852, App	C 542	92.5	6.9	2520	16	US-10-084-839-505	Sequence 505, App
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C 475	92.5	6.9	2517	10	US-09-864-636A-501	Sequence 501, App	C 548	92.5	6.9	2520	16	US-10-084-839-2711	Sequence 2711, App
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C 484	92.5	6.9	2517	10	US-09-758-282-74	Sequence 74, Appl	C 557	92.5	6.9	2526	9	US-09-777-430A-22	Sequence 22, Appl
C 485	92.5	6.9	2517	10	US-09-758-282-238	Sequence 238, App	C 558	92.5	6.9	2526	9	US-09-777-430A-25	Sequence 25, Appl
C 486	92.5	6.9	2517	11	US-09-864-426A-69	Sequence 69, Appl	C 559	92.5	6.9	2526	10	US-09-864-636A-103	Sequence 103, App
C 487	92.5	6.9	2517	11	US-09-864-426A-128	Sequence 128, App	C 560	92.5	6.9	2526	10	US-09-864-636A-104	Sequence 104, App
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C 494	92.5	6.9	2517	11	US-09-864-426A-521	Sequence 521, App	C 567	92.5	6.9	2526	10	US-09-864-636A-349	Sequence 349, App
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C 496	92.5	6.9	2517	11	US-09-864-426A-529	Sequence 529, App	C 569	92.5	6.9	2526	10	US-09-864-636A-375	Sequence 375, App
C 497	92.5	6.9	2517	11	US-09-864-426A-533	Sequence 533, App	C 570	92.5	6.9	2526	10	US-09-864-636A-379	Sequence 379, App
C 498	92.5	6.9	2517	11	US-09-864-426A-537	Sequence 537, App	C 571	92.5	6.9	2526	10	US-09-864-636A-383	Sequence 383, App
C 499	92.5	6.9	2517	16	US-10-084-839-69	Sequence 69, Appl	C 572	92.5	6.9	2526	10	US-09-864-636A-387	Sequence 387, App
C 500	92.5	6.9	2517	16	US-10-084-839-128	Sequence 128, App	C 573	92.5	6.9	2526	10	US-09-864-636A-391	Sequence 391, App



C 574	92.5	6.9	2526	10	US-09-864-636A-395	Sequence 395, App	C 647	92.5	6.9	2526	16	US-10-084-839-2725	Sequence 2725, Ap
C 575	92.5	6.9	2526	10	US-09-864-636A-399	Sequence 399, App	C 648	92.5	6.9	2526	16	US-10-084-839-2727	Sequence 2727, Ap
C 576	92.5	6.9	2526	10	US-09-864-636A-452	Sequence 452, App	C 649	92.5	6.9	2526	16	US-10-084-839-2729	Sequence 2729, Ap
C 577	92.5	6.9	2526	10	US-09-864-636A-455	Sequence 455, App	C 650	92.5	6.9	2526	16	US-10-084-839-2731	Sequence 2731, Ap
C 578	92.5	6.9	2526	10	US-09-864-636A-459	Sequence 459, App	C 651	92.5	6.9	2526	16	US-10-084-839-2733	Sequence 2733, Ap
C 579	92.5	6.9	2526	10	US-09-864-636A-471	Sequence 471, App	C 652	92.5	6.9	2526	16	US-10-084-839-2735	Sequence 2735, Ap
C 580	92.5	6.9	2526	10	US-09-864-636A-497	Sequence 497, App	C 653	92.5	6.9	2526	16	US-10-084-839-2765	Sequence 2765, Ap
C 581	92.5	6.9	2526	10	US-09-864-636A-558	Sequence 558, App	C 654	92.5	6.9	2526	16	US-10-084-839-2767	Sequence 2767, Ap
C 582	92.5	6.9	2526	10	US-09-758-282-64	Sequence 64, Appl	C 655	92.5	6.9	2526	16	US-10-084-839-2773	Sequence 2773, Ap
C 583	92.5	6.9	2526	10	US-09-758-282-70	Sequence 70, Appl	C 656	92.5	6.9	2526	16	US-10-084-839-2777	Sequence 2777, Ap
C 584	92.5	6.9	2526	10	US-09-758-282-162	Sequence 162, App	C 657	92.5	6.9	2526	16	US-10-084-839-2786	Sequence 2786, Ap
C 585	92.5	6.9	2526	10	US-09-758-282-165	Sequence 165, App	C 658	92.5	6.9	2526	16	US-10-084-839-2832	Sequence 2832, Ap
C 586	92.5	6.9	2526	10	US-09-758-282-211	Sequence 211, App	C 659	92.5	6.9	2526	16	US-10-084-839-2838	Sequence 2838, Ap
C 587	92.5	6.9	2526	10	US-09-758-282-213	Sequence 213, App	C 660	92.5	6.9	2526	16	US-10-084-839-2840	Sequence 2840, Ap
C 588	92.5	6.9	2526	10	US-09-758-282-215	Sequence 215, App	C 661	92.5	6.9	2526	16	US-10-084-839-2842	Sequence 2842, Ap
C 589	92.5	6.9	2526	10	US-09-758-282-258	Sequence 258, App	C 662	92.5	6.9	2526	16	US-10-084-839-2844	Sequence 2844, Ap
C 590	92.5	6.9	2526	11	US-09-864-426A-103	Sequence 103, App	C 663	92.5	6.9	2526	16	US-10-084-839-2846	Sequence 2846, Ap
C 591	92.5	6.9	2526	11	US-09-864-426A-104	Sequence 104, App	C 664	92.5	6.9	2526	16	US-10-084-839-2848	Sequence 2848, Ap
C 592	92.5	6.9	2526	11	US-09-864-426A-117	Sequence 117, App	C 665	92.5	6.9	2532	10	US-09-864-636A-463	Sequence 463, App
C 593	92.5	6.9	2526	11	US-09-864-426A-118	Sequence 118, App	C 666	92.5	6.9	2532	10	US-09-864-636A-467	Sequence 467, App
C 594	92.5	6.9	2526	11	US-09-864-426A-119	Sequence 119, App	C 667	92.5	6.9	2532	11	US-09-864-426A-463	Sequence 463, App
C 595	92.5	6.9	2526	11	US-09-864-426A-132	Sequence 132, App	C 668	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 596	92.5	6.9	2526	11	US-09-864-426A-267	Sequence 267, App	C 669	92.5	6.9	2532	16	US-10-084-839-463	Sequence 463, App
C 597	92.5	6.9	2526	11	US-09-864-426A-273	Sequence 273, App	C 670	92.5	6.9	2532	16	US-10-084-839-467	Sequence 467, App
C 598	92.5	6.9	2526	11	US-09-864-426A-349	Sequence 349, App	C 671	92.5	6.9	2532	16	US-10-084-839-2769	Sequence 2769, Ap
C 599	92.5	6.9	2526	11	US-09-864-426A-373	Sequence 373, App	C 672	92.5	6.9	2532	16	US-10-084-839-2771	Sequence 2771, Ap
C 600	92.5	6.9	2526	11	US-09-864-426A-375	Sequence 375, App	C 673	92.5	6.9	2532	10	US-09-864-636A-563	Sequence 563, App
C 601	92.5	6.9	2526	11	US-09-864-426A-379	Sequence 379, App	C 674	92.5	6.9	2619	11	US-09-864-426A-563	Sequence 563, App
C 602	92.5	6.9	2526	11	US-09-864-426A-383	Sequence 383, App	C 675	92.5	6.9	2619	16	US-10-084-839-563	Sequence 563, App
C 603	92.5	6.9	2526	11	US-09-864-426A-387	Sequence 387, App	C 676	92.5	6.9	2619	16	US-10-084-839-5816	Sequence 5816, Ap
C 604	92.5	6.9	2526	11	US-09-864-426A-391	Sequence 391, App	C 677	92.5	6.9	2643	10	US-09-864-636A-559	Sequence 559, App
C 605	92.5	6.9	2526	11	US-09-864-426A-395	Sequence 395, App	C 678	92.5	6.9	2643	11	US-09-864-426A-559	Sequence 559, App
C 606	92.5	6.9	2526	11	US-09-864-426A-399	Sequence 399, App	C 679	92.5	6.9	2643	16	US-10-084-839-559	Sequence 559, App
C 607	92.5	6.9	2526	11	US-09-864-426A-452	Sequence 452, App	C 680	92.5	6.9	2643	16	US-10-084-839-2814	Sequence 2814, Ap
C 608	92.5	6.9	2526	11	US-09-864-426A-455	Sequence 455, App	C 681	92.5	6.9	3135	10	US-09-864-636A-481	Sequence 481, App
C 609	92.5	6.9	2526	11	US-09-864-426A-459	Sequence 459, App	C 682	92.5	6.9	3135	11	US-09-864-426A-481	Sequence 481, App
C 610	92.5	6.9	2526	11	US-09-864-426A-471	Sequence 471, App	C 683	92.5	6.9	3135	16	US-10-084-839-481	Sequence 481, App
C 611	92.5	6.9	2526	11	US-09-864-426A-497	Sequence 497, App	C 684	92.5	6.9	3135	16	US-10-084-839-2777	Sequence 2777, Ap
C 612	92.5	6.9	2526	11	US-09-864-426A-558	Sequence 558, App	C 685	92	6.9	813	17	US-10-369-493-33103	Sequence 33103, A
C 613	92.5	6.9	2526	16	US-10-084-839-103	Sequence 103, App	C 686	92	6.9	942	10	US-09-942-025-8	Sequence 8, Appli
C 614	92.5	6.9	2526	16	US-10-084-839-104	Sequence 104, App	C 687	92	6.9	1130	17	US-10-282-122A-19437	Sequence 19437, A
C 615	92.5	6.9	2526	16	US-10-084-839-117	Sequence 117, App	C 688	92	6.9	1932	17	US-10-267-502-88	Sequence 88, Appl
C 616	92.5	6.9	2526	16	US-10-084-839-118	Sequence 118, App	C 689	92	6.9	67311	10	US-09-942-025-1	Sequence 1, Appli
C 617	92.5	6.9	2526	16	US-10-084-839-119	Sequence 119, App	C 690	91.5	6.8	903	15	US-10-156-761-642	Sequence 642, App
C 618	92.5	6.9	2526	16	US-10-084-839-132	Sequence 132, App	C 691	91.5	6.8	1092	18	US-10-437-963-97637	Sequence 97637, A
C 619	92.5	6.9	2526	16	US-10-084-839-267	Sequence 267, App	C 692	91.5	6.8	1116	17	US-10-282-122A-32148	Sequence 32148, A
C 620	92.5	6.9	2526	16	US-10-084-839-273	Sequence 273, App	C 693	91.5	6.8	1149	15	US-10-156-761-5745	Sequence 5745, Ap
C 621	92.5	6.9	2526	16	US-10-084-839-349	Sequence 349, App	C 694	91.5	6.8	1896	15	US-10-156-761-5658	Sequence 5658, Ap
C 622	92.5	6.9	2526	16	US-10-084-839-373	Sequence 373, App	C 695	91.5	6.8	2253	17	US-10-282-122A-30610	Sequence 30610, A
C 623	92.5	6.9	2526	16	US-10-084-839-375	Sequence 375, App	C 696	91.5	6.8	2499	10	US-09-864-636A-79	Sequence 79, Appl
C 624	92.5	6.9	2526	16	US-10-084-839-379	Sequence 379, App	C 697	91.5	6.8	2499	10	US-09-758-282-94	Sequence 94, Appl
C 625	92.5	6.9	2526	16	US-10-084-839-383	Sequence 383, App	C 698	91.5	6.8	2499	11	US-09-864-426A-79	Sequence 79, Appl
C 626	92.5	6.9	2526	16	US-10-084-839-387	Sequence 387, App	C 699	91.5	6.8	2499	16	US-10-084-839-79	Sequence 79, Appl
C 627	92.5	6.9	2526	16	US-10-084-839-391	Sequence 391, App	C 700	91.5	6.8	2499	16	US-10-084-839-2682	Sequence 2682, Ap
C 628	92.5	6.9	2526	16	US-10-084-839-395	Sequence 395, App	C 701	91.5	6.8	2505	10	US-09-864-636A-155	Sequence 155, App
C 629	92.5	6.9	2526	16	US-10-084-839-399	Sequence 399, App	C 702	91.5	6.8	2505	10	US-09-758-282-266	Sequence 266, App
C 630	92.5	6.9	2526	16	US-10-084-839-452	Sequence 452, App	C 703	91.5	6.8	2505	11	US-09-864-426A-155	Sequence 155, App
C 631	92.5	6.9	2526	16	US-10-084-839-455	Sequence 455, App	C 704	91.5	6.8	2505	16	US-10-084-839-155	Sequence 155, App
C 632	92.5	6.9	2526	16	US-10-084-839-459	Sequence 459, App	C 705	91.5	6.8	2505	16	US-10-084-839-2709	Sequence 2709, Ap
C 633	92.5	6.9	2526	16	US-10-084-839-471	Sequence 471, App	C 706	91.5	6.8	2511	9	US-09-777-430A-9	Sequence 9, Appli
C 634	92.5	6.9	2526	16	US-10-084-839-497	Sequence 497, App	C 707	91.5	6.8	2511	10	US-09-864-636A-244	Sequence 244, App
C 635	92.5	6.9	2526	16	US-10-084-839-558	Sequence 558, App	C 708	91.5	6.8	2511	11	US-09-758-282-3	Sequence 3, Appli
C 636	92.5	6.9	2526	16	US-10-084-839-2701	Sequence 2701, App	C 709	91.5	6.8	2511	11	US-09-864-426A-244	Sequence 244, App
C 637	92.5	6.9	2526	16	US-10-084-839-2702	Sequence 2702, App	C 710	91.5	6.8	2511	16	US-10-084-839-244	Sequence 244, App
C 638	92.5	6.9	2526	16	US-10-084-839-2703	Sequence 2703, App	C 711	91.5	6.8	2511	16	US-10-084-839-2713	Sequence 2713, Ap
C 639	92.5	6.9	2526	16	US-10-084-839-2704	Sequence 2704, App	C 712	91.5	6.8	2653	18	US-10-469-558-1	Sequence 1, Appli
C 640	92.5	6.9	2526	16	US-10-084-839-2705	Sequence 2705, App	C 713	91.5	6.8	2731748	18	US-10-297-465A-1	Sequence 1, Appli
C 641	92.5	6.9	2526	16	US-10-084-839-2707	Sequence 2707, App	C 714	91.5	6.8	2731748	18	US-10-297-465A-1	Sequence 1, Appli
C 642	92.5	6.9	2526	16	US-10-084-839-2716	Sequence 2716, App	C 715	91	6.8	798	18	US-10-425-115-60646	Sequence 60646, A
C 643	92.5	6.9	2526	16	US-10-084-839-2718	Sequence 2718, App	C 716	91	6.8	846	17	US-10-282-122A-23727	Sequence 23727, A
C 644	92.5	6.9	2526	16	US-10-084-839-2720	Sequence 2720, App	C 717	91	6.8	1209	17	US-10-425-114-16417	Sequence 16417, A
C 645	92.5	6.9	2526	16	US-10-084-839-2721	Sequence 2721, App	C 718	91	6.8	1400	17	US-10-437-963-22255	Sequence 22255, A
C 646	92.5	6.9	2526	16	US-10-084-839-2723	Sequence 2723, App	C 719	91	6.8	1590	17	US-10-282-122A-41291	Sequence 41291, A

C 720	91	6.8	2064	15	US-10-156-761-2302	Sequence 2902, Ap	1394	88.5	6.6	1392	15	US-10-156-761-6437	Sequence 6437, Ap
C 721	91	6.8	2299	18	US-10-466-531-49	Sequence 49, Appl	1395	88.5	6.6	1437	17	US-10-369-493-31948	Sequence 31948, A
C 722	91	6.8	2454	15	US-10-156-761-2410	Sequence 2410, Ap	1396	88.5	6.6	1566	18	US-10-437-963-1947	Sequence 1947, Ap
C 754	91	6.8	2749	10	US-09-991-428-516	Sequence 516, App	1397	88.5	6.6	1696	17	US-10-120-988-151	Sequence 151, App
C 844	91	6.8	2749	14	US-10-167-749-215	Sequence 215, App	1398	88.5	6.6	2038	18	US-10-739-930-4499	Sequence 4499, Ap
C 969	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl	1399	88.5	6.6	2413	9	US-09-931-087A-2	Sequence 2, Appl
C 973	91	6.8	2749	15	US-10-223-084-59	Sequence 59, Appl	1400	88.5	6.6	2413	16	US-10-062-923-2	Sequence 2, Appl
C 974	91	6.8	2749	15	US-10-223-088-59	Sequence 59, Appl	1401	88.5	6.6	2454	14	US-10-198-846-13360	Sequence 13360, A
C 975	91	6.8	2749	15	US-10-223-090-59	Sequence 59, Appl	1402	88.5	6.6	3060	18	US-10-837-318-46	Sequence 46, Appl
C 976	91	6.8	2749	15	US-10-223-087-59	Sequence 59, Appl	1403	88.5	6.6	3060	18	US-10-837-318-46	Sequence 46, Appl
C 978	91	6.8	2749	15	US-10-223-083-59	Sequence 59, Appl	1404	88.5	6.6	3060	19	US-10-926-223-56	Sequence 56, Appl
C 979	91	6.8	2749	15	US-10-223-089-59	Sequence 59, Appl	1405	88.5	6.6	3060	19	US-10-926-223-56	Sequence 56, Appl
C 1151	91	6.8	2749	16	US-10-223-081-59	Sequence 59, Appl	1406	88.5	6.6	3289	18	US-10-723-860-6374	Sequence 6374, A
C 1171	91	6.8	2749	16	US-10-223-082-59	Sequence 59, Appl	1407	88.5	6.6	3413	17	US-10-424-599-52304	Sequence 52304, A
C 1240	91	6.8	2749	17	US-10-170-481A-215	Sequence 215, App	1408	88.5	6.6	22459	11	US-09-973-278-883	Sequence 883, App
C 1242	91	6.8	2749	17	US-10-210-028-215	Sequence 215, App	1409	88.5	6.6	30350	13	US-10-118-328-3	Sequence 3, Appl
C 1302	91	6.8	2749	17	US-10-163-521A-215	Sequence 215, App	1410	88.5	6.6	30350	18	US-10-694-438-3	Sequence 3, Appl
C 1311	91	6.8	2749	17	US-10-305-654-59	Sequence 59, Appl	1411	88.5	6.6	37116	17	US-10-107-431-279	Sequence 279, App
C 1324	91	6.8	2749	19	US-10-081-056-59	Sequence 59, Appl	1412	88.5	6.6	84428	17	US-10-229-148B-1	Sequence 1, Appl
C 1329	91	6.8	2749	19	US-10-918-851-215	Sequence 215, App	1413	88.5	6.6	109519	11	US-09-758-759-1	Sequence 1, Appl
C 1340	91	6.8	2749	19	US-10-931-886-385	Sequence 385, App	1414	88	6.6	160361	17	US-10-235-192A-35	Sequence 35, Appl
C 1341	91	6.8	2749	19	US-10-805-667-215	Sequence 215, App	1415	88	6.6	813	17	US-10-369-493-33037	Sequence 33037, A
C 1342	91	6.8	2749	19	US-10-805-667-215	Sequence 215, App	1416	88	6.6	852	17	US-10-389-647-34	Sequence 34, Appl
C 1344	91	6.8	2749	19	US-10-437-963-96859	Sequence 96859, A	1417	88	6.6	931	18	US-10-767-701-2040	Sequence 2040, Ap
C 1345	90.5	6.7	1023	17	US-10-369-493-31552	Sequence 31552, A	1418	88	6.6	1043	18	US-10-425-115-143306	Sequence 143306, A
C 1346	90.5	6.7	1248	15	US-10-156-761-1741	Sequence 1741, Ap	1419	88	6.6	1087	18	US-10-425-115-143306	Sequence 143306, A
C 1347	90.5	6.7	1611	17	US-10-260-238-1334	Sequence 1334, Ap	1420	88	6.6	1281	17	US-10-369-493-44439	Sequence 44439, A
C 1348	90.5	6.7	1820	18	US-10-437-963-49451	Sequence 49451, A	1421	88	6.6	1461	15	US-10-156-761-1666	Sequence 1666, Ap
C 1349	90.5	6.7	2526	10	US-09-864-636A-102	Sequence 102, App	1422	88	6.6	1464	17	US-10-424-599-128274	Sequence 128274, A
C 1350	90.5	6.7	2526	10	US-09-758-282-159	Sequence 159, App	1423	88	6.6	1694	18	US-10-437-963-97638	Sequence 97638, A
C 1351	90.5	6.7	2526	11	US-09-864-426A-102	Sequence 102, App	1424	88	6.6	2006	18	US-10-437-963-18431	Sequence 18431, A
C 1352	90.5	6.7	2526	16	US-10-084-839-102	Sequence 102, App	1425	88	6.6	2402	17	US-10-369-493-32004	Sequence 32004, A
C 1353	90.5	6.7	2526	16	US-10-084-839-2700	Sequence 2700, Ap	1426	88	6.6	2487	17	US-10-282-122A-32996	Sequence 32996, A
C 1354	90.5	6.7	2538	18	US-10-425-115-174346	Sequence 174346, A	1427	88	6.6	2517	10	US-09-864-636A-127	Sequence 127, App
C 1355	90.5	6.7	135638	16	US-10-314-657-1	Sequence 1, Appl	1428	88	6.6	2517	10	US-09-758-282-235	Sequence 235, App
C 1356	90.5	6.7	3309400	9	US-09-738-626-1	Sequence 875, App	1429	88	6.6	2517	16	US-10-084-839-127	Sequence 127, App
C 1357	90	6.7	662	18	US-10-437-963-875	Sequence 875, App	1430	88	6.6	2528	18	US-10-437-963-81418	Sequence 81418, A
C 1358	90	6.7	1195	18	US-10-425-115-26858	Sequence 26858, A	1431	88	6.6	2565	15	US-10-156-761-3914	Sequence 3914, Ap
C 1359	90	6.7	1338	17	US-10-369-493-45528	Sequence 45528, A	1432	88	6.6	3426	15	US-10-156-761-5493	Sequence 5493, Ap
C 1360	90	6.7	1443	15	US-10-156-761-559	Sequence 559, App	1433	88	6.6	3730	9	US-09-917-800A-476	Sequence 476, App
C 1361	90	6.7	2160	17	US-10-221-596B-23	Sequence 23, Appl	1434	88	6.6	3885	13	US-10-087-192-2021	Sequence 2021, Ap
C 1362	90	6.7	3084	18	US-10-437-963-1495	Sequence 1495, Ap	1435	88	6.6	4750	18	US-10-723-860-2201	Sequence 2201, Ap
C 1363	90	6.7	45814	13	US-10-087-192-256	Sequence 256, App	1436	88	6.6	4874	18	US-10-331-053-65	Sequence 65, Appl
C 1364	89.5	6.7	849	15	US-10-156-761-925	Sequence 925, App	1437	88	6.6	5130	18	US-10-437-963-59667	Sequence 59667, A
C 1365	89.5	6.7	1026	17	US-10-425-114-28163	Sequence 28163, A	1438	88	6.6	11007	17	US-10-402-842-5	Sequence 5, Appl
C 1366	89.5	6.7	1052	18	US-10-716-803-10	Sequence 10, Appl	1439	88	6.6	47988	17	US-10-402-842-1	Sequence 1, Appl
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C 1369	89.5	6.7	1710	18	US-10-437-963-24299	Sequence 24299, A	1442	87.5	6.5	1053	15	US-10-181-319-5	Sequence 5, Appl
C 1370	89.5	6.7	2418	17	US-10-369-493-40581	Sequence 40581, A	1443	87.5	6.5	1104	18	US-10-437-963-24858	Sequence 24858, A
C 1371	89.5	6.7	10846	17	US-10-074-024-577	Sequence 577, App	1444	87.5	6.5	1287	15	US-10-156-761-3398	Sequence 3398, Ap
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C 1374	89	6.6	1291	18	US-10-437-963-73204	Sequence 73204, A	1447	87.5	6.5	1402	9	US-09-814-777A-102	Sequence 102, App
C 1375	89	6.6	1374	17	US-10-282-122A-25943	Sequence 25943, A	1448	87.5	6.5	1803	17	US-10-369-493-26552	Sequence 26552, A
C 1376	89	6.6	1428	18	US-10-739-930-2348	Sequence 2348, Ap	1449	87.5	6.5	1823	18	US-10-437-963-48275	Sequence 48275, A
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C 1393	88.5	6.6	1263	17	US-10-282-122A-11556	Sequence 11556, A	1466	87.5	6.5	9745	17	US-10-227-577-2259	Sequence 2259, Ap

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c1469	87.5	6.5	12149	17	US-10-227-577-2258	Sequence 2258, Ap
c1470	87.5	6.5	25801	13	US-10-181-319-13	Sequence 13, Appl
c1471	87.5	6.5	98546	13	US-10-087-192-1414	Sequence 1414, Ap
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum Match 100%

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	401	29.9	891	3	US-09-452-239-1
4	396	29.5	1058	3	US-09-452-239-11
5	394	29.3	1078	3	US-09-452-239-41
6	392.5	29.2	962	3	US-09-452-239-23
7	392.5	29.2	1023	3	US-09-452-239-25
8	389	29.0	997	3	US-09-452-239-13
9	387	28.8	953	3	US-09-452-239-45
10	386.5	28.8	967	3	US-09-452-239-5
11	386	28.7	1012	3	US-09-615-192A-94
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C 89	102.5	7.6	8793	4	US-09-902-540-1042	Sequence 1042, App	162	94.5	7.0	9623	4	US-09-949-016-14362	Sequence 14362, A
C 90	102	7.6	1813	5	US-09-902-540-1042	Sequence 1042, App	163	94.5	7.0	16347	4	US-09-949-016-14645	Sequence 14645, A
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C 95	100.5	7.5	1979	2	US-08-649-619B-1	Sequence 3, Appli	168	94	7.0	2313	4	US-09-252-991A-11939	Sequence 11939, A
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C 119	98.5	7.3	77536	4	US-09-940-316B-1	Sequence 1, Appli	192	92.5	6.9	2511	4	US-09-577-304A-59	Sequence 59, Appli
120	98	7.3	1713	4	US-09-252-991A-109	Sequence 109, App	193	92.5	6.9	2511	4	US-09-777-430C-12	Sequence 12, Appli
C 121	97.5	7.3	657	4	US-09-351-150A-14	Sequence 9351, App	194	92.5	6.9	2514	4	US-09-758-282B-260	Sequence 260, App
C 122	97.5	7.3	1632	4	US-09-252-991A-11756	Sequence 14, Appli	195	92.5	6.9	2514	4	US-09-577-304A-211	Sequence 211, App
C 123	97.5	7.3	2232	4	US-09-252-991A-11756	Sequence 11756, A	196	92.5	6.9	2517	4	US-09-758-282B-74	Sequence 74, Appli
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C 130	97	7.2	1101	4	US-09-252-991A-10597	Sequence 10597, A	203	92.5	6.9	2526	4	US-09-758-282B-162	Sequence 162, App
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C 132	97	7.2	11502	4	US-09-902-540-1064	Sequence 1064, App	205	92.5	6.9	2526	4	US-09-758-282B-211	Sequence 211, App
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C 136	96.5	7.2	1254	4	US-09-252-991A-12420	Sequence 12420, A	209	92.5	6.9	2526	4	US-09-577-304A-64	Sequence 64, Appli
C 137	96.5	7.2	6083	4	US-09-902-540-763	Sequence 763, App	210	92.5	6.9	2526	4	US-09-577-304A-70	Sequence 70, Appli
C 138	96	7.1	3135	4	US-09-252-991A-5922	Sequence 5922, App	211	92.5	6.9	2526	4	US-09-577-304A-162	Sequence 162, App
C 139	96	7.1	9097	4	US-09-902-540-947	Sequence 947, App	212	92.5	6.9	2526	4	US-09-577-304A-211	Sequence 211, App
C 140	96	7.1	14541	4	US-09-902-540-1159	Sequence 1159, App	213	92.5	6.9	2526	4	US-09-577-304A-213	Sequence 213, App
C 141	96	7.1	22301	4	US-09-902-540-1208	Sequence 1208, App	214	92.5	6.9	2526	4	US-09-577-304A-215	Sequence 215, App
C 142	95.5	7.1	852	4	US-09-252-991A-7607	Sequence 7607, App	215	92.5	6.9	2526	4	US-09-577-304A-215	Sequence 215, App
C 143	95.5	7.1	1452	4	US-09-252-991A-3933	Sequence 3933, App	216	92.5	6.9	2526	4	US-09-577-304A-258	Sequence 258, App
C 144	95.5	7.1	1794	5	US-09-902-540-947	Sequence 947, App	217	92.5	6.9	2526	4	US-09-777-430C-14	Sequence 14, Appli
C 145	95.5	7.1	1794	5	US-09-902-540-947	Sequence 3, Appli	218	92.5	6.9	2526	4	US-09-777-430C-19	Sequence 19, Appli
C 146	95.5	7.1	1977	4	US-09-902-540-4798	Sequence 4798, App	219	92.5	6.9	2526	4	US-09-777-430C-22	Sequence 22, Appli
C 147	95.5	7.1	3048	5	US-09-902-540-4798	Sequence 1, Appli	220	92.5	6.9	2526	4	US-09-777-430C-25	Sequence 25, Appli
C 148	95.5	7.1	3048	5	US-09-902-540-4798	Sequence 1, Appli	221	92	6.9	1407	4	US-09-252-991A-13018	Sequence 13018, A
C 149	95.5	7.1	4284	4	US-09-252-991A-4006	Sequence 4006, App	222	92	6.9	2558	4	US-09-902-540-6342	Sequence 6342, App
C 150	95.5	7.1	29103	4	US-09-902-540-1236	Sequence 1236, App	223	92	6.9	2560	4	US-09-902-540-8919	Sequence 8919, App
C 151	95	7.1	3810	4	US-09-902-540-3021	Sequence 3021, App	224	92	6.9	6645	4	US-09-902-540-8919	Sequence 8919, App
C 152	95	7.1	3812	4	US-09-902-540-641	Sequence 641, App	225	92	6.9	10210	4	US-09-902-540-938	Sequence 938, App
C 153	95	7.1	13579	4	US-09-902-540-1101	Sequence 1101, App	226	92	6.9	67156	4	US-09-949-016-12284	Sequence 12284, A
C 154	94.5	7.0	1638	4	US-09-902-540-8744	Sequence 8744, App	227	92	6.9	67157	4	US-09-949-016-15558	Sequence 15558, A
C 155	94.5	7.0	2304	1	US-08-464-266-1	Sequence 1, Appli	228	91.5	6.8	1197	4	US-09-252-991A-6737	Sequence 6737, App
C 156	94.5	7.0	2304	1	US-08-464-272-1	Sequence 1, Appli	229	91.5	6.8	1272	4	US-09-252-991A-6952	Sequence 6952, App
C 157	94.5	7.0	2304	3	US-08-464-514-1	Sequence 1, Appli	230	91.5	6.8	2346	4	US-09-252-991A-6782	Sequence 6782, App
C 158	94.5	7.0	2304	3	US-08-486-403-1	Sequence 1, Appli	231	91.5	6.8	2499	4	US-09-758-282B-94	Sequence 94, Appli

C 232	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl	C 305	88.5	6.6	1455	4	US-09-252-991A-158	Sequence 158, App
C 233	91.5	6.8	2505	1	US-07-977-434-9	Sequence 9, Appl1	306	88.5	6.6	1566	4	US-09-902-540-7706	Sequence 7706, App
C 234	91.5	6.8	2505	1	US-08-458-819-9	Sequence 9, Appl1	307	88.5	6.6	1696	4	US-09-774-528-151	Sequence 151, App
C 235	91.5	6.8	2505	4	US-09-684-938-159	Sequence 159, App	308	88.5	6.6	2413	3	US-09-367-206-2	Sequence 2, Appl1
C 236	91.5	6.8	2505	4	US-09-308-825A-159	Sequence 159, App	309	88.5	6.6	2507	2	US-08-471-066B-1	Sequence 1, Appl1
C 237	91.5	6.8	2505	4	US-09-758-282B-266	Sequence 266, App	310	88.5	6.6	2511	4	US-09-252-991A-9132	Sequence 9132, App
C 238	91.5	6.8	2505	4	US-09-577-304A-266	Sequence 266, App	311	88.5	6.6	2670	4	US-09-902-540-517	Sequence 517, App
C 239	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appl1	312	88.5	6.6	3916	4	US-09-902-540-463	Sequence 463, App
C 240	91.5	6.8	2511	4	US-09-684-938-161	Sequence 161, App	313	88.5	6.6	6611	4	US-09-902-540-762	Sequence 762, App
C 241	91.5	6.8	2511	4	US-09-308-825A-161	Sequence 161, App	314	88.5	6.6	30350	4	US-10-118-328-3	Sequence 3, Appl1
C 242	91.5	6.8	2511	4	US-09-758-282B-3	Sequence 3, Appl1	315	88.5	6.6	35614	4	US-09-902-540-1259	Sequence 1259, App
C 243	91.5	6.8	2511	4	US-09-577-304A-3	Sequence 3, Appl1	316	88	6.6	1446	4	US-09-902-540-5188	Sequence 5188, App
C 244	91.5	6.8	2511	4	US-09-777-430C-9	Sequence 9, Appl1	317	88	6.6	1530	4	US-09-902-540-8329	Sequence 8329, App
C 245	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl	318	88	6.6	2517	4	US-09-902-540-235	Sequence 235, App
C 246	91.5	6.8	2640	1	US-08-459-383-30	Sequence 30, Appl	319	88	6.6	2517	4	US-09-577-304A-235	Sequence 235, App
C 247	91.5	6.8	2943	4	US-09-379-530B-4	Sequence 4, Appl1	320	88	6.6	7518	4	US-09-902-540-870	Sequence 870, App
C 248	91.5	6.8	3006	4	US-09-252-991A-9720	Sequence 9720, App	321	88	6.6	8604	4	US-09-902-540-5331	Sequence 5331, App
C 249	91.5	6.8	3660	4	US-09-252-991A-12269	Sequence 12269, App	322	88	6.6	29899	4	US-09-902-540-1365	Sequence 1265, App
C 250	91.5	6.8	5226	4	US-09-902-540-3953	Sequence 3953, App	323	88	6.6	34199	4	US-09-902-540-1365	Sequence 1265, App
C 251	91.5	6.8	9556	4	US-09-902-540-929	Sequence 929, App	324	88	6.6	35399	4	US-09-902-540-1260	Sequence 1260, App
C 252	91.5	6.8	22156	4	US-09-902-540-1195	Sequence 1195, App	325	88	6.6	36171	4	US-09-949-016-13876	Sequence 13876, App
C 253	91	6.8	906	4	US-09-489-039A-3080	Sequence 3080, App	326	88	6.6	36274	4	US-09-949-016-13876	Sequence 13876, App
C 254	91	6.8	966	4	US-09-252-991A-13273	Sequence 13273, App	327	87.5	6.5	669	4	US-09-902-540-7715	Sequence 7715, App
C 255	91	6.8	1083	4	US-09-252-991A-7327	Sequence 7327, App	328	87.5	6.5	849	4	US-09-252-991A-617	Sequence 617, App
C 256	91	6.8	1200	4	US-09-252-991A-14709	Sequence 14709, App	329	87.5	6.5	1062	4	US-09-902-540-3096	Sequence 3096, App
C 257	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, App	330	87.5	6.5	1575	4	US-09-252-991A-3100	Sequence 3100, App
C 258	91	6.8	1299	4	US-09-252-991A-14277	Sequence 14277, App	331	87.5	6.5	1866	4	US-09-252-991A-16213	Sequence 16213, App
C 259	91	6.8	1428	4	US-09-252-991A-13126	Sequence 13126, App	332	87.5	6.5	1956	4	US-09-252-991A-3189	Sequence 3189, App
C 260	91	6.8	1449	4	US-09-252-991A-14921	Sequence 14921, App	333	87.5	6.5	2379	4	US-09-252-991A-686	Sequence 686, App
C 261	91	6.8	1515	4	US-09-252-991A-12966	Sequence 12966, App	334	87.5	6.5	2499	4	US-09-252-991A-696	Sequence 696, App
C 262	91	6.8	1824	4	US-09-252-991A-14307	Sequence 14307, App	335	87.5	6.5	2526	4	US-09-577-304A-156	Sequence 156, App
C 263	90.5	6.7	2496	4	US-09-252-991A-13526	Sequence 13526, App	336	87.5	6.5	2655	4	US-09-902-540-6674	Sequence 6674, App
C 264	90.5	6.7	2526	4	US-09-758-282B-159	Sequence 159, App	337	87.5	6.5	2655	4	US-09-902-540-523	Sequence 523, App
C 265	90.5	6.7	2526	4	US-09-577-304A-159	Sequence 159, App	338	87.5	6.5	3798	4	US-09-902-540-523	Sequence 523, App
C 266	90.5	6.7	2622	4	US-09-252-991A-13933	Sequence 13933, App	339	87.5	6.5	10059	4	US-09-949-016-16323	Sequence 16323, App
C 267	90.5	6.7	3065	3	US-09-171-710-3	Sequence 3, Appl1	340	87.5	6.5	14634	4	US-09-949-016-17384	Sequence 17384, App
C 268	90.5	6.7	9198	4	US-09-902-540-966	Sequence 966, App	341	87.5	6.5	15499	4	US-09-902-540-1140	Sequence 1140, App
C 269	90.5	6.7	14555	4	US-09-902-540-1096	Sequence 1096, App	342	87.5	6.5	28783	4	US-09-902-540-1242	Sequence 1242, App
C 270	90.5	6.7	1629	4	US-09-614-912-203	Sequence 203, App	343	87.5	6.5	34316	4	US-09-902-540-1257	Sequence 1257, App
C 271	90	6.7	1069	4	US-09-902-540-6825	Sequence 6825, App	344	87.5	6.5	57267	4	US-09-949-016-11899	Sequence 11899, App
C 272	90	6.7	1702	4	US-09-902-540-5141	Sequence 5141, App	345	87.5	6.5	101015	4	US-09-949-016-16981	Sequence 16981, App
C 273	90	6.7	1701	4	US-09-902-540-5141	Sequence 5141, App	346	87	6.5	720	4	US-09-902-540-4895	Sequence 4895, App
C 274	90	6.7	1929	4	US-09-252-991A-7017	Sequence 7017, App	347	87	6.5	930	4	US-09-252-991A-6618	Sequence 6618, App
C 275	90	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App	348	87	6.5	1074	4	US-09-351-150A-36	Sequence 36, Appl
C 276	90	6.7	4407	4	US-09-902-540-569	Sequence 569, App	349	87	6.5	11508	4	US-09-252-991A-14214	Sequence 14214, App
C 277	90	6.7	6404	4	US-09-902-540-760	Sequence 760, App	350	87	6.5	1308	4	US-09-252-991A-6649	Sequence 6649, App
C 278	90	6.7	11854	4	US-09-902-540-1037	Sequence 1037, App	351	87	6.5	1353	4	US-09-902-540-4241	Sequence 4241, App
C 279	90	6.7	19112	4	US-09-902-540-1181	Sequence 1181, App	352	87	6.5	1377	4	US-09-351-150A-12	Sequence 12, Appl
C 280	90	6.7	32666	4	US-09-949-016-16086	Sequence 16086, App	353	87	6.5	1535	1	US-08-910-973-10	Sequence 10, Appl
C 281	89.5	6.7	962	3	US-08-765-907A-16	Sequence 16, Appl	354	87	6.5	1535	3	US-09-499-227-10	Sequence 10, Appl
C 282	89.5	6.7	962	4	US-09-987-614A-16	Sequence 16, Appl	355	87	6.5	1625	4	US-09-799-451-594	Sequence 594, App
C 283	89.5	6.7	1052	2	US-08-403-852D-10	Sequence 10, Appl	356	87	6.5	1650	4	US-09-252-991A-10150	Sequence 10150, App
C 284	89.5	6.7	1052	3	US-08-510-646B-10	Sequence 10, Appl	357	87	6.5	1725	4	US-09-252-991A-9926	Sequence 9926, App
C 285	89.5	6.7	1052	3	US-09-231-818-10	Sequence 10, Appl	358	87	6.5	2145	4	US-09-252-991A-13235	Sequence 13235, App
C 286	89.5	6.7	1052	4	US-09-635-359B-10	Sequence 10, Appl	359	87	6.5	3390	4	US-09-489-039A-3029	Sequence 3029, App
C 287	89.5	6.7	1366	4	US-09-252-991A-13397	Sequence 13397, App	360	87	6.5	3741	4	US-09-252-991A-6569	Sequence 6569, App
C 288	89.5	6.7	1359	4	US-09-252-991A-13492	Sequence 13492, App	361	87	6.5	4431	4	US-09-252-991A-12856	Sequence 12856, App
C 289	89.5	6.7	1605	4	US-09-252-991A-3610	Sequence 3610, App	362	87	6.5	4455	4	US-09-902-540-7119	Sequence 7119, App
C 290	89.5	6.7	2019	4	US-09-902-540-9185	Sequence 9185, App	363	87	6.5	4458	4	US-09-902-540-650	Sequence 650, App
C 291	89.5	6.7	3270	4	US-09-252-991A-3763	Sequence 3763, App	364	87	6.5	7463	4	US-09-902-540-928	Sequence 928, App
C 292	89.5	6.7	9556	4	US-09-902-540-982	Sequence 982, App	365	87	6.5	10095	3	US-08-822-586-45	Sequence 45, Appl
C 293	89.5	6.7	25686	4	US-09-902-540-1246	Sequence 1246, App	366	87	6.5	16448	4	US-09-902-540-9686	Sequence 9686, App
C 294	89	6.6	5481	4	US-09-902-540-7351	Sequence 7351, App	367	87	6.5	16450	4	US-09-902-540-1098	Sequence 1098, App
C 295	89	6.6	6402	4	US-09-902-540-702	Sequence 702, App	368	87	6.5	19598	4	US-09-902-540-1143	Sequence 1143, App
C 296	89	6.6	9369	4	US-10-237-551-190	Sequence 190, App	369	87	6.5	24494	4	US-09-351-150A-1	Sequence 1, Appl
C 297	89	6.6	9369	4	US-10-237-551-247	Sequence 247, App	370	87	6.5	28493	4	US-09-902-540-1241	Sequence 1241, App
C 298	88.5	6.6	969	4	US-09-252-991A-8841	Sequence 8841, App	371	86.5	6.4	888	4	US-09-540-236-1514	Sequence 1514, App
C 299	88.5	6.6	1008	4	US-09-252-991A-8953	Sequence 8953, App	372	86.5	6.4	1043	4	US-09-902-540-2570	Sequence 2570, App
C 300	88.5	6.6	1035	4	US-09-252-991A-185	Sequence 185, App	373	86.5	6.4	1086	4	US-09-252-991A-11554	Sequence 11554, App
C 301	88.5	6.6	1074	4	US-09-252-991A-162	Sequence 162, App	374	86.5	6.4	1251	4	US-09-252-991A-3770	Sequence 3770, App
C 302	88.5	6.6	1293	4	US-09-252-991A-12484	Sequence 12484, App	375	86.5	6.4	1368	4	US-09-902-540-8624	Sequence 8624, App
C 303	88.5	6.6	1305	4	US-09-902-540-6655	Sequence 6655, App	376	86.5	6.4	1425	4	US-09-252-991A-6019	Sequence 6019, App
C 304	88.5	6.6	1422	4	US-09-252-991A-12989	Sequence 12989, App	377	86.5	6.4	1643	4	US-09-902-540-6808	Sequence 6808, App

378	86.5	6.4	1707	4	US-09-489-039A-2690	Sequence 2690, Ap	451	84.5	6.3	1524	4	US-09-252-991A-9472	Sequence 9472, Ap
379	86.5	6.4	1399	4	US-09-252-991A-6290	Sequence 6290, Ap	452	84.5	6.3	2406	4	US-09-252-991A-11299	Sequence 11299, A
380	86.5	6.4	1299	4	US-09-252-991A-726	Sequence 726, App	c 453	84.5	6.3	2517	4	US-09-758-282B-80	Sequence 80, Appl
381	86.5	6.4	2625	4	US-09-902-540-8554	Sequence 8554, Ap	c 454	84.5	6.3	2517	4	US-09-577-304A-80	Sequence 80, Appl
382	86.5	6.4	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	c 455	84.5	6.3	2526	4	US-09-758-282B-92	Sequence 92, Appl
383	86.5	6.4	4282	4	US-09-902-540-563	Sequence 563, App	c 456	84.5	6.3	2526	4	US-09-577-304A-92	Sequence 92, Appl
384	86.5	6.4	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	c 457	84.5	6.3	3162	4	US-09-902-540-373	Sequence 373, App
385	86.5	6.4	7001	1	US-08-258-261B-1	Sequence 1, Appl	c 458	84.5	6.3	3358	3	US-09-248-571-2	Sequence 2, Appl
386	86.5	6.4	7001	1	US-08-456-837-1	Sequence 1, Appl	c 459	84.5	6.3	3358	3	US-09-553-736-2	Sequence 2, Appl
387	86.5	6.4	7001	1	US-08-457-342-1	Sequence 1, Appl	c 460	84.5	6.3	8614	4	US-09-502-540-787	Sequence 787, App
388	86.5	6.4	7001	1	US-08-457-646A-1	Sequence 1, Appl	c 461	84.5	6.3	8773	4	US-09-902-540-955	Sequence 955, App
389	86.5	6.4	7001	1	US-08-458-076A-1	Sequence 1, Appl	c 462	84.5	6.3	10178	4	US-09-902-540-977	Sequence 977, App
390	86.5	6.4	7001	1	US-08-457-335A-1	Sequence 1, Appl	c 463	84.5	6.3	19455	4	US-09-902-540-1147	Sequence 1147, Ap
391	86.5	6.4	7001	1	US-08-761-258-6	Sequence 6, Appl	464	84.5	6.3	22311	4	US-09-949-016-12344	Sequence 12344, A
392	86.5	6.4	7001	1	US-08-729-214-1	Sequence 1, Appl	465	84.5	6.3	22312	4	US-09-949-016-17217	Sequence 17217, A
393	86.5	6.4	7001	2	US-08-977-306-6	Sequence 6, Appl	c 465	84.5	6.3	34446	3	US-09-103-330-35	Sequence 35, Appl
394	86.5	6.4	7001	3	US-09-028-934-1	Sequence 1, Appl	467	84.5	6.3	49225	4	US-09-902-540-1269	Sequence 1269, Ap
395	86.5	6.4	7562	4	US-09-902-540-902	Sequence 902, App	468	84.5	6.3	146307	4	US-09-949-016-14881	Sequence 14881, A
396	86.5	6.4	7982	4	US-09-902-540-911	Sequence 911, App	469	84.5	6.3	146307	4	US-09-949-016-14882	Sequence 14882, A
397	86.5	6.4	8037	4	US-09-774-528-209	Sequence 209, App	470	84.5	6.3	146307	4	US-09-949-016-14883	Sequence 14883, A
398	86.5	6.4	13855	4	US-09-902-540-1117	Sequence 1117, Ap	471	84.5	6.3	146307	4	US-09-949-016-14884	Sequence 14884, A
399	86.5	6.4	19068	4	US-09-902-540-1123	Sequence 1123, Ap	472	84.5	6.3	146307	4	US-09-949-016-14885	Sequence 14885, A
c 400	86.5	6.4	26640	4	US-09-949-016-17431	Sequence 17431, A	473	84.5	6.3	146307	4	US-09-949-016-14886	Sequence 14886, A
c 401	86.5	6.4	30780	4	US-09-902-540-1243	Sequence 1243, Ap	474	84.5	6.3	146307	4	US-09-949-016-14887	Sequence 14887, A
c 402	86.5	6.4	53500	4	US-09-266-965-76	Sequence 76, Appl	475	84.5	6.3	146307	4	US-09-949-016-14888	Sequence 14888, A
c 403	86.5	6.4	62909	4	US-09-596-002-32	Sequence 32, Appl	476	84.5	6.3	148405	4	US-09-949-016-11747	Sequence 11747, A
c 404	86	6.4	822	4	US-09-252-991A-6178	Sequence 6178, Ap	477	84.5	6.3	148405	4	US-09-949-016-12835	Sequence 12835, A
c 405	86	6.4	1143	4	US-09-902-540-3850	Sequence 3850, Ap	478	84.5	6.3	148405	4	US-09-949-016-12836	Sequence 12836, A
c 406	86	6.4	1221	4	US-09-252-991A-7107	Sequence 7107, Ap	479	84.5	6.3	148405	4	US-09-949-016-12837	Sequence 12837, A
c 407	86	6.4	1488	4	US-09-252-991A-9231	Sequence 9231, Ap	480	84	6.3	314	3	US-09-060-756-582	Sequence 582, App
c 408	86	6.4	2019	4	US-09-252-991A-8818	Sequence 8818, Ap	481	84	6.3	314	4	US-09-583-110-637	Sequence 637, App
c 409	86	6.4	2094	4	US-09-252-991A-7438	Sequence 7438, Ap	482	84	6.3	759	4	US-09-583-110-637	Sequence 637, App
c 410	86	6.4	2517	4	US-09-758-282B-174	Sequence 174, App	483	84	6.3	780	4	US-09-902-540-2969	Sequence 2969, Ap
c 411	86	6.4	2517	4	US-09-577-304A-174	Sequence 174, App	484	84	6.3	971	1	US-08-253-155A-11	Sequence 11, Appl
c 412	86	6.4	2814	4	US-09-252-991A-15765	Sequence 15765, A	c 485	84	6.3	1065	4	US-09-252-991A-16320	Sequence 16320, A
c 413	86	6.4	2937	4	US-09-902-540-6675	Sequence 6675, Ap	486	84	6.3	1332	4	US-09-252-991A-15961	Sequence 15961, A
c 414	86	6.4	3012	4	US-09-252-991A-7498	Sequence 7498, Ap	c 487	84	6.3	1341	4	US-09-252-991A-16544	Sequence 16544, A
415	86	6.4	3357	4	US-09-252-991A-15868	Sequence 15868, A	c 488	84	6.3	1405	1	US-08-035-558-3	Sequence 3, Appl
416	86	6.4	3550	4	US-09-902-540-524	Sequence 524, App	c 489	84	6.3	1405	2	US-08-682-847-5	Sequence 5, Appl
417	86	6.4	10528	4	US-09-902-540-945	Sequence 945, App	c 490	84	6.3	1405	3	US-09-063-676-1	Sequence 1, Appl
418	86	6.4	20740	4	US-09-902-540-1223	Sequence 1223, Ap	c 491	84	6.3	1407	1	US-09-902-540-4833	Sequence 4833, Ap
419	86	6.4	21964	4	US-09-902-540-1190	Sequence 1190, Ap	492	84	6.3	1785	1	US-07-865-662F-4	Sequence 4, Appl
c 420	86	6.4	47981	4	US-09-679-279-1	Sequence 1, Appl	493	84	6.3	1785	3	US-08-374-219B-4	Sequence 4, Appl
c 421	85.5	6.4	909	4	US-09-252-991A-12929	Sequence 12929, A	494	84	6.3	2055	4	US-09-252-991A-1845	Sequence 1845, Ap
c 422	85.5	6.4	1047	4	US-09-902-540-4239	Sequence 4239, Ap	495	84	6.3	2067	4	US-09-252-991A-1398	Sequence 1398, Ap
c 423	85.5	6.4	1269	4	US-09-252-991A-8698	Sequence 8698, Ap	c 496	84	6.3	2100	4	US-09-252-991A-1209	Sequence 1209, Ap
c 424	85.5	6.4	1344	4	US-09-252-991A-9081	Sequence 9081, Ap	c 497	84	6.3	2480	4	US-09-064-199-15	Sequence 15, Appl
c 425	85.5	6.4	17622	4	US-09-902-540-1125	Sequence 1125, Ap	498	84	6.3	2595	4	US-09-902-540-3202	Sequence 3202, Ap
c 426	85.5	6.4	29598	3	US-09-341-587-6	Sequence 6, Appl	499	84	6.3	3393	1	US-08-295-502-1	Sequence 1, Appl
c 427	85.5	6.4	106929	4	US-09-949-016-12060	Sequence 12060, A	500	84	6.3	3393	5	PCT-US95-10691-1	Sequence 1, Appl
c 428	85.5	6.4	106929	4	US-09-949-016-16618	Sequence 16618, A	501	84	6.3	4346	4	US-09-064-199-12	Sequence 12, Appl
c 429	85.5	6.4	152481	4	US-09-949-016-12521	Sequence 12521, A	502	84	6.3	4366	4	US-09-064-199-14	Sequence 14, Appl
c 430	85.5	6.4	152798	4	US-09-949-016-12775	Sequence 12775, A	503	84	6.3	4418	4	US-09-064-199-13	Sequence 13, Appl
c 431	85.5	6.4	152822	4	US-09-949-016-17519	Sequence 17519, A	504	84	6.3	4431	4	US-09-064-199-8	Sequence 8, Appl
c 432	85.5	6.4	152822	4	US-09-949-016-17519	Sequence 17519, A	505	84	6.3	4441	3	US-09-641-999-2	Sequence 2, Appl
c 433	85.5	6.4	157866	4	US-09-949-016-12982	Sequence 12982, A	506	84	6.3	4441	4	US-09-064-199-10	Sequence 10, Appl
c 434	85.5	6.4	157866	4	US-09-949-016-12983	Sequence 12983, A	507	84	6.3	4543	2	US-08-519-547A-5	Sequence 5, Appl
c 435	85.5	6.4	157866	4	US-09-949-016-12984	Sequence 12984, A	508	84	6.3	4549	4	US-09-064-199-9	Sequence 9, Appl
c 436	85	6.3	666	4	US-09-252-991A-7202	Sequence 7202, Ap	509	84	6.3	4564	4	US-09-064-199-2	Sequence 2, Appl
c 437	85	6.3	798	4	US-09-543-681A-2640	Sequence 2640, Ap	510	84	6.3	4649	4	US-09-064-199-11	Sequence 11, Appl
c 438	85	6.3	984	4	US-09-902-540-3562	Sequence 3562, Ap	511	84	6.3	4746	4	US-09-064-199-7	Sequence 7, Appl
c 439	85	6.3	1902	4	US-09-902-540-8758	Sequence 8758, Ap	512	84	6.3	5105	4	US-09-064-199-3	Sequence 3, Appl
c 440	85	6.3	16924	4	US-09-902-540-1178	Sequence 1178, Ap	513	84	6.3	5463	4	US-09-064-199-1	Sequence 1, Appl
c 441	85	6.3	19019	4	US-09-902-540-1171	Sequence 1171, Ap	514	84	6.3	7404	4	US-09-902-540-3115	Sequence 3115, Ap
c 442	85	6.3	21296	4	US-09-949-016-14504	Sequence 14504, A	515	84	6.3	7734	4	US-09-949-016-1095	Sequence 1095, Ap
c 443	85	6.3	21296	4	US-09-949-016-14505	Sequence 14505, A	516	84	6.3	8145	4	US-09-949-016-1093	Sequence 1093, Ap
c 444	85	6.3	21296	4	US-09-949-016-15701	Sequence 15701, A	517	84	6.3	8220	4	US-09-949-016-1094	Sequence 1094, Ap
c 445	85	6.3	21296	4	US-09-949-016-15702	Sequence 15702, A	518	84	6.3	8280	4	US-09-949-016-5	Sequence 5, Appl
c 446	85	6.3	23496	4	US-09-902-540-5645	Sequence 5645, Ap	519	84	6.3	8738	4	US-09-902-540-873	Sequence 873, App
c 447	85	6.3	25254	4	US-09-902-540-1233	Sequence 1233, Ap	c 520	84	6.3	9054	4	US-09-949-016-13588	Sequence 13588, A
c 448	85	6.3	51354	4	US-09-902-540-1270	Sequence 1270, Ap	521	84	6.3	10391	4	US-09-902-540-958	Sequence 958, App
c 449	85	6.3	536165	4	US-09-214-808-1	Sequence 1, Appl	522	84	6.3	15644	4	US-09-902-540-1133	Sequence 1133, Ap
c 450	84.5	6.3	1260	4	US-09-252-991A-6317	Sequence 6317, Ap	c 523	84	6.3	18809	4	US-09-902-540-1141	Sequence 1141, Ap



524	84	6.3	19455	4	US-09-902-540-1147	Sequence 1147, Ap	597	83	6.2	43380	2	US-08-804-227C-1	Sequence 1, Appli
525	84	6.3	24741	4	US-09-949-016-15547	Sequence 15547, A	598	83	6.2	77826	4	US-09-949-016-12608	Sequence 12608, A
526	84	6.3	25733	4	US-09-902-540-1215	Sequence 1215, Ap	599	82.5	6.1	651	4	US-09-252-991A-2095	Sequence 2095, Ap
527	84	6.3	26012	4	US-09-902-540-1212	Sequence 1212, Ap	600	82.5	6.1	786	4	US-09-902-540-5164	Sequence 5164, Ap
528	84	6.3	26659	4	US-09-902-540-1237	Sequence 1237, Ap	c 601	82.5	6.1	816	4	US-09-252-991A-507	Sequence 507, App
529	84	6.3	27219	4	US-09-902-540-1244	Sequence 1244, Ap	602	82.5	6.1	930	4	US-09-902-540-8427	Sequence 8427, Ap
530	84	6.3	27579	4	US-09-949-016-13465	Sequence 13465, A	c 603	82.5	6.1	957	4	US-09-252-991A-6278	Sequence 6278, Ap
531	84	6.3	42232	4	US-09-949-016-11917	Sequence 11917, A	604	82.5	6.1	1209	4	US-09-252-991A-572	Sequence 572, App
532	84	6.3	42234	4	US-09-949-016-13705	Sequence 13705, A	605	82.5	6.1	1245	4	US-09-252-991A-594	Sequence 594, App
533	84	6.3	46603	4	US-09-949-016-15636	Sequence 15636, A	606	82.5	6.1	1623	4	US-09-613-303-3	Sequence 3, Appli
534	83.5	6.2	601	4	US-09-949-016-171096	Sequence 171096,	607	82.5	6.1	1623	4	US-10-267-311-3	Sequence 3, Appli
535	83.5	6.2	601	4	US-09-949-016-171226	Sequence 171226,	608	82.5	6.1	1764	4	US-09-252-991A-6133	Sequence 6133, Ap
536	83.5	6.2	1107	4	US-09-902-540-8772	Sequence 8772, Ap	c 609	82.5	6.1	1785	4	US-09-252-991A-4278	Sequence 4278, Ap
537	83.5	6.2	1251	4	US-09-252-991A-8004	Sequence 8004, Ap	610	82.5	6.1	1879	4	US-09-614-748A-10	Sequence 10, Appli
538	83.5	6.2	1308	4	US-09-252-991A-7182	Sequence 7182, Ap	611	82.5	6.1	1886	1	US-07-980-526-1	Sequence 10, Appli
539	83.5	6.2	1344	4	US-09-252-991A-6363	Sequence 6363, Ap	612	82.5	6.1	1920	4	US-09-613-303-16	Sequence 16, Appli
540	83.5	6.2	1550	3	US-09-234-332-3	Sequence 3, Appli	613	82.5	6.1	1920	4	US-10-267-311-16	Sequence 16, Appli
541	83.5	6.2	1671	4	US-09-252-991A-6188	Sequence 6188, Ap	614	82.5	6.1	1947	4	US-09-613-303-28	Sequence 28, Appli
542	83.5	6.2	1767	1	US-08-399-646-1	Sequence 1, Appli	615	82.5	6.1	1947	4	US-10-267-311-28	Sequence 28, Appli
543	83.5	6.2	1767	1	US-08-607-321-1	Sequence 1, Appli	c 616	82.5	6.1	1956	4	US-09-252-991A-12032	Sequence 12032, A
544	83.5	6.2	1767	2	US-08-961-240-1	Sequence 1, Appli	617	82.5	6.1	2017	4	US-09-614-748A-8	Sequence 8, Appli
545	83.5	6.2	1767	2	US-08-605-501-1	Sequence 1, Appli	c 618	82.5	6.1	2067	4	US-09-252-991A-527	Sequence 527, App
546	83.5	6.2	1854	4	US-09-902-540-17177	Sequence 1717, Ap	619	82.5	6.1	2499	4	US-09-758-282B-96	Sequence 96, Appli
547	83.5	6.2	2161	1	US-08-399-646-11	Sequence 11, Appli	c 620	82.5	6.1	2499	4	US-09-577-304A-96	Sequence 96, Appli
548	83.5	6.2	2161	1	US-08-607-321-11	Sequence 11, Appli	c 621	82.5	6.1	2517	4	US-09-758-282B-78	Sequence 78, Appli
549	83.5	6.2	2161	2	US-08-961-240-11	Sequence 11, Appli	c 622	82.5	6.1	2517	4	US-09-758-282B-84	Sequence 84, Appli
550	83.5	6.2	2161	2	US-08-605-501-11	Sequence 11, Appli	c 623	82.5	6.1	2517	4	US-09-758-282B-86	Sequence 86, Appli
551	83.5	6.2	2484	4	US-09-252-991A-7462	Sequence 7462, Ap	c 624	82.5	6.1	2517	4	US-09-758-282B-102	Sequence 102, App
552	83.5	6.2	2499	4	US-09-758-282B-98	Sequence 98, Appli	c 625	82.5	6.1	2517	4	US-09-758-282B-105	Sequence 105, App
553	83.5	6.2	2499	4	US-09-577-304A-98	Sequence 98, Appli	c 626	82.5	6.1	2517	4	US-09-758-282B-108	Sequence 108, App
554	83.5	6.2	3251	3	US-09-085-199B-6	Sequence 6, Appli	c 627	82.5	6.1	2517	4	US-09-758-282B-111	Sequence 111, App
555	83.5	6.2	3876	4	US-09-849-602-4	Sequence 4, Appli	c 628	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App
556	83.5	6.2	4162	4	US-09-902-540-664	Sequence 664, App	c 629	82.5	6.1	2517	4	US-09-577-304A-78	Sequence 78, Appli
557	83.5	6.2	7515	4	US-09-949-016-583	Sequence 583, App	c 630	82.5	6.1	2517	4	US-09-577-304A-84	Sequence 84, Appli
558	83.5	6.2	9185	4	US-09-902-540-931	Sequence 931, App	c 631	82.5	6.1	2517	4	US-09-577-304A-86	Sequence 86, Appli
559	83.5	6.2	11219	1	US-07-642-734C-1	Sequence 1, Appli	c 632	82.5	6.1	2517	4	US-09-577-304A-102	Sequence 102, App
560	83.5	6.2	11219	3	US-08-439-009A-1	Sequence 1, Appli	c 633	82.5	6.1	2517	4	US-09-577-304A-105	Sequence 105, App
561	83.5	6.2	11706	4	US-09-902-540-1038	Sequence 1038, Ap	c 634	82.5	6.1	2517	4	US-09-577-304A-108	Sequence 108, App
562	83.5	6.2	13624	4	US-09-902-540-1053	Sequence 1053, Ap	c 635	82.5	6.1	2517	4	US-09-577-304A-111	Sequence 111, App
563	83.5	6.2	14018	4	US-09-949-016-17114	Sequence 17114, A	c 636	82.5	6.1	2517	4	US-09-577-304A-135	Sequence 135, App
564	83.5	6.2	112807	4	US-09-949-016-12420	Sequence 12420, A	c 637	82.5	6.1	2526	4	US-09-758-282B-90	Sequence 90, Appli
565	83.5	6.2	112807	4	US-09-949-016-12794	Sequence 12794, A	c 638	82.5	6.1	2526	4	US-09-577-304A-90	Sequence 90, Appli
566	83.5	6.2	112808	4	US-09-949-016-16589	Sequence 16589, A	639	82.5	6.1	2766	4	US-09-252-991A-3756	Sequence 3756, Ap
567	83.5	6.2	112808	4	US-09-949-016-16590	Sequence 16590, A	640	82.5	6.1	2847	4	US-09-613-303-20	Sequence 20, Appli
568	83	6.2	774	4	US-09-252-991A-13331	Sequence 13331, A	641	82.5	6.1	2847	4	US-10-267-311-20	Sequence 20, Appli
569	83	6.2	924	4	US-09-902-540-3612	Sequence 3612, Ap	642	82.5	6.1	2874	4	US-09-252-991A-3837	Sequence 3837, Ap
570	83	6.2	933	4	US-09-252-991A-10917	Sequence 10917, A	643	82.5	6.1	3390	4	US-09-252-991A-11981	Sequence 11981, A
571	83	6.2	964	4	US-09-513-999C-14934	Sequence 14934, A	644	82.5	6.1	4380	3	US-08-955-565A-3	Sequence 3, Appli
572	83	6.2	1152	4	US-09-252-991A-5237	Sequence 5237, Ap	645	82.5	6.1	6553	4	US-09-902-540-885	Sequence 885, App
573	83	6.2	1617	3	US-09-265-013-2	Sequence 2, Appli	646	82.5	6.1	6553	4	US-09-949-016-15370	Sequence 15370, A
574	83	6.2	1660	4	US-09-902-540-378	Sequence 378, App	647	82.5	6.1	15923	4	US-09-902-540-1095	Sequence 1095, Ap
575	83	6.2	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	648	82.5	6.1	18551	4	US-09-902-540-1187	Sequence 1187, Ap
576	83	6.2	2046	4	US-09-252-991A-5266	Sequence 5266, Ap	649	82.5	6.1	28804	2	US-08-592-874-1	Sequence 1, Appli
577	83	6.2	2328	4	US-09-252-991A-11890	Sequence 11890, A	c 650	82.5	6.1	28804	3	US-09-096-942-2	Sequence 2, Appli
578	83	6.2	4143	4	US-09-252-991A-9151	Sequence 9151, Ap	c 651	82.5	6.1	28804	3	US-09-096-942-2	Sequence 2, Appli
579	83	6.2	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	c 652	82.5	6.1	125672	4	US-09-949-016-16956	Sequence 16956, A
580	83	6.2	4430	4	US-09-902-540-491	Sequence 491, App	653	82	6.1	780	1	US-09-107-433-1646	Sequence 1646, Ap
581	83	6.2	7308	3	US-09-011-745-3	Sequence 3, Appli	654	82	6.1	789	1	US-08-181-335B-3	Sequence 3, Appli
582	83	6.2	7308	3	US-09-011-745-4	Sequence 4, Appli	655	82	6.1	789	1	US-08-181-335B-5	Sequence 5, Appli
583	83	6.2	7616	3	US-09-011-745-2	Sequence 2, Appli	656	82	6.1	789	1	US-08-181-335B-6	Sequence 6, Appli
584	83	6.2	8202	1	US-08-258-420-13	Sequence 13, Appli	657	82	6.1	789	5	PCT-US95-00129-3	Sequence 3, Appli
585	83	6.2	8332	3	US-08-850-961-1	Sequence 1, Appli	658	82	6.1	789	5	PCT-US95-00129-5	Sequence 5, Appli
586	83	6.2	8332	3	US-09-479-776-1	Sequence 1, Appli	659	82	6.1	789	5	PCT-US95-00129-6	Sequence 6, Appli
587	83	6.2	8332	3	US-09-309-572-11	Sequence 11, Appli	660	82	6.1	852	4	US-09-252-991A-6125	Sequence 6125, Ap
588	83	6.2	8332	3	US-09-315-127-1	Sequence 1, Appli	c 661	82	6.1	1068	4	US-09-252-991A-6432	Sequence 6432, Ap
589	83	6.2	8332	3	US-09-265-013-1	Sequence 1, Appli	662	82	6.1	1218	4	US-09-902-540-9113	Sequence 9113, Ap
590	83	6.2	8332	4	US-09-554-572-25	Sequence 25, Appli	663	82	6.1	1237	4	US-09-902-540-9113	Sequence 2125, Ap
591	83	6.2	8332	4	US-09-718-096-11	Sequence 11, Appli	664	82	6.1	1665	4	US-09-902-540-7864	Sequence 7864, Ap
592	83	6.2	8332	4	US-09-001-039B-15	Sequence 15, Appli	665	82	6.1	1737	4	US-09-252-991A-2085	Sequence 2085, Ap
593	83	6.2	18848	4	US-09-902-540-1174	Sequence 1174, Ap	666	82	6.1	1761	4	US-09-902-540-3727	Sequence 3727, Ap
594	83	6.2	26104	4	US-09-949-016-14045	Sequence 14045, A	c 667	82	6.1	2517	4	US-09-758-282B-138	Sequence 138, App
595	83	6.2	35399	4	US-09-902-540-1260	Sequence 1260, Ap	c 668	82	6.1	2517	4	US-09-577-304A-138	Sequence 138, App
596	83	6.2	42450	4	US-09-815-048-3	Sequence 3, Appli	669	82	6.1	2667	4	US-09-902-540-9380	Sequence 9380, Ap

670	82	6.1	3186	4	US-09-489-039A-5569	Sequence 5569, Ap	c 743	81	6.0	2499	1	US-08-458-819-1	Sequence 1, Appli
671	82	6.1	3236	3	US-08-961-527-222	Sequence 222, App	c 744	81	6.0	2499	3	US-07-602-848E-1	Sequence 1, Appli
672	82	6.1	3378	4	US-09-252-991A-2158	Sequence 2158, Ap	c 745	81	6.0	2499	3	US-09-587-855-1	Sequence 1, Appli
673	82	6.1	3381	4	US-09-902-540-7493	Sequence 7493, Ap	c 746	81	6.0	2499	3	US-09-777-537-1	Sequence 1, Appli
674	82	6.1	3397	4	US-09-902-540-5402	Sequence 5402, Ap	c 747	81	6.0	2499	3	US-09-777-538-1	Sequence 1, Appli
675	82	6.1	4235	4	US-09-902-540-9587	Sequence 9587, Ap	c 748	81	6.0	2499	4	US-09-758-282B-100	Sequence 100, App
676	82	6.1	5661	3	US-08-938-105-2	Sequence 2, Appli	c 749	81	6.0	2499	4	US-09-577-304A-100	Sequence 100, Appl
677	82	6.1	6269	4	US-09-902-540-726	Sequence 726, App	c 750	81	6.0	2499	5	PCT-US91-07035-1	Sequence 1, Appli
678	82	6.1	7861	4	US-09-774-528-305	Sequence 305, App	c 751	81	6.0	2505	2	US-08-757-653-167	Sequence 167, App
679	82	6.1	8820	4	US-09-902-540-974	Sequence 974, App	c 752	81	6.0	2505	2	US-08-823-516-65	Sequence 65, Appl
680	82	6.1	11566	4	US-09-902-540-1088	Sequence 1088, Ap	c 753	81	6.0	2505	3	US-08-759-038-106	Sequence 106, App
681	82	6.1	11566	4	US-09-902-540-1088	Sequence 1088, Ap	c 754	81	6.0	2505	3	US-08-758-314-106	Sequence 106, App
682	82	6.1	12707	4	US-09-949-016-14243	Sequence 14243, A	c 755	81	6.0	2505	4	US-09-684-938-106	Sequence 106, App
683	82	6.1	12707	4	US-09-949-016-14243	Sequence 14243, A	c 756	81	6.0	2505	4	US-09-308-825A-106	Sequence 106, App
684	82	6.1	13027	4	US-09-902-540-1074	Sequence 1074, A	c 757	81	6.0	2505	4	US-09-758-282B-55	Sequence 55, Appl
685	82	6.1	34552	4	US-09-902-540-1262	Sequence 1262, Ap	c 758	81	6.0	2505	4	US-09-940-244-65	Sequence 65, Appl
686	82	6.1	111677	4	US-09-949-016-16946	Sequence 16946, A	c 759	81	6.0	2505	4	US-09-577-304A-55	Sequence 55, Appl
687	81.5	6.1	744	4	US-09-252-991A-15563	Sequence 15563, A	c 760	81	6.0	2506	1	US-08-073-384C-1	Sequence 1, Appli
688	81.5	6.1	837	4	US-09-252-991A-5702	Sequence 5702, Ap	c 761	81	6.0	2506	1	US-08-254-359A-1	Sequence 1, Appli
689	81.5	6.1	1080	4	US-09-248-796A-4099	Sequence 4099, Ap	c 762	81	6.0	2506	1	US-08-483-043-1	Sequence 1, Appli
690	81.5	6.1	1104	4	US-09-902-540-3201	Sequence 3201, Ap	c 763	81	6.0	2506	1	US-08-481-238-1	Sequence 1, Appli
691	81.5	6.1	1161	4	US-09-892-188B-1	Sequence 1, Appli	c 764	81	6.0	2506	2	US-08-484-956-1	Sequence 1, Appli
692	81.5	6.1	1221	4	US-09-252-991A-7990	Sequence 7990, Ap	c 765	81	6.0	2506	2	US-08-757-653-1	Sequence 1, Appli
693	81.5	6.1	1233	4	US-09-252-991A-8268	Sequence 8268, Ap	c 766	81	6.0	2506	2	US-08-599-491-1	Sequence 1, Appli
694	81.5	6.1	1245	4	US-09-252-991A-5725	Sequence 5725, Ap	c 767	81	6.0	2506	2	US-08-756-386-1	Sequence 1, Appli
695	81.5	6.1	1302	4	US-09-252-991A-8677	Sequence 8677, Ap	c 768	81	6.0	2506	2	US-08-823-516-1	Sequence 1, Appli
696	81.5	6.1	1362	4	US-09-252-991A-8259	Sequence 8259, Ap	c 769	81	6.0	2506	3	US-08-682-853A-1	Sequence 1, Appli
697	81.5	6.1	1424	4	US-09-902-540-3125	Sequence 3125, Ap	c 770	81	6.0	2506	3	US-08-753-038-1	Sequence 1, Appli
698	81.5	6.1	1428	4	US-09-902-540-7081	Sequence 7081, Ap	c 771	81	6.0	2506	3	US-08-758-314-1	Sequence 1, Appli
699	81.5	6.1	1503	4	US-09-252-991A-13684	Sequence 13684, A	c 772	81	6.0	2506	3	US-09-350-309-1	Sequence 1, Appli
700	81.5	6.1	1584	4	US-09-252-991A-625	Sequence 625, App	c 773	81	6.0	2506	3	US-08-520-946-1	Sequence 1, Appli
701	81.5	6.1	1674	4	US-09-252-991A-3990	Sequence 3990, Ap	c 774	81	6.0	2506	4	US-09-684-938-1	Sequence 1, Appli
702	81.5	6.1	1746	4	US-09-252-991A-13461	Sequence 13461, A	c 775	81	6.0	2506	4	US-09-308-825A-1	Sequence 1, Appli
703	81.5	6.1	1983	4	US-09-252-991A-15635	Sequence 15635, A	c 776	81	6.0	2506	4	US-09-758-282B-1	Sequence 1, Appli
704	81.5	6.1	2190	4	US-09-252-991A-10256	Sequence 10256, A	c 777	81	6.0	2506	4	US-09-655-378A-1	Sequence 1, Appli
705	81.5	6.1	2211	4	US-09-252-991A-15685	Sequence 15685, A	c 778	81	6.0	2506	4	US-09-940-244-1	Sequence 1, Appli
706	81.5	6.1	2325	4	US-09-252-991A-8052	Sequence 8052, Ap	c 779	81	6.0	2506	4	US-09-333-145-1	Sequence 1, Appli
707	81.5	6.1	2403	4	US-09-252-991A-8064	Sequence 8064, Ap	c 780	81	6.0	2506	4	US-09-577-304A-1	Sequence 1, Appli
708	81.5	6.1	3537	4	US-09-902-540-8144	Sequence 8144, Ap	c 781	81	6.0	2514	4	US-09-758-282B-264	Sequence 264, App
709	81.5	6.1	4242	4	US-09-252-991A-7056	Sequence 7056, Ap	c 782	81	6.0	2514	4	US-09-577-304A-264	Sequence 264, App
710	81.5	6.1	4346	4	US-09-919-039-112	Sequence 112, App	c 783	81	6.0	2517	4	US-09-758-282B-62	Sequence 62, Appl
711	81.5	6.1	6410	4	US-09-902-540-835	Sequence 835, App	c 784	81	6.0	2517	4	US-09-758-282B-71	Sequence 71, Appl
712	81.5	6.1	9007	4	US-09-902-540-908	Sequence 908, App	c 785	81	6.0	2517	4	US-09-758-282B-82	Sequence 82, Appl
713	81.5	6.1	9497	4	US-09-902-540-1054	Sequence 1054, Ap	c 786	81	6.0	2517	4	US-09-758-282B-88	Sequence 88, Appl
714	81.5	6.1	10023	4	US-09-252-991A-6997	Sequence 6997, Ap	c 787	81	6.0	2517	4	US-09-758-282B-114	Sequence 114, App
715	81.5	6.1	15268	4	US-09-902-540-1142	Sequence 1142, Ap	c 788	81	6.0	2517	4	US-09-758-282B-117	Sequence 117, App
716	81.5	6.1	23796	4	US-09-949-016-17581	Sequence 17581, A	c 789	81	6.0	2517	4	US-09-758-282B-120	Sequence 120, App
717	81.5	6.1	23951	4	US-09-902-540-1245	Sequence 1245, Ap	c 790	81	6.0	2517	4	US-09-758-282B-123	Sequence 123, App
718	81.5	6.1	30135	4	US-09-902-540-1249	Sequence 1249, Ap	c 791	81	6.0	2517	4	US-09-758-282B-126	Sequence 126, App
719	81.5	6.1	39920	4	US-09-949-016-16316	Sequence 16316, A	c 792	81	6.0	2517	4	US-09-758-282B-129	Sequence 129, App
720	81.5	6.1	41768	4	US-09-902-540-1366	Sequence 1366, Ap	c 793	81	6.0	2517	4	US-09-758-282B-132	Sequence 132, App
721	81.5	6.1	43507	4	US-09-949-016-13297	Sequence 13297, A	c 794	81	6.0	2517	4	US-09-758-282B-141	Sequence 141, App
722	81.5	6.1	186734	4	US-09-949-016-14870	Sequence 14870, A	c 795	81	6.0	2517	4	US-09-758-282B-147	Sequence 147, App
723	81.5	6.1	193689	4	US-09-949-016-12350	Sequence 12350, A	c 796	81	6.0	2517	4	US-09-758-282B-149	Sequence 149, App
724	81.5	6.1	193689	4	US-09-949-016-13088	Sequence 13088, A	c 797	81	6.0	2517	4	US-09-758-282B-152	Sequence 152, App
725	81	6.0	915	4	US-09-489-039A-2253	Sequence 2253, Ap	c 798	81	6.0	2517	4	US-09-758-282B-168	Sequence 168, App
726	81	6.0	999	2	US-08-960-756-3	Sequence 3, Appli	c 799	81	6.0	2517	4	US-09-758-282B-177	Sequence 177, App
727	81	6.0	1152	4	US-09-266-965-45	Sequence 45, Appli	c 800	81	6.0	2517	4	US-09-758-282B-180	Sequence 180, App
728	81	6.0	1307	2	US-08-960-022-17	Sequence 17, Appli	c 801	81	6.0	2517	4	US-09-758-282B-183	Sequence 183, App
729	81	6.0	1470	4	US-09-252-991A-3389	Sequence 3389, Ap	c 802	81	6.0	2517	4	US-09-758-282B-186	Sequence 186, App
730	81	6.0	1584	4	US-09-489-039A-2524	Sequence 2524, Ap	c 803	81	6.0	2517	4	US-09-758-282B-189	Sequence 189, App
731	81	6.0	1682	3	US-09-096-399-1	Sequence 1, Appli	c 804	81	6.0	2517	4	US-09-758-282B-199	Sequence 199, App
732	81	6.0	1696	3	US-09-096-399-3	Sequence 3, Appli	c 805	81	6.0	2517	4	US-09-758-282B-201	Sequence 201, App
733	81	6.0	1722	4	US-09-902-540-9668	Sequence 9668, Ap	c 806	81	6.0	2517	4	US-09-758-282B-203	Sequence 203, App
734	81	6.0	1854	4	US-09-902-540-340	Sequence 340, App	c 807	81	6.0	2517	4	US-09-758-282B-205	Sequence 205, App
735	81	6.0	1899	4	US-09-640-958-3	Sequence 3, Appli	c 808	81	6.0	2517	4	US-09-758-282B-217	Sequence 217, App
736	81	6.0	1904	4	US-09-640-958-9	Sequence 9, Appli	c 809	81	6.0	2517	4	US-09-758-282B-220	Sequence 220, App
737	81	6.0	1944	4	US-09-252-991A-16245	Sequence 16245, A	c 810	81	6.0	2517	4	US-09-758-282B-225	Sequence 225, App
738	81	6.0	1965	4	US-09-640-958-11	Sequence 11, Appli	c 811	81	6.0	2517	4	US-09-758-282B-227	Sequence 227, App
739	81	6.0	2004	4	US-09-902-540-5312	Sequence 5312, Ap	c 812	81	6.0	2517	4	US-09-758-282B-229	Sequence 229, App
740	81	6.0	2208	4	US-09-902-540-6293	Sequence 6293, Ap	c 813	81	6.0	2517	4	US-09-758-282B-231	Sequence 231, App
741	81	6.0	2291	4	US-09-902-540-376	Sequence 376, App	c 814	81	6.0	2517	4	US-09-758-282B-233	Sequence 233, App
742	81	6.0	2499	1	US-07-977-434-1	Sequence 1, Appli	c 815	81	6.0	2517	4	US-09-577-304A-62	Sequence 62, Appl

C 816	81	6.0	2517	4	US-09-577-304A-71	Sequence 71, Appl	C 889	80.5	6.0	672	4	US-09-252-991A-9638	Sequence 9638, Ap
C 817	81	6.0	2517	4	US-09-577-304A-82	Sequence 82, Appl	890	80.5	6.0	807	4	US-09-489-039A-139	Sequence 139, App
C 818	81	6.0	2517	4	US-09-577-304A-88	Sequence 88, Appl	891	80.5	6.0	885	4	US-09-902-540-8054	Sequence 8054, Ap
C 819	81	6.0	2517	4	US-09-577-304A-114	Sequence 114, App	892	80.5	6.0	936	4	US-09-489-039A-2270	Sequence 2270, App
C 820	81	6.0	2517	4	US-09-577-304A-117	Sequence 117, App	893	80.5	6.0	957	4	US-09-252-991A-3959	Sequence 3959, Ap
C 821	81	6.0	2517	4	US-09-577-304A-120	Sequence 120, App	C 894	80.5	6.0	1005	4	US-09-902-540-5305	Sequence 5305, Ap
C 822	81	6.0	2517	4	US-09-577-304A-123	Sequence 123, App	C 895	80.5	6.0	1095	4	US-09-902-540-7866	Sequence 7866, Ap
C 823	81	6.0	2517	4	US-09-577-304A-126	Sequence 126, App	C 896	80.5	6.0	1362	4	US-09-252-991A-3943	Sequence 3943, Ap
C 824	81	6.0	2517	4	US-09-577-304A-129	Sequence 129, App	C 897	80.5	6.0	1449	4	US-09-252-991A-1976	Sequence 1976, Ap
C 825	81	6.0	2517	4	US-09-577-304A-132	Sequence 132, App	C 898	80.5	6.0	1524	4	US-09-807-897-3	Sequence 3, Appli
C 826	81	6.0	2517	4	US-09-577-304A-141	Sequence 141, App	C 899	80.5	6.0	1596	4	US-09-252-991A-10119	Sequence 10119, A
C 827	81	6.0	2517	4	US-09-577-304A-147	Sequence 147, App	C 900	80.5	6.0	1605	4	US-09-252-991A-10729	Sequence 10729, A
C 828	81	6.0	2517	4	US-09-577-304A-149	Sequence 149, App	C 901	80.5	6.0	1866	2	US-08-648-657-14	Sequence 14, Appl
C 829	81	6.0	2517	4	US-09-577-304A-152	Sequence 152, App	C 902	80.5	6.0	1818	4	US-09-902-540-4605	Sequence 4605, Ap
C 830	81	6.0	2517	4	US-09-577-304A-158	Sequence 158, App	903	80.5	6.0	1854	4	US-09-902-540-5512	Sequence 5512, Ap
C 831	81	6.0	2517	4	US-09-577-304A-177	Sequence 177, App	904	80.5	6.0	2155	4	US-09-620-312D-65	Sequence 65, Appl
C 832	81	6.0	2517	4	US-09-577-304A-180	Sequence 180, App	C 905	80.5	6.0	2220	2	US-08-864-224-1	Sequence 1, Appli
C 833	81	6.0	2517	4	US-09-577-304A-183	Sequence 183, App	C 906	80.5	6.0	2220	4	US-09-122-384-1	Sequence 1, Appli
C 834	81	6.0	2517	4	US-09-577-304A-186	Sequence 186, App	907	80.5	6.0	2325	4	US-09-252-991A-218	Sequence 218, App
C 835	81	6.0	2517	4	US-09-577-304A-189	Sequence 189, App	C 908	80.5	6.0	2493	4	US-09-252-991A-5433	Sequence 5433, Ap
C 836	81	6.0	2517	4	US-09-577-304A-199	Sequence 199, App	C 909	80.5	6.0	2505	4	US-09-334-818A-1	Sequence 1, Appli
C 837	81	6.0	2517	4	US-09-577-304A-201	Sequence 201, App	C 910	80.5	6.0	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
C 838	81	6.0	2517	4	US-09-577-304A-203	Sequence 203, App	C 911	80.5	6.0	2571	4	US-09-252-991A-1279	Sequence 1279, Ap
C 839	81	6.0	2517	4	US-09-577-304A-205	Sequence 205, App	C 912	80.5	6.0	2571	4	US-09-252-991A-8489	Sequence 8489, Ap
C 840	81	6.0	2517	4	US-09-577-304A-217	Sequence 217, App	C 913	80.5	6.0	2784	4	US-09-252-991A-1394	Sequence 1394, App
C 841	81	6.0	2517	4	US-09-577-304A-220	Sequence 220, App	914	80.5	6.0	2946	4	US-09-252-991A-227	Sequence 227, App
C 842	81	6.0	2517	4	US-09-577-304A-225	Sequence 225, App	C 915	80.5	6.0	4284	4	US-09-252-991A-10434	Sequence 10434, A
C 843	81	6.0	2517	4	US-09-577-304A-227	Sequence 227, App	C 916	80.5	6.0	4563	4	US-09-252-991A-4765	Sequence 4765, Ap
C 844	81	6.0	2517	4	US-09-577-304A-229	Sequence 229, App	C 917	80.5	6.0	4631	4	US-09-902-540-720	Sequence 720, App
C 845	81	6.0	2517	4	US-09-577-304A-231	Sequence 231, App	918	80.5	6.0	6794	4	US-09-902-540-736	Sequence 736, App
C 846	81	6.0	2517	4	US-09-577-304A-233	Sequence 233, App	919	80.5	6.0	7160	4	US-09-902-540-821	Sequence 821, Appl
C 847	81	6.0	2526	4	US-09-758-282B-76	Sequence 76, Appl	C 920	80.5	6.0	7266	3	US-08-713-118-1	Sequence 1, Appli
C 848	81	6.0	2526	4	US-09-758-282B-240	Sequence 240, App	C 921	80.5	6.0	7266	3	US-09-452-007-1	Sequence 1, Appli
C 849	81	6.0	2526	4	US-09-758-282B-262	Sequence 262, App	C 922	80.5	6.0	8614	4	US-09-902-540-787	Sequence 787, Appl
C 850	81	6.0	2526	4	US-09-577-304A-76	Sequence 76, Appl	C 923	80.5	6.0	11254	4	US-09-902-540-1040	Sequence 1040, Ap
C 851	81	6.0	2526	4	US-09-577-304A-240	Sequence 240, App	C 924	80.5	6.0	11813	1	US-08-484-044-10	Sequence 10, Appl
C 852	81	6.0	2526	4	US-09-577-304A-262	Sequence 262, App	C 925	80.5	6.0	12849	4	US-09-902-540-963	Sequence 963, Appl
C 853	81	6.0	2626	1	US-08-156-020-1	Sequence 1, Appli	C 926	80.5	6.0	12849	4	US-09-902-540-1143	Sequence 1143, Ap
C 854	81	6.0	2626	1	US-08-156-020-3	Sequence 3, Appli	C 927	80.5	6.0	19598	4	US-09-902-540-1230	Sequence 1230, Ap
C 855	81	6.0	2626	1	US-08-156-020-5	Sequence 5, Appli	C 928	80.5	6.0	24754	4	US-09-902-540-1324	Sequence 1224, Ap
C 856	81	6.0	2626	1	US-08-156-020-7	Sequence 7, Appli	C 929	80.5	6.0	25497	1	US-09-902-540-1324	Sequence 1, Appli
C 857	81	6.0	2626	1	US-08-156-020-9	Sequence 9, Appli	C 930	80.5	6.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 858	81	6.0	2626	3	US-08-978-806-1	Sequence 1, Appli	C 931	80.5	6.0	50341	1	US-08-247-901C-1	Sequence 1, Appli
C 859	81	6.0	2727	4	US-09-623-326-3	Sequence 3, Appli	C 932	80.5	6.0	50341	2	US-09-075-904-1	Sequence 1, Appli
C 860	81	6.0	2727	4	US-09-623-326-4	Sequence 4, Appli	C 933	80.5	6.0	52297	3	US-09-426-436-1	Sequence 1, Appli
C 861	81	6.0	2733	4	US-09-623-326-1	Sequence 1, Appli	934	80.5	6.0	52297	3	US-08-705-557-1	Sequence 1, Appli
C 862	81	6.0	2733	4	US-09-623-326-2	Sequence 2, Appli	C 935	80.5	6.0	767577	4	US-09-949-016-12147	Sequence 12147, A
C 863	81	6.0	2763	4	US-09-623-326-5	Sequence 5, Appli	C 936	80.5	6.0	767577	4	US-09-949-016-17361	Sequence 17361, A
C 864	81	6.0	2850	4	US-09-623-326-6	Sequence 6, Appli	C 937	80.5	6.0	618	4	US-09-489-039A-1035	Sequence 1035, Ap
C 865	81	6.0	2949	4	US-09-623-326-6	Sequence 6, Appli	C 938	80.5	6.0	855	4	US-09-252-991A-9422	Sequence 9422, Ap
C 866	81	6.0	3114	4	US-09-252-991A-225	Sequence 225, App	C 939	80.5	6.0	969	4	US-09-902-540-9029	Sequence 9029, Ap
C 867	81	6.0	3261	4	US-09-252-991A-8480	Sequence 8480, Ap	C 940	80.5	6.0	1008	1	US-08-347-826A-3	Sequence 3, Appli
C 868	81	6.0	3345	4	US-09-252-991A-8394	Sequence 8394, Ap	C 941	80.5	6.0	1101	4	US-09-252-991A-9455	Sequence 9455, Ap
C 869	81	6.0	3402	4	US-09-252-991A-1374	Sequence 1374, App	C 942	80.5	6.0	1122	4	US-09-252-991A-8798	Sequence 8798, Ap
C 870	81	6.0	3687	4	US-09-252-991A-1193	Sequence 1193, App	C 943	80.5	6.0	1221	4	US-09-902-540-5071	Sequence 5071, Ap
C 871	81	6.0	3864	4	US-09-252-991A-13035	Sequence 13035, A	944	80.5	6.0	1417	4	US-09-902-540-9159	Sequence 9159, Ap
C 872	81	6.0	3876	4	US-09-252-991A-2933	Sequence 2933, Ap	945	80.5	6.0	1417	4	US-09-902-540-9159	Sequence 31, Appl
C 873	81	6.0	4366	4	US-09-252-991A-1234	Sequence 1234, Ap	946	80.5	6.0	1524	4	US-09-489-039A-3444	Sequence 3444, Ap
C 874	81	6.0	5337	4	US-09-902-540-810	Sequence 810, App	947	80.5	6.0	1791	4	US-09-252-991A-9892	Sequence 9892, Ap
C 875	81	6.0	5849	3	US-09-134-246-6	Sequence 6, Appli	948	80.5	6.0	2083	4	US-09-489-039A-4049	Sequence 4049, Ap
C 876	81	6.0	5849	4	US-09-664-186-6	Sequence 6, Appli	C 949	80.5	6.0	2346	4	US-09-774-528-344	Sequence 344, App
C 877	81	6.0	6714	1	US-08-021-623C-5	Sequence 5, Appli	C 950	80.5	6.0	2350	4	US-09-949-016-342	Sequence 342, App
C 878	81	6.0	6732	4	US-09-976-594-99	Sequence 99, Appl	C 951	80.5	6.0	2379	4	US-09-252-991A-9252	Sequence 9252, Ap
C 879	81	6.0	8321	4	US-09-902-540-979	Sequence 979, App	C 952	80.5	6.0	3033	4	US-09-724-797-81	Sequence 81, Appl
C 880	81	6.0	10263	4	US-09-902-540-1024	Sequence 1024, App	C 953	80.5	6.0	3841	4	US-09-902-540-607	Sequence 607, App
C 881	81	6.0	21119	3	US-09-453-702B-111	Sequence 111, App	954	80.5	6.0	3860	4	US-09-902-540-2038	Sequence 2038, Ap
C 882	81	6.0	30360	4	US-09-949-016-15716	Sequence 15716, A	C 955	80.5	6.0	6401	3	US-09-221-017B-804	Sequence 804, App
C 883	81	6.0	35614	4	US-09-902-540-1259	Sequence 1259, App	C 956	80.5	6.0	9053	4	US-09-902-540-815	Sequence 815, App
C 884	81	6.0	38494	4	US-08-311-731A-24	Sequence 24, Appl	C 957	80.5	6.0	10280	4	US-09-902-540-980	Sequence 980, App
C 885	81	6.0	38675	4	US-08-311-731A-135	Sequence 135, App	C 958	80.5	6.0	12865	4	US-09-902-540-1048	Sequence 1048, Ap
C 886	81	6.0	50309	4	US-09-949-016-14112	Sequence 14112, A	C 959	80.5	6.0	17173	4	US-09-902-540-1122	Sequence 1122, Ap
C 887	81	6.0	50937	3	US-09-428-517-1	Sequence 1, Appli	960	80.5	6.0	18324	4	US-09-902-540-1136	Sequence 1136, Ap
C 888	81	6.0	53500	4	US-09-266-965-76	Sequence 76, Appl	C 961	80.5	6.0	26930	4	US-09-902-540-1228	Sequence 1228, Ap

962	80	6.0	28194	4	US-09-302-540-1250	Sequence 1250, Ap	1035	79.5	5.9	17245	4	US-09-902-540-1073	Sequence 1073, Ap
963	80	6.0	35630	4	US-09-949-016-13832	Sequence 13832, A	1036	79.5	5.9	23233	4	US-09-902-540-1184	Sequence 1184, Ap
964	79.5	5.9	786	4	US-09-902-540-5264	Sequence 5264, Ap	1037	79.5	5.9	28762	4	US-09-902-540-1232	Sequence 1232, Ap
965	79.5	5.9	828	4	US-09-252-991A-11099	Sequence 11099, A	1038	79.5	5.9	30783	4	US-09-902-540-1358	Sequence 1256, Ap
966	79.5	5.9	850	1	US-08-114-461-2	Sequence 2, Appl	1039	79.5	5.9	34662	4	US-09-902-540-1558	Sequence 1261, Ap
967	79.5	5.9	850	1	US-08-192-156-2	Sequence 2, Appl	c1040	79.5	5.9	39113	4	US-09-949-016-15634	Sequence 15634, A
968	79.5	5.9	850	1	US-08-370-789-2	Sequence 2, Appl	c1041	79.5	5.9	41927	4	US-09-902-540-1268	Sequence 1268, Ap
969	79.5	5.9	852	4	US-09-252-991A-10276	Sequence 10276, A	1042	79.5	5.9	193303	4	US-09-497-855A-37	Sequence 37, Appl
970	79.5	5.9	882	4	US-09-252-991A-16022	Sequence 16022, A	1043	79.5	5.9	193303	4	US-09-497-855A-44	Sequence 44, Appl
971	79.5	5.9	1065	4	US-09-370-767-12932	Sequence 12932, A	c1044	79	5.9	939	4	US-09-252-991A-734	Sequence 734, App
972	79.5	5.9	1191	4	US-09-302-540-4712	Sequence 4712, Ap	c1045	79	5.9	1122	4	US-09-252-991A-3305	Sequence 3305, Ap
973	79.5	5.9	1317	4	US-09-252-991A-10989	Sequence 10989, A	c1046	79	5.9	1161	4	US-09-252-991A-11607	Sequence 11607, A
974	79.5	5.9	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	c1047	79	5.9	1174	5	PCT-US95-07554-3	Sequence 3, Appl
975	79.5	5.9	1377	4	US-09-489-039A-6783	Sequence 6783, Ap	1048	79	5.9	1194	4	US-09-252-991A-7454	Sequence 7454, Ap
976	79.5	5.9	1458	4	US-09-302-540-3540	Sequence 3540, Ap	1049	79	5.9	1209	4	US-09-902-540-6604	Sequence 6604, Ap
977	79.5	5.9	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	1050	79	5.9	1209	4	US-09-902-540-7412	Sequence 7412, Ap
978	79.5	5.9	1473	4	US-09-302-540-3378	Sequence 3378, Ap	1051	79	5.9	1221	4	US-09-252-991A-7020	Sequence 7020, Ap
979	79.5	5.9	1715	1	US-07-847-743B-24	Sequence 24, Appl	c1052	79	5.9	1229	4	US-09-949-016-5000	Sequence 5000, Ap
980	79.5	5.9	1715	1	US-08-456-201-24	Sequence 24, Appl	c1053	79	5.9	1263	4	US-09-252-991A-7692	Sequence 7692, Ap
981	79.5	5.9	1715	1	US-08-456-201-24	Sequence 24, Appl	c1054	79	5.9	1305	4	US-09-252-991A-11762	Sequence 11762, A
982	79.5	5.9	1715	5	PCT-US92-04295A-24	Sequence 24, Appl	1055	79	5.9	1350	4	US-09-252-991A-1330	Sequence 1330, Ap
983	79.5	5.9	1731	4	US-09-252-991A-15928	Sequence 15928, A	1056	79	5.9	1488	4	US-09-252-991A-197	Sequence 197, App
984	79.5	5.9	1872	4	US-09-252-991A-13815	Sequence 13815, A	1057	79	5.9	1560	4	US-09-252-991A-166	Sequence 166, App
985	79.5	5.9	1964	4	US-09-774-528-308	Sequence 308, App	1058	79	5.9	1650	4	US-09-344-510B-9	Sequence 9, Appl
986	79.5	5.9	2077	4	US-09-921-099A-16	Sequence 16, Appl	1059	79	5.9	1692	4	US-09-252-991A-7872	Sequence 7872, Ap
987	79.5	5.9	2232	4	US-09-489-039A-3302	Sequence 3302, Ap	1060	79	5.9	1800	4	US-09-252-991A-679	Sequence 679, App
988	79.5	5.9	2431	1	US-07-847-743B-25	Sequence 25, Appl	1061	79	5.9	1816	1	US-07-865-662F-5	Sequence 5, Appl
989	79.5	5.9	2431	1	US-08-456-201-25	Sequence 25, Appl	1062	79	5.9	1816	3	US-08-374-219B-5	Sequence 5, Appl
990	79.5	5.9	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	1063	79	5.9	1822	1	US-07-865-662F-6	Sequence 6, Appl
991	79.5	5.9	2431	5	US-09-849-334-1	Sequence 1, Appl	1064	79	5.9	1822	3	US-08-374-219B-6	Sequence 6, Appl
992	79.5	5.9	2469	4	US-10-274-878-1	Sequence 1, Appl	1065	79	5.9	1938	4	US-09-543-681A-3585	Sequence 3585, Ap
993	79.5	5.9	2469	4	US-10-274-878-1	Sequence 1, Appl	1066	79	5.9	1995	4	US-09-902-540-9209	Sequence 9209, Ap
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995	79.5	5.9	2472	3	US-08-743-168B-35	Sequence 35, Appl	c1068	79	5.9	2244	5	PCT-US95-09323-10	Sequence 10, Appl
996	79.5	5.9	2472	3	US-08-743-168B-37	Sequence 37, Appl	1069	79	5.9	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
997	79.5	5.9	2478	4	US-09-252-991A-592	Sequence 592, Appl	c1070	79	5.9	2334	1	US-08-476-519-1	Sequence 1, Appl
998	79.5	5.9	2490	1	US-07-847-743B-23	Sequence 23, Appl	c1071	79	5.9	2334	5	PCT-US95-09323-1	Sequence 1, Appl
999	79.5	5.9	2490	1	US-08-456-201-23	Sequence 23, Appl	c1072	79	5.9	2418	4	US-09-252-991A-2294	Sequence 2294, Ap
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1001	79.5	5.9	2490	5	PCT-US92-04295A-23	Sequence 23, Appl	c1074	79	5.9	2610	4	US-09-252-991A-175	Sequence 175, App
1002	79.5	5.9	2502	4	US-09-252-991A-15767	Sequence 15767, A	1075	79	5.9	2817	4	US-09-252-991A-7311	Sequence 7311, Ap
1003	79.5	5.9	2517	4	US-09-758-282B-144	Sequence 144, App	c1076	79	5.9	2880	4	US-09-252-991A-7187	Sequence 7187, Ap
1004	79.5	5.9	2517	4	US-09-577-304A-144	Sequence 144, App	c1077	79	5.9	2943	4	US-09-379-530B-3	Sequence 3, Appl
1005	79.5	5.9	2742	4	US-09-252-991A-5556	Sequence 5556, Ap	1078	79	5.9	3113	4	US-09-902-540-500	Sequence 500, App
1006	79.5	5.9	2778	4	US-09-252-991A-10486	Sequence 10486, A	1079	79	5.9	3134	1	US-07-865-662F-7	Sequence 7, Appl
1007	79.5	5.9	2825	4	US-09-949-016-1895	Sequence 1895, Ap	1080	79	5.9	3134	3	US-08-374-219B-7	Sequence 7, Appl
1008	79.5	5.9	3293	2	US-08-442-809A-75	Sequence 75, Appl	c1081	79	5.9	3373	1	US-08-273-411-2	Sequence 2, Appl
1009	79.5	5.9	3321	4	US-09-252-991A-5668	Sequence 5668, Ap	c1082	79	5.9	3374	4	US-09-949-016-5482	Sequence 5482, Ap
1010	79.5	5.9	3339	4	US-09-252-991A-10685	Sequence 10685, A	c1083	79	5.9	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
1011	79.5	5.9	4824	4	US-09-902-540-9627	Sequence 9627, Ap	1084	79	5.9	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
1012	79.5	5.9	5499	4	US-09-902-540-2892	Sequence 2892, Ap	1085	79	5.9	5001	4	US-09-902-540-8618	Sequence 8618, Ap
1013	79.5	5.9	6131	4	US-09-949-016-2451	Sequence 2451, Ap	1086	79	5.9	5032	4	US-09-344-510B-8	Sequence 8, Appl
1014	79.5	5.9	6250	4	US-09-949-016-13222	Sequence 13222, A	c1087	79	5.9	5464	4	US-09-902-540-717	Sequence 717, App
1015	79.5	5.9	6575	3	US-08-949-386-3	Sequence 3, Appl	1088	79	5.9	5630	4	US-09-903-540-764	Sequence 764, App
1016	79.5	5.9	6575	3	US-08-450-562-3	Sequence 3, Appl	1089	79	5.9	5743	4	US-09-949-016-12687	Sequence 12687, A
1017	79.5	5.9	6575	3	US-08-984-709A-3	Sequence 3, Appl	1090	79	5.9	5743	4	US-09-949-016-14451	Sequence 14451, A
1018	79.5	5.9	6575	3	US-08-450-273-3	Sequence 3, Appl	1091	79	5.9	5825	4	US-09-949-016-4382	Sequence 4382, Ap
1019	79.5	5.9	6575	3	US-08-450-273-3	Sequence 3, Appl	1092	79	5.9	5878	4	US-09-949-016-939	Sequence 939, App
1020	79.5	5.9	6725	3	US-08-949-386-36	Sequence 36, Appl	c1093	79	5.9	6119	4	US-09-903-540-713	Sequence 713, App
1021	79.5	5.9	6725	3	US-08-450-562-36	Sequence 36, Appl	1094	79	5.9	6975	4	US-09-902-540-2386	Sequence 2386, Ap
1022	79.5	5.9	6725	3	US-08-984-709A-36	Sequence 36, Appl	1095	79	5.9	8091	4	US-09-230-652-1	Sequence 1, Appl
1023	79.5	5.9	6725	3	US-08-450-273-36	Sequence 36, Appl	c1096	79	5.9	8174	1	US-07-914-281-5	Sequence 5, Appl
1024	79.5	5.9	6725	4	US-08-450-273-36	Sequence 36, Appl	c1097	79	5.9	8174	1	US-08-393-246-5	Sequence 5, Appl
1025	79.5	5.9	9839	4	US-09-902-540-996	Sequence 996, App	c1098	79	5.9	8174	1	US-08-525-058A-5	Sequence 5, Appl
1026	79.5	5.9	11220	4	US-09-949-016-5061	Sequence 5061, Ap	c1099	79	5.9	8174	2	US-08-696-731-5	Sequence 5, Appl
1027	79.5	5.9	11706	4	US-09-902-540-1038	Sequence 1038, Ap	c1100	79	5.9	8174	3	US-09-042-531-5	Sequence 5, Appl
1028	79.5	5.9	14382	4	US-09-902-540-1145	Sequence 1145, Ap	c1101	79	5.9	8174	5	PCT-US91-00899-3	Sequence 3, Appl
1029	79.5	5.9	15872	3	US-09-105-537-1	Sequence 1, Appl	1102	79	5.9	8257	3	US-09-484-970B-65	Sequence 65, Appl
1030	79.5	5.9	15872	4	US-09-091-609-1	Sequence 1, Appl	c1103	79	5.9	8580	4	US-09-949-016-17224	Sequence 17224, A
1031	79.5	5.9	15872	4	US-09-091-609-3	Sequence 3, Appl	1104	79	5.9	10301	4	US-09-902-540-985	Sequence 985, App
1032	79.5	5.9	15923	4	US-09-902-540-1095	Sequence 1095, Ap	1105	79	5.9	11101	4	US-09-902-540-1005	Sequence 1005, Ap
1033	79.5	5.9	16187	4	US-09-902-540-1093	Sequence 1093, Ap	c1106	79	5.9	11276	4	US-09-902-540-1034	Sequence 1034, Ap
1034	79.5	5.9	17228	4	US-09-902-540-1170	Sequence 1170, Ap	c1107	79	5.9	12183	4	US-09-902-540-1066	Sequence 1066, Ap

1108	79	5.9	13332	4	US-09-902-540-1047	Sequence 1047, Ap	1181	78.5	5.8	11873	2	US-08-970-269A-32	Sequence 32, Appl
1109	79	5.9	14158	4	US-09-902-540-1069	Sequence 1069, Ap	1182	78.5	5.8	11873	3	US-09-407-562-32	Sequence 32, Appl
1110	79	5.9	14570	4	US-09-902-540-1012	Sequence 1012, Ap	1183	78.5	5.8	11878	2	US-08-970-269A-31	Sequence 31, Appl
1111	79	5.9	15840	4	US-09-902-540-1134	Sequence 1134, Ap	1184	78.5	5.8	11878	3	US-09-407-562-31	Sequence 31, Appl
1112	79	5.9	16080	4	US-09-724-566A-48	Sequence 48, Appl	1185	78.5	5.8	12898	4	US-09-902-540-1000	Sequence 1000, Ap
1113	79	5.9	16080	4	US-09-471-669A-48	Sequence 48, Appl	1186	78.5	5.8	14823	4	US-09-902-540-1087	Sequence 1087, Ap
1114	79	5.9	17315	4	US-09-902-540-1103	Sequence 1103, Ap	1187	78.5	5.8	14427	4	US-09-902-540-1100	Sequence 1100, Ap
1115	79	5.9	19222	4	US-09-902-540-1192	Sequence 1192, Ap	1188	78.5	5.8	15482	4	US-09-902-540-1067	Sequence 1067, Ap
1116	79	5.9	20113	4	US-09-902-540-1173	Sequence 1173, Ap	1189	78.5	5.8	15666	4	US-09-949-016-15929	Sequence 15929, A
1117	79	5.9	29103	4	US-09-902-540-1236	Sequence 1236, Ap	1190	78.5	5.8	33230	4	US-09-949-016-16732	Sequence 16732, A
1118	79	5.9	29977	4	US-09-949-016-17452	Sequence 17452, A	1191	78.5	5.8	34001	4	US-09-596-002-18	Sequence 18, Appl
1119	79	5.9	34446	3	US-09-103-330-35	Sequence 35, Appl	1192	78.5	5.8	152582	4	US-09-949-016-12086	Sequence 12086, A
1120	79	5.9	34741	4	US-09-949-016-12475	Sequence 12475, A	1193	78.5	5.8	152583	4	US-09-949-016-17390	Sequence 17390, A
1121	79	5.9	34745	4	US-09-949-016-16024	Sequence 16024, A	1194	78.5	5.8	152583	4	US-09-949-016-17391	Sequence 17391, A
1122	79	5.9	45314	4	US-09-949-016-14927	Sequence 14927, A	1195	78.5	5.8	202111	4	US-09-949-016-13877	Sequence 13877, A
1123	79	5.9	60990	4	US-09-949-016-14080	Sequence 14080, A	1196	78.5	5.8	434	4	US-09-513-999C-2126	Sequence 2126, Ap
1124	79	5.9	69701	4	US-09-949-016-14187	Sequence 14187, A	1197	78.5	5.8	477	4	US-09-621-976-18886	Sequence 18886, A
1125	79	5.9	73308	4	US-09-949-016-16326	Sequence 16326, A	1198	78.5	5.8	601	4	US-09-949-016-17924	Sequence 17924, A
1126	79	5.9	106315	4	US-09-949-016-16613	Sequence 16613, A	1199	78.5	5.8	601	4	US-09-949-016-17678	Sequence 17678, A
1127	79	5.9	137000	4	US-10-172-911-11	Sequence 11, Appl	1200	78.5	5.8	651	4	US-09-252-991A-11549	Sequence 11549, A
1128	79	5.9	1830121	4	US-09-557-884-1	Sequence 1, Appl	1201	78.5	5.8	732	4	US-09-252-991A-3444	Sequence 3444, Ap
1129	79	5.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl	1202	78.5	5.8	735	4	US-09-328-352-1496	Sequence 1496, Ap
1130	78.5	5.8	601	4	US-09-949-016-148878	Sequence 148878, A	1203	78.5	5.8	735	4	US-09-328-352-1496	Sequence 1496, Ap
1131	78.5	5.8	618	4	US-09-902-540-4243	Sequence 4243, Ap	1204	78.5	5.8	756	4	US-09-252-991A-216	Sequence 216, Ap
1132	78.5	5.8	681	4	US-09-252-991A-3852	Sequence 3852, Ap	1205	78.5	5.8	768	4	US-09-902-540-5226	Sequence 5226, Ap
1133	78.5	5.8	791	3	US-08-858-207A-219	Sequence 219, Ap	1206	78.5	5.8	915	4	US-09-252-991A-9133	Sequence 9133, Ap
1134	78.5	5.8	801	4	US-09-489-039A-5911	Sequence 5911, Ap	1207	78.5	5.8	933	4	US-09-902-540-3236	Sequence 3236, Ap
1135	78.5	5.8	831	4	US-09-252-991A-5052	Sequence 5052, Ap	1208	78.5	5.8	981	4	US-09-252-991A-431	Sequence 431, Appl
1136	78.5	5.8	933	4	US-09-252-991A-3415	Sequence 3415, Ap	1209	78.5	5.8	993	4	US-09-252-991A-8950	Sequence 8950, Ap
1137	78.5	5.8	1014	4	US-09-252-991A-195	Sequence 195, Appl	1210	78.5	5.8	1077	4	US-09-902-540-8685	Sequence 8685, Ap
1138	78.5	5.8	1245	4	US-09-252-991A-5535	Sequence 5535, Ap	1211	78.5	5.8	1115	4	US-09-902-540-539	Sequence 539, Appl
1139	78.5	5.8	1488	4	US-09-023-655-880	Sequence 880, Appl	1212	78.5	5.8	1188	4	US-09-902-540-5270	Sequence 5270, Ap
1140	78.5	5.8	1527	4	US-09-244-111-7	Sequence 7, Appl	1213	78.5	5.8	1199	1	US-08-395-800A-5	Sequence 5, Appl1
1141	78.5	5.8	1546	3	US-09-383-318A-1	Sequence 1, Appl	1214	78.5	5.8	1305	4	US-09-252-991A-9360	Sequence 9360, Ap
1142	78.5	5.8	1557	4	US-09-902-540-8222	Sequence 8222, Ap	1215	78.5	5.8	1308	4	US-09-902-540-8199	Sequence 8199, Ap
1143	78.5	5.8	1563	4	US-09-902-540-4269	Sequence 4269, Ap	1216	78.5	5.8	1335	4	US-09-252-991A-1685	Sequence 1685, Ap
1144	78.5	5.8	1626	4	US-09-902-540-200	Sequence 200, Appl	1217	78.5	5.8	1407	4	US-09-252-991A-15866	Sequence 15866, A
1145	78.5	5.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap	1218	78.5	5.8	1461	4	US-09-398-522-113	Sequence 113, Appl
1146	78.5	5.8	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	1219	78.5	5.8	1638	4	US-09-902-540-8744	Sequence 8744, Ap
1147	78.5	5.8	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	1220	78.5	5.8	1644	4	US-09-252-991A-6563	Sequence 6563, Ap
1148	78.5	5.8	1743	4	US-09-949-016-945	Sequence 945, Appl	1221	78.5	5.8	1708	4	US-09-902-540-5058	Sequence 5058, Ap
1149	78.5	5.8	1743	4	US-09-949-016-2709	Sequence 2709, Ap	1222	78.5	5.8	1710	4	US-09-252-991A-10677	Sequence 10677, A
1150	78.5	5.8	1831	4	US-09-759-451-646	Sequence 646, Appl	1223	78.5	5.8	1731	4	US-09-252-991A-15928	Sequence 15928, A
1151	78.5	5.8	1869	4	US-09-252-991A-3231	Sequence 3231, Ap	1224	78.5	5.8	1791	4	US-09-252-991A-6662	Sequence 6662, Ap
1152	78.5	5.8	1901	4	US-09-902-540-6375	Sequence 6375, Ap	1225	78.5	5.8	2163	4	US-09-252-991A-3010	Sequence 3010, Ap
1153	78.5	5.8	1986	4	US-09-252-991A-1654	Sequence 1654, Ap	1226	78.5	5.8	2226	4	US-09-252-991A-10491	Sequence 10491, A
1154	78.5	5.8	2054	4	US-09-902-540-418	Sequence 418, Appl	1227	78.5	5.8	2230	4	US-09-902-540-6807	Sequence 6807, Ap
1155	78.5	5.8	2166	2	US-08-408-095-30	Sequence 30, Appl	1228	78.5	5.8	2290	4	US-09-907-794A-72	Sequence 72, Appl
1156	78.5	5.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	1229	78.5	5.8	2290	4	US-09-905-125A-72	Sequence 72, Appl
1157	78.5	5.8	2341	4	US-09-902-540-395	Sequence 395, Appl	1230	78.5	5.8	2290	4	US-09-902-775A-72	Sequence 72, Appl
1158	78.5	5.8	2499	4	US-09-758-282B-51	Sequence 51, Appl	1231	78.5	5.8	2290	4	US-09-906-700-72	Sequence 72, Appl
1159	78.5	5.8	2499	4	US-09-758-282B-250	Sequence 250, Appl	1232	78.5	5.8	2290	4	US-09-903-603A-72	Sequence 72, Appl
1160	78.5	5.8	2499	4	US-09-577-304A-51	Sequence 51, Appl	1233	78.5	5.8	2290	4	US-09-904-920A-72	Sequence 72, Appl
1161	78.5	5.8	2499	4	US-09-577-304A-250	Sequence 250, Appl	1234	78.5	5.8	2290	4	US-09-909-064-72	Sequence 72, Appl
1162	78.5	5.8	2511	4	US-09-252-991A-9494	Sequence 9494, Ap	1235	78.5	5.8	2290	4	US-09-906-618-72	Sequence 72, Appl
1163	78.5	5.8	2514	4	US-09-758-282B-260	Sequence 260, Appl	1236	78.5	5.8	2290	4	US-09-903-603A-72	Sequence 72, Appl
1164	78.5	5.8	2514	4	US-09-758-282B-264	Sequence 264, Appl	1237	78.5	5.8	2348	4	US-09-724-566A-42	Sequence 42, Appl
1165	78.5	5.8	2514	4	US-09-577-304A-260	Sequence 260, Appl	1238	78.5	5.8	2348	4	US-09-724-566A-44	Sequence 44, Appl
1166	78.5	5.8	2514	4	US-09-577-304A-264	Sequence 264, Appl	1239	78.5	5.8	2348	4	US-09-471-669A-42	Sequence 42, Appl
1167	78.5	5.8	2583	4	US-09-252-991A-9541	Sequence 9541, Ap	1240	78.5	5.8	2348	4	US-09-471-669A-44	Sequence 44, Appl
1168	78.5	5.8	2911	3	US-09-171-710-1	Sequence 1, Appl	1241	78.5	5.8	2502	4	US-09-252-991A-15767	Sequence 15767, A
1169	78.5	5.8	3024	1	US-07-923-976-7	Sequence 7, Appl	1242	78.5	5.8	2505	2	US-08-757-653-187	Sequence 187, Appl
1170	78.5	5.8	3264	4	US-09-252-991A-12013	Sequence 12013, A	1243	78.5	5.8	2505	2	US-08-757-653-189	Sequence 189, Appl
1171	78.5	5.8	3279	4	US-09-252-991A-11905	Sequence 11905, A	1244	78.5	5.8	2505	2	US-08-823-516-68	Sequence 68, Appl
1172	78.5	5.8	3279	4	US-09-902-540-7318	Sequence 7318, Ap	1245	78.5	5.8	2505	2	US-08-823-516-70	Sequence 70, Appl
1173	78.5	5.8	3625	4	US-09-023-655-1180	Sequence 1180, Ap	1246	78.5	5.8	2505	3	US-08-759-038-139	Sequence 129, Appl
1174	78.5	5.8	3702	4	US-09-252-991A-6666	Sequence 6666, Ap	1247	78.5	5.8	2505	3	US-08-759-038-131	Sequence 131, Appl
1175	78.5	5.8	3771	4	US-09-902-540-559	Sequence 559, Appl	1248	78.5	5.8	2505	3	US-08-758-314-129	Sequence 129, Appl
1176	78.5	5.8	4632	4	US-09-902-540-8368	Sequence 8368, Ap	1249	78.5	5.8	2505	3	US-08-758-314-131	Sequence 131, Appl
1177	78.5	5.8	4704	4	US-09-252-991A-3906	Sequence 3906, Ap	1250	78.5	5.8	2505	4	US-09-684-938-139	Sequence 129, Appl
1178	78.5	5.8	5318	4	US-09-902-540-849	Sequence 849, Appl	1251	78.5	5.8	2505	4	US-09-684-938-131	Sequence 131, Appl
1179	78.5	5.8	5656	4	US-09-902-540-694	Sequence 694, Appl	1252	78.5	5.8	2505	4	US-09-308-825A-129	Sequence 129, Appl
1180	78.5	5.8	5868	4	US-09-949-016-16884	Sequence 16884, A	1253	78.5	5.8	2505	4	US-09-308-825A-131	Sequence 131, Appl

c1254	78	5.8	2505	4	US-09-940-244-68	Sequence 68, Appl	c1327	77.5	5.8	2013	4	US-09-903-540-5920	Sequence 5920, Ap
c1255	78	5.8	2505	4	US-09-940-244-70	Sequence 70, Appl	1328	77.5	5.8	2039	4	US-09-903-540-179	Sequence 179, App
c1256	78	5.8	2317	4	US-09-758-282B-171	Sequence 171, App	1329	77.5	5.8	2153	2	US-08-577-492-31	Sequence 31, Appl
c1257	78	5.8	2317	4	US-09-577-304A-171	Sequence 171, App	1330	77.5	5.8	2153	3	US-09-079-630-31	Sequence 31, Appl
c1258	78	5.8	2781	4	US-09-252-991A-15980	Sequence 15980, A	1331	77.5	5.8	2377	4	US-09-920-668-3	Sequence 3, Appl
c1259	78	5.8	2888	3	US-08-765-907A-1	Sequence 1, Appl	1332	77.5	5.8	2658	4	US-09-252-991A-9558	Sequence 9558, Ap
c1260	78	5.8	2888	4	US-09-987-614A-1	Sequence 1, Appl	1333	77.5	5.8	2658	4	US-09-252-991A-14053	Sequence 14053, A
c1261	78	5.8	2952	4	US-09-252-991A-16297	Sequence 16297, A	1334	77.5	5.8	2703	4	US-09-903-540-8634	Sequence 8634, Ap
c1262	78	5.8	3294	4	US-09-252-991A-6008	Sequence 6008, Ap	1335	77.5	5.8	2733	4	US-09-902-540-3104	Sequence 3104, Ap
c1263	78	5.8	3486	4	US-09-252-991A-6301	Sequence 6301, Ap	1336	77.5	5.8	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
c1264	78	5.8	3648	4	US-09-902-540-624	Sequence 624, App	1337	77.5	5.8	2822	4	US-09-949-016-1184	Sequence 1184, Ap
c1265	78	5.8	4239	4	US-09-815-048-1	Sequence 1, Appl	1338	77.5	5.8	2853	4	US-09-949-016-4282	Sequence 4282, Ap
c1266	78	5.8	4493	4	US-09-949-016-14034	Sequence 14034, A	1339	77.5	5.8	2874	4	US-09-252-991A-14101	Sequence 14101, A
c1267	78	5.8	4800	4	US-09-902-540-562	Sequence 562, App	1340	77.5	5.8	3331	4	US-09-976-594-131	Sequence 131, App
c1268	78	5.8	4835	3	US-08-976-259-58	Sequence 58, Appl	1341	77.5	5.8	3402	4	US-09-252-991A-15560	Sequence 15560, A
c1269	78	5.8	4835	4	US-09-956-004-58	Sequence 58, Appl	1342	77.5	5.8	3606	4	US-09-252-991A-15688	Sequence 15688, A
c1270	78	5.8	6625	4	US-09-949-016-13534	Sequence 13534, A	1343	77.5	5.8	3846	4	US-09-903-540-2520	Sequence 2520, Ap
c1271	78	5.8	7419	4	US-09-252-991A-481	Sequence 481, App	1344	77.5	5.8	4084	4	US-09-903-540-6397	Sequence 6397, App
c1272	78	5.8	7449	4	US-09-252-991A-396	Sequence 396, App	1345	77.5	5.8	4530	4	US-09-799-451-881	Sequence 881, App
c1273	78	5.8	7760	4	US-09-902-540-845	Sequence 845, App	1346	77.5	5.8	6063	4	US-09-903-540-801	Sequence 807, App
c1274	78	5.8	12950	4	US-09-902-540-1036	Sequence 1036, Ap	1347	77.5	5.8	6599	4	US-09-902-540-724	Sequence 724, App
c1275	78	5.8	14431	4	US-09-902-540-1149	Sequence 1149, Ap	1348	77.5	5.8	8320	4	US-09-902-540-913	Sequence 913, App
c1276	78	5.8	16265	4	US-09-902-540-1126	Sequence 1126, Ap	1349	77.5	5.8	8931	3	US-09-028-934-28	Sequence 28, Appl
c1277	78	5.8	16427	4	US-09-902-540-1160	Sequence 1160, Ap	1350	77.5	5.8	9335	4	US-09-902-540-940	Sequence 940, App
c1278	78	5.8	17348	4	US-09-949-016-17403	Sequence 17403, A	1351	77.5	5.8	11382	4	US-09-902-540-904	Sequence 904, App
c1279	78	5.8	17592	4	US-09-902-540-1138	Sequence 1138, Ap	1352	77.5	5.8	14464	4	US-09-902-540-1135	Sequence 1135, Ap
c1280	78	5.8	17612	3	US-08-911-853-29	Sequence 29, Appl	1353	77.5	5.8	15499	4	US-09-902-540-1140	Sequence 1140, Ap
c1281	78	5.8	17612	3	US-09-479-409-29	Sequence 29, Appl	1354	77.5	5.8	17503	4	US-09-902-540-1114	Sequence 1114, Ap
c1282	78	5.8	17612	3	US-09-479-453-29	Sequence 29, Appl	1355	77.5	5.8	23677	4	US-09-902-540-1218	Sequence 1218, Ap
c1283	78	5.8	18609	3	US-08-943-731-1	Sequence 1, Appl	1356	77.5	5.8	26289	4	US-09-902-540-1210	Sequence 1210, Ap
c1284	78	5.8	19726	4	US-09-902-540-1164	Sequence 1164, Ap	1357	77.5	5.8	36470	4	US-08-311-731A-123	Sequence 123, App
c1285	78	5.8	24741	4	US-09-949-016-15547	Sequence 15547, A	1358	77.5	5.8	64518	4	US-09-949-016-17289	Sequence 17289, A
c1286	78	5.8	27490	4	US-09-902-540-1227	Sequence 1227, Ap	1359	77.5	5.8	119981	4	US-09-949-016-11844	Sequence 11844, A
c1287	78	5.8	28257	4	US-09-949-016-13076	Sequence 13076, A	1360	77.5	5.8	119982	4	US-09-949-016-13606	Sequence 13606, A
c1288	78	5.8	30783	4	US-09-902-540-1258	Sequence 1258, Ap	1361	77	5.7	601	4	US-09-949-016-91732	Sequence 91732, A
c1289	78	5.8	37861	4	US-09-949-016-15872	Sequence 16872, A	1362	77	5.7	601	4	US-09-949-016-109219	Sequence 109219, A
c1290	78	5.8	41106	4	US-09-949-016-15796	Sequence 15796, A	1363	77	5.7	601	4	US-09-949-016-109220	Sequence 109220, A
c1291	78	5.8	43717	4	US-09-949-016-16821	Sequence 16821, A	1364	77	5.7	601	4	US-09-949-016-194673	Sequence 194673, A
c1292	78	5.8	50725	4	US-09-902-540-1271	Sequence 1271, Ap	1365	77	5.7	645	4	US-09-252-991A-7665	Sequence 7665, Ap
c1293	78	5.8	197336	4	US-09-949-016-12881	Sequence 12881, A	1366	77	5.7	669	4	US-09-252-991A-5618	Sequence 5618, Ap
c1294	78	5.8	197337	4	US-09-949-016-14376	Sequence 14376, A	1367	77	5.7	810	4	US-09-540-236-319	Sequence 319, App
c1295	78	5.8	203475	4	US-09-949-016-14516	Sequence 14516, A	1368	77	5.7	810	4	US-09-902-540-3599	Sequence 3599, Ap
c1296	78	5.8	203475	4	US-09-949-016-14517	Sequence 14517, A	1369	77	5.7	990	4	US-09-902-540-4759	Sequence 4759, Ap
c1297	78	5.8	203475	4	US-09-949-016-14518	Sequence 14518, A	1370	77	5.7	1005	4	US-09-902-540-5305	Sequence 5305, Ap
c1298	78	5.8	203475	4	US-09-949-016-14519	Sequence 14519, A	1371	77	5.7	1032	4	US-09-252-991A-748	Sequence 748, App
c1299	78	5.8	203475	4	US-09-949-016-17226	Sequence 17226, A	1372	77	5.7	1128	4	US-09-252-991A-9049	Sequence 9049, Ap
c1300	78	5.8	203475	4	US-09-949-016-17227	Sequence 17227, A	1373	77	5.7	1152	4	US-09-252-991A-8964	Sequence 8964, Ap
c1301	78	5.8	203475	4	US-09-949-016-17228	Sequence 17228, A	1374	77	5.7	1257	4	US-09-252-991A-15524	Sequence 15524, A
c1302	78	5.8	203475	4	US-09-949-016-17229	Sequence 17229, A	1375	77	5.7	1461	4	US-09-902-540-7265	Sequence 7265, Ap
c1303	78	5.8	234288	4	US-09-949-016-17272	Sequence 17272, A	1376	77	5.7	1582	3	US-09-180-109A-32	Sequence 32, Appl
c1304	77.5	5.8	429	4	US-09-252-991A-12815	Sequence 12815, A	1377	77	5.7	1585	4	US-09-949-016-617	Sequence 617, App
c1305	77.5	5.8	477	4	US-09-902-540-4517	Sequence 4517, Ap	1378	77	5.7	1587	4	US-09-023-655-1192	Sequence 1192, Ap
c1306	77.5	5.8	654	4	US-09-489-039A-618	Sequence 618, App	1379	77	5.7	1686	2	US-08-648-657-2	Sequence 2, Appl
c1307	77.5	5.8	894	4	US-09-252-991A-6276	Sequence 6276, Ap	1380	77	5.7	1689	2	US-08-648-657-1	Sequence 2, Appl
c1308	77.5	5.8	1041	4	US-09-252-991A-4916	Sequence 4916, Ap	1381	77	5.7	1776	4	US-09-902-540-7046	Sequence 7046, Ap
c1309	77.5	5.8	1101	4	US-09-902-540-4233	Sequence 4233, Ap	1382	77	5.7	1836	4	US-09-252-991A-1026	Sequence 1026, Ap
c1310	77.5	5.8	1155	1	US-08-434-151-1	Sequence 1, Appl	1383	77	5.7	1848	1	US-08-635-137-1	Sequence 1, Appl
c1311	77.5	5.8	1155	1	US-08-208-889A-1	Sequence 1, Appl	1384	77	5.7	1848	3	US-09-136-981-1	Sequence 1, Appl
c1312	77.5	5.8	1155	2	US-08-433-271-1	Sequence 1, Appl	1385	77	5.7	1965	4	US-09-252-991A-8852	Sequence 8852, Ap
c1313	77.5	5.8	1155	2	US-08-715-259-1	Sequence 1, Appl	1386	77	5.7	2070	4	US-09-902-540-9138	Sequence 9138, Ap
c1314	77.5	5.8	1200	4	US-09-252-991A-5386	Sequence 5386, Ap	1387	77	5.7	2157	4	US-09-252-991A-9125	Sequence 9125, Ap
c1315	77.5	5.8	1227	4	US-09-489-039A-5352	Sequence 5352, Ap	1388	77	5.7	2397	4	US-09-252-991A-8738	Sequence 8738, Ap
c1316	77.5	5.8	1266	4	US-09-252-991A-15755	Sequence 15755, A	1389	77	5.7	2415	4	US-09-252-991A-7480	Sequence 7480, Ap
c1317	77.5	5.8	1451	4	US-09-902-540-7976	Sequence 7976, Ap	1390	77	5.7	2588	2	US-08-796-414B-6	Sequence 6, Appl
c1318	77.5	5.8	1491	4	US-09-252-991A-14743	Sequence 14743, A	1391	77	5.7	2667	4	US-09-252-991A-7216	Sequence 7216, Ap
c1319	77.5	5.8	1500	4	US-09-252-991A-4920	Sequence 4920, Ap	1392	77	5.7	2689	1	US-08-465-795-2	Sequence 2, Appl
c1320	77.5	5.8	1536	4	US-09-902-540-8768	Sequence 8768, Ap	1393	77	5.7	2865	4	US-09-252-991A-4675	Sequence 4675, Ap
c1321	77.5	5.8	1539	4	US-09-252-991A-14886	Sequence 14886, A	1394	77	5.7	2872	3	US-09-327-487A-2	Sequence 2, Appl
c1322	77.5	5.8	1599	4	US-09-252-991A-5850	Sequence 5850, Ap	1395	77	5.7	3195	4	US-09-252-991A-937	Sequence 937, App
c1323	77.5	5.8	1614	4	US-09-252-991A-15010	Sequence 15010, A	1396	77	5.7	3739	4	US-09-902-540-477	Sequence 477, App
c1324	77.5	5.8	1620	4	US-09-252-991A-4922	Sequence 4922, Ap	1397	77	5.7	3837	4	US-09-902-540-9503	Sequence 9503, Ap
c1325	77.5	5.8	1863	4	US-09-252-991A-5819	Sequence 5819, Ap	1398	77	5.7	4324	4	US-09-902-540-684	Sequence 684, App
c1326	77.5	5.8	1992	4	US-09-252-991A-9693	Sequence 9693, Ap	1399	77	5.7	4497	4	US-09-252-991A-14663	Sequence 14663, A

1400	77	5.7	4532	4	US-09-902-540-626	Sequence 626, App	cl473	76.5	5.7	1825	4	US-09-907-794A-1	Sequence 1, Appli
1401	77	5.7	5589	1	US-08-465-795-1	Sequence 1, Appli	cl474	76.5	5.7	1825	4	US-09-905-125A-1	Sequence 1, Appli
1402	77	5.7	6363	4	US-09-902-540-707	Sequence 707, App	cl475	76.5	5.7	1825	4	US-09-902-775A-1	Sequence 1, Appli
1403	77	5.7	6751	4	US-09-761-466-5	Sequence 5, Appli	cl476	76.5	5.7	1825	4	US-09-906-700-1	Sequence 1, Appli
1404	77	5.7	6909	3	US-09-199-637A-111	Sequence 111, App	cl477	76.5	5.7	1825	4	US-09-903-603A-1	Sequence 1, Appli
1405	77	5.7	7515	4	US-09-902-540-888	Sequence 888, App	cl478	76.5	5.7	1825	4	US-09-904-920A-1	Sequence 1, Appli
1406	77	5.7	7880	4	US-09-902-540-898	Sequence 898, App	cl479	76.5	5.7	1825	4	US-09-905-064-1	Sequence 1, Appli
1407	77	5.7	8051	2	US-08-576-626A-2	Sequence 2, Appli	cl480	76.5	5.7	1825	4	US-09-905-381A-1	Sequence 1, Appli
1408	77	5.7	9603	3	US-09-203-895-1	Sequence 1, Appli	cl481	76.5	5.7	1825	4	US-09-906-618-1	Sequence 1, Appli
1409	77	5.7	10178	4	US-09-902-540-977	Sequence 977, App	cl482	76.5	5.7	1854	4	US-09-252-991A-4542	Sequence 4542, Ap
1410	77	5.7	10311	4	US-09-902-540-957	Sequence 957, App	cl483	76.5	5.7	1875	4	US-09-252-991A-3919	Sequence 3919, Ap
1411	77	5.7	10392	4	US-09-902-540-1081	Sequence 1081, Ap	cl484	76.5	5.7	1875	4	US-09-252-991A-8812	Sequence 8812, Ap
1412	77	5.7	11476	4	US-09-902-540-955	Sequence 955, App	cl485	76.5	5.7	1828	3	US-09-352-153-43	Sequence 43, Appl
1413	77	5.7	11563	4	US-09-902-540-1019	Sequence 1019, Ap	cl486	76.5	5.7	1928	4	US-09-771-045B-43	Sequence 43, Appl
1414	77	5.7	11854	4	US-09-902-540-1037	Sequence 1037, Ap	cl487	76.5	5.7	2010	4	US-09-902-540-9547	Sequence 9547, Ap
1415	77	5.7	13234	4	US-09-902-540-986	Sequence 986, App	cl488	76.5	5.7	2028	4	US-09-252-991A-12590	Sequence 12590, A
1416	77	5.7	15271	4	US-09-902-540-1051	Sequence 1051, Ap	cl489	76.5	5.7	2040	4	US-09-252-991A-10540	Sequence 10540, A
1417	77	5.7	16013	4	US-09-949-016-12988	Sequence 12988, A	cl490	76.5	5.7	2046	4	US-09-490-291-3	Sequence 3, Appli
1418	77	5.7	19085	4	US-09-949-016-16361	Sequence 16361, A	cl491	76.5	5.7	2076	4	US-09-490-291-5	Sequence 5, Appli
1419	77	5.7	20740	4	US-09-902-540-1223	Sequence 1223, Ap	cl492	76.5	5.7	2116	4	US-09-023-655-1256	Sequence 1256, Ap
1420	77	5.7	26492	4	US-09-902-540-1234	Sequence 1234, Ap	cl493	76.5	5.7	2176	6	5320958-1	Patent No. 5320958
1421	77	5.7	26928	4	US-09-544-398B-6	Sequence 6, Appli	cl494	76.5	5.7	2176	6	5320958-1	Patent No. 5320958
1422	77	5.7	26928	1	US-08-543-771B-6	Sequence 6, Appli	cl495	76.5	5.7	2196	4	US-09-252-991A-9319	Sequence 9319, Ap
1423	77	5.7	28958	1	US-08-258-261B-6	Sequence 6, Appli	cl496	76.5	5.7	2356	4	US-09-949-016-1984	Sequence 1984, Ap
1424	77	5.7	28958	1	US-08-456-837-6	Sequence 6, Appli	cl497	76.5	5.7	2356	4	US-09-252-991A-9238	Sequence 9238, Ap
1425	77	5.7	28958	1	US-08-457-342-6	Sequence 6, Appli	cl498	76.5	5.7	2517	4	US-09-252-991A-7209	Sequence 7209, Ap
1426	77	5.7	28958	1	US-08-457-646A-6	Sequence 6, Appli	cl499	76.5	5.7	2541	4	US-09-252-991A-7209	Sequence 9, Appli
1427	77	5.7	28958	1	US-08-458-076A-6	Sequence 6, Appli	cl500	76.5	5.7	2626	1	US-08-156-020-9	Sequence 9, Appli
1428	77	5.7	28958	1	US-08-764-233A-4	Sequence 4, Appli	cl501	76.5	5.7	2699	4	US-09-902-540-6501	Sequence 6501, Ap
1429	77	5.7	28958	1	US-08-457-335A-6	Sequence 6, Appli							
1430	77	5.7	28958	1	US-08-729-214-6	Sequence 6, Appli							
1431	77	5.7	28958	3	US-09-028-934-6	Sequence 6, Appli							
1432	77	5.7	51928	4	US-09-949-016-13184	Sequence 13184, A							
1433	77	5.7	60276	4	US-09-949-016-15004	Sequence 15004, A							
1434	77	5.7	60338	4	US-09-949-016-15694	Sequence 15694, A							
1435	77	5.7	100848	4	US-09-596-002-39	Sequence 39, Appl							
1436	77	5.7	154600	4	US-09-949-016-14757	Sequence 14757, A							
1437	77	5.7	229354	4	US-09-705-400-64	Sequence 64, Appl							
1438	76.5	5.7	552	4	US-09-252-991A-9619	Sequence 9619, Ap							
1439	76.5	5.7	601	4	US-09-949-016-43908	Sequence 43908, A							
1440	76.5	5.7	783	4	US-09-252-991A-7428	Sequence 7428, Ap							
1441	76.5	5.7	858	4	US-09-543-681A-639	Sequence 639, App							
1442	76.5	5.7	882	4	US-09-328-352-710	Sequence 710, App							
1443	76.5	5.7	939	4	US-09-252-991A-9154	Sequence 9154, Ap							
1444	76.5	5.7	1026	4	US-09-655-908-19	Sequence 19, Appl							
1445	76.5	5.7	1089	4	US-09-252-991A-1313	Sequence 1313, Ap							
1446	76.5	5.7	1107	4	US-09-252-991A-3881	Sequence 3881, Ap							
1447	76.5	5.7	1131	4	US-09-252-991A-2322	Sequence 2322, Ap							
1448	76.5	5.7	1215	4	US-09-252-991A-2513	Sequence 2513, Ap							
1449	76.5	5.7	1215	4	US-09-252-991A-2595	Sequence 2595, Ap							
1450	76.5	5.7	1227	4	US-09-252-991A-9232	Sequence 9232, Ap							
1451	76.5	5.7	1239	4	US-09-252-991A-13781	Sequence 13781, A							
1452	76.5	5.7	1245	4	US-09-252-991A-4611	Sequence 4611, Ap							
1453	76.5	5.7	1251	4	US-09-252-991A-16089	Sequence 16089, A							
1454	76.5	5.7	1269	4	US-09-902-540-6879	Sequence 6879, Ap							
1455	76.5	5.7	1341	4	US-09-902-540-6759	Sequence 6759, Ap							
1456	76.5	5.7	1386	4	US-09-949-016-3585	Sequence 3585, Ap							
1457	76.5	5.7	1443	4	US-09-252-991A-10295	Sequence 10295, A							
1458	76.5	5.7	1503	3	US-09-463-702A-33	Sequence 33, Appl							
1459	76.5	5.7	1503	4	US-09-699-135-33	Sequence 33, Appl							
1460	76.5	5.7	1515	4	US-09-902-540-6108	Sequence 6108, Ap							
1461	76.5	5.7	1519	4	US-09-902-540-279	Sequence 279, App							
1462	76.5	5.7	1527	4	US-09-252-991A-16194	Sequence 16194, A							
1463	76.5	5.7	1557	1	US-08-481-130-26	Sequence 26, Appl							
1464	76.5	5.7	1557	1	US-08-656-984A-26	Sequence 26, Appl							
1465	76.5	5.7	1557	1	US-08-485-604-26	Sequence 26, Appl							
1466	76.5	5.7	1557	2	US-08-487-595-26	Sequence 26, Appl							
1467	76.5	5.7	1566	4	US-09-252-991A-14361	Sequence 14361, A							
1468	76.5	5.7	1569	4	US-09-252-991A-15857	Sequence 15857, A							
1469	76.5	5.7	1662	4	US-09-252-991A-16399	Sequence 16399, A							
1470	76.5	5.7	1866	4	US-09-252-991A-10406	Sequence 10406, A							
1471	76.5	5.7	1883	4	US-09-882-694B-30	Sequence 30, Appl							
1472	76.5	5.7	1824	4	US-09-252-991A-4025	Sequence 4025, Ap							

## ALIGNMENTS

RESULT 1  
 US-09-252-991A-3196  
 ; Sequence 3196, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: ABRUINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 3196  
 ; LENGTH: 846  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-3196

Alignment Scores:  
 Pred. No.: 1,226-39 Length: 846  
 Score: 429.00 Matches: 102  
 Percent Similarity: 55.1% Conservative: 31  
 Best Local Similarity: 42.3% Mismatches: 82  
 Query Match: 31.94% Indels: 26  
 DB: 4 Gaps: 5

US-10-017-407A-306 (1-262) x US-09-252-991A-3196 (1-846)

QY	38	TPAARGIYARGARGGLUCGLNCysLeuLeuProProGlu		-----	50
DB	145	TGCGCGGG-----TGC-----		CTGAGCGCGGAGGTCCGGGGCCATC	183
QY	51	-----		-----	62
DB	184	ATGACCCACCGCACCTCAATCTCAGCACACCTTATCGTACCTGCTGCGCTTCG		-----	243
QY	63	MetArgGluHisProAlaLeuArgSerLeuLeuThrLeuGlnProGlnGly		-----	82



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Db 244 CTGGCGGAAACCCCGTGTATGATCCCGCTTCGCGAGGAAACCGGAAGCTGCCAACGCA 303
Qy 83 AspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGln 102
Db 304 CGCTGGCAGATCGCCCGCAGCAGGCGCCAGTTTCATCGCCTTGTGTGACCTGTATCGGC 363
Qy 103 AlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeu 122
Db 364 GCGCGCGCGCGCTGGAGGTGGCAGCTTCACCGGCTACAGCGCTGTGATGGCTAC 423
Qy 123 AlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProGluLeu 142
Db 424 GCCCTGGCGAGCAGCGGCGTCTTACCTGTTCGACCTGCCCGGAGCTACCACTGACT 483
Qy 143 GlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysPro 162
Db 484 GCGCGCGCTACTTGGCGGCAAGCGCTGTTCGAGGAGCGATCGAGTACGCTCGGGGCC 543
Qy 163 AlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAla 182
Db 544 GCGCTGGAAACCTGGCTGCTGTTCGAGAGGCGCTGCCGCGGAGTTCCACCTGGCC 603
Qy 183 ValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeu 202
Db 604 TTCATCGACGCGCAGCAAGCCCAACTACCCCGAATACCTGGAGCGCGCTGGCGCTGGTG 663
Qy 203 ArgProGlyLysLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu----- 220
Db 664 CGCCACGGTGGCTGTGCTTTTCGACAACTGTCTGTGGAGCGCGCGGTGTCTGGAAGCG 723
Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArg 240
Db 724 CAGCCGAAAGTGGGATACCGCGGC-----ATCCACAGCTCAACTGGCGCTGAAG 777
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuLeuAlaPhe 260
Db 778 AACGACGCGCGGTGGACTACTCGTGTCTGCGGATCGCGGACGCGGCTGTGCTGCGC 837
Qy 261 Lys 261
Db 838 AAG 840
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## RESULT 2

US-09-452-239-21

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; Sequence 21, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Glycine max
US-09-452-239-21
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## Alignment Scores:

Pred. No.:	7,63e-37	Length:	980
Score:	405.50	Matches:	92
Percent Similarity:	57.2%	Conservative:	45
Best Local Similarity:	38.1%	Mismatches:	93
Query Match:	30.19%	Indels:	10
DB:	3	Gaps:	3

US-10-017-407A-306 (1-262) x US-09-452-239-21 (1-980)

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Qy 32 GlyArgCysProTrpArgGlyArgGluGlnCysLeuLeuProGluAs 51
Db 48 GGAACAGAAAAACCACTCTTCGGCATCAAGATCTCGGTCAACAAGCTCTCTTCAGAG 107
Qy 51 pSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLe 69
Db 108 TGATCCTCTATCATATATATCTTGAACCAAGTGTCTCTCAAGAGAGCAGAGTGCTT 167
Qy 69 uArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysG 89
Db 168 GAAAGAGATAGCAAGATGACTGCAAAAACACCCACTGAACATCATCGCAACACCAAGCAG 227
Qy 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysLysAlaLeuAspLe 109
Db 228 CGAAGGACAACCTTCGAGCATGCTTTGTAAGCTCAGCAATTCAAAGAACGCTTCGAAT 287
Qy 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 288 TGGTGTATTCACTGGTACTCTCTCTCCACTGCCCTGGCTCTTCCCTCGATGATAA 347
Qy 129 gValValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGl 149
Db 348 GATCTTGGCTTGGATGTGAATCGCAATCTATGATGTAGGATGCCAAATAATTCAAAA 407
Qy 149 nAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGl 169
Db 408 AGCTGGATGGCTCAAGATTGATTTCAGAGAGGAGCTGCTCTTCGGTTTCTTGACGA 467
Qy 169 uLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValAlaAspLeu 188
Db 468 GATGCTTAAAGATGAAATAAAAGGGTCTGTGATTCGTTTTCGTGGATGCTGATAA 527
Qy 188 sGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyLeu 208
Db 528 GGACAATTACTTGAACCTACCAAGAGGGTACTAGAGCTTGTGAAGATTGGAGGACTGAT 587
Qy 208 uAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAl 228
Db 588 CGGATACGATAACACCTTATGGGTGGATCTGTGGCTGCACCCCGATGACCAATTGAT 647
Qy 228 aAlaGluCys-----ValArgAsnLeuAsnGluArgGileArgAs 242
Db 648 GGATTACATTAAAGCTCTTCGCGGCCATGTGATGGAGCTCAACAAGTATCTGGCTCAAGA 707
Qy 242 pValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIl 262
Db 708 TTCGAGGATCGAGATTTTCCAGCTCCCGGTGGTGGATTACCTGTGCGCGCGCAT 767
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262 e 262

768 C 768

## RESULT 3

US-09-452-239-1

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; Sequence 1, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (806)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (810)
US-09-452-239-1

Alignment Scores:
Pred. No.: 2,17e-36 Length: 891
Score: 401.00 Matches: 100
Percent Similarity: 56.03% Conservative: 44
Best Local Similarity: 38.91% Mismatches: 88
Query Match: 29.86% Indels: 25
DB: 3 Gaps: 6

US-10-017-407A-306 (1-262) x US-09-452-239-1 (1-891)

QY 17 GlySerAlaLeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArg----- 34
DB 107 GCGCGCGCGCGCGCGAGCAGCA-----GGCCAAACGCGCAACGG 145
QY 35 -----CysProProTrpArgGlyArgGluGlnCysLeuLeuProGluAsp 51
DB 146 CGAGCAGAGACGCGGCACCTCCGAGGTGCGCCAAAGAG-----CCTGCTCAAGAG 196
QY 52 SerArg-LeuTrpGlnTyLeuLeuSerArgSerMet-----ArgGluHisProAlaLe 69
DB 197 CGAGGACCTTACCACTATCTCGACACGAGCGTGATCCCGCGGGAGCGGAGGACAT 256
QY 69 uArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGln 89
DB 257 GAAGGAGCTCCGCGAGATCACCGCCCAAGCACCATGACACCTGATGACGACCTCCGCGCA 316
QY 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaIleAlaLeuAspLe 109
DB 317 CGAGGGCGAGTTCTTCAACATGCTCATCAAGCTCATCGCGCGCCCAAGAACCATGAGAT 376
QY 109 uGlyThrPheThrGlyTyTrSerAlaLeuAlaLeuAlaLeuLeuProAlaAspGlyAr 129
DB 377 CGCGGTCTACACCGGTACTCGTCTCTCGCCACCGCGCTCGACTCCCGGAGAGCGGCAC 436
QY 129 gValValThrCysGluValAspAlaGlnProGluLeuGlyArgProLeuTrpArgGln 149
DB 437 GATCTTGGCCATGGACATCAACCGCGAGAACTACGAGCTAGGCTTCCCTGCATCAACAA 496
QY 149 nAlaGluAlaGluHisIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGln 169
DB 497 GCGCGCGGTGGGCCCAAGATGACATTCCGCGAGGCGCGCGCTCCCGTCTCGACGA 556
QY 169 uLeuLeuAlaAlaGlyGluAla---GlyThrPheAspValAlaValAlaAspAlaAspLy 188
DB 557 CTTCTGTGGGACAGAGCAGCAGCGGTCTGCTCGACTTCGCTTCTGTGGACGCGCACAA 616
QY 188 sGluAsnCysSerAlaTyTrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLe 208
DB 617 CGACAACTACCTCAGCTACCAACGAGCGGTCTGTAAGCTGGTGGAGCGCGCGGCTCAT 676
QY 208 uAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAl 228
DB 677 CGGCTACGCAACACGCTGTGGAAACCGCTCCGCTGCTCCCGCAGCAGCGCGCCATGGG 736
QY 228 a-----AlaGluCysValArgAsnLeuLeuAsnGluArgIleArgAs 242
DB 737 CAAGTACATCCGGTTCTACCGGACATTCGTTCTCGCCCTCAACAGCGCGCTCCGCCCGCA 796
QY 242 pValArgValTyIleSerLeuLeuProLeuGlyAspGlyLeuThrLeu 258
DB 797 CGACCGCGGTNAGANTCTGCCAGCTCCCGCTCGCGCAGCGGCTCACGCTC 845

RESULT 4
US-09-452-239-11
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; Sequence 11, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-452-239-11

Alignment Scores:
Pred. No.: 1.06e-35 Length: 1058
Score: 396.00 Matches: 97
Percent Similarity: 55.86% Conservative: 46
Best Local Similarity: 37.89% Mismatches: 93
Query Match: 29.49% Indels: 20
DB: 3 Gaps: 5

US-10-017-407A-306 (1-262) x US-09-452-239-11 (1-1058)

QY 18 SerAlaLeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProPro 37
DB 120 AGCAGCGCAATGGGAGCAGCGCGCGAGC-----AGAAAGA----- 155
QY 38 TrpArgGlyArgGluGlnCysLeuLeu-ProProGluAspSerArg-LeuTrpGln 57
DB 156 ---CGCGGACCTCGGAGGTGCGGCCCAAGAGCTCTCAAGCGCAGCATCTCTACAGT 212
QY 57 TyLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLeuArgLeu 75
DB 213 ACATCTGGAGACGAGCGGTGATCCCGCGGAGCAGCAGTGATGAAGGAGTCCCGCAGG 272
QY 75 euThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeu 95
DB 273 TCACCGCCCAACCAACCATGGAACCTGTGACGACGCTCGCGCGGAGGGGCAATTCTCTGA 332
QY 95 laAsnLeuAlaArgLeuIleGlnAlaIleAlaLeuAspLeuGlyThrPheThrGlyT 115
DB 333 ACCTGCTGTGAAGCTCATCGCGGCCCAAGAACCATGAGATCGCGCTCTACCGGCT 392
QY 115 TySerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValThrCysGluV 135
DB 393 ACTCCCTCTCGCCACCGCCCTCGCCATCCCGACGACGACGATCTTGGCGATGACA 452
QY 135 alAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHis 155
DB 453 TCAACCGGAGAACTACGAGCTGGGCTCCCGTCGATCGAGAGGGGAGGTGGCGCAC 512
QY 155 yAlaAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeu---AlaAlaG 174
DB 513 AGATTCACCTTCGCGGAGGAGGACCGCGCTCCCGTGTGAGCCAGCTGGTGGAGGAGGAGG 572
QY 174 lYgluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCysSerAlat 194
DB 573 GCAACCATCGGTCTGCTCGACTTCGTGTCGACGCGCCGACAGGACAACTACTCTCAACT 632
QY 194 TyTrpGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal 214
DB 633 ACCACGAGCGGTGATGAAGCTGGTCAAGGTGCGCGGCTCGTCTGCTGACGACACACGC 692
QY 214 euTrpArgGlyLysValLeuGlnProProLysGlyAspValAla----- 228
DB 693 TCTGGAACGCGCTCCGCTCGTCTCCCGCGCAGCGCCCTCATGCGCAAGTACATCCGCTACT 752
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QY 229 --AlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIles 248
Db 753 ACCGGACCTCGTCTGAGCTCAACAGGCGCTCGCGCGGACACCGCGTGGAGATCT 812
QY 248 exLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 813 GCCAGCTCCCGTCCGCGGCGGATCACCTCTCGCGCGCGTCT 856

RESULT 5
US-09-452-239-41
; Sequence 41, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 41
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-452-239-41

Alignment Scores:
Pred. No.: 1,85e-35 Length: 1078
Score: 394.00 Matches: 102
Percent Similarity: 54.14% Conservative: 42
Best Local Similarity: 38.35% Mismatches: 100
Query Match: 29.34% Indels: 23
DB: 6 Gaps: 6

US-10-017-407A-306 (1-262) x US-09-452-239-41 (1-1078)
QY 6 ProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAlaLeuGlyAlaAla--- 24
Db 97 CCAGCAATGCCACCGCAGCGCGGCGCAC-GGCGCGGCGGCCCAAGGACCGCGCGC 155
QY 25 -----PheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGlyArgArg 42
Db 156 CAACGGTTCGAGCAGGT-----CACGCGCCACTCCGAGGTGGCCA 197
QY 43 GluGlnCysLeuLeuProGluAspSerArg-LeuTrpGlnTyrLeuLeuSerArgSe 62
Db 198 CAAGAG-----CCTGCTCAGAGCGACGCGCTCTACAGATACATCTCGAGACGAG 248
QY 62 rMet-----ArgGluHisProAlaLeuArgSerLeuArgLeuLeuGluGlnPr 80
Db 249 CGTGATCCCGCGGACGACGATGTCATGAGGAGTCCGCGGATCACCGCCCAACCC 308
QY 80 oGlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLe 100
Db 309 ATGGAACCTGATGACGACGCTCGCGCGGCGGCGGCGGCTCTCAACATCTGCTCAAGT 368
QY 100 uileGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLe 120
Db 369 CATCGGCGCAAGAGACCATGAGATGGCGTCTACACCGGCTACTCCTCTCGGCAC 428
QY 120 uAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPr 140
Db 429 CGGGCTCGGCTCCCGGACGCGGACCATCTTGGCCATGGACATCAACCGCGGAGACTA 488
QY 140 oGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLe 160
Db 489 CGAGCTGGGGCTCGCGTGTGATCGAGAAAGCGCGGTGGCGCAAGATCGACTTCGCGCA 548

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QY 160 ulysProAlaLeuGluThrLeuAspGluLeuLeuAla---AlaGlyGluAlaGlyThrPh 179
Db 549 GGGCCCGCGCTGCGGTGCTGACCGCTGCGGAGGAGGAGGCAACACCGGACCTT 608
QY 179 eAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLe 199
Db 609 CGACTTCGTCTTGTGTGAGCGCGGCAAGGACAACTACCTCAACTACCGAGCGCTCAT 668
QY 199 uGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysVa 219
Db 669 GAAGCTCGTCAAGCTCGCGCGCTCTCGGTACGACACACGCTCTGGAACGGCTCCGT 728
QY 219 lLeuGlnProProLysGlyAspValAla-----AlaGluCysValAr 233
Db 729 CGTGTCTCCCGCGGAGCGGCCCATCGGCAAGTACATCGCTACTACCGGACTTCGTCT 788
QY 233 gAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeuLeuProLeuGl 253
Db 789 CGACCTCAACAGGCGCTCGCGCGGACCGCGCGTGGAGATCTGCCAGCTCCCGTCGG 848
QY 253 yAspGlyLeuThrLeu 258
Db 849 CGACGGCATCACCCCTC 864

RESULT 6
US-09-452-239-23
; Sequence 23, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (22)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (68)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (866)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (902)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (905)
US-09-452-239-23

Alignment Scores:
Pred. No.: 2.31e-35 Length: 962
Score: 392.50 Matches: 88
Percent Similarity: 58.11% Conservative: 41
Best Local Similarity: 39.64% Mismatches: 84
Query Match: 29.23% Indels: 9
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x US-09-452-239-23 (1-962)
QY 50 GluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67

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Db 125 CAGAGCGATGCCTCTATCAGTATATCTTAAACACAGTGTGTACCAAGAGAGCATGAG 184
Qy 68 AlaLeuArgSerLeuArgLeuThrLeuGluGlnProGlnGlyAspSerMetThr 87
   ::::: ||||| ::::: |||||
Db 185 AGCTTGAAGGAGCTACGAGAGTTGACGGAACACACCTTGGAACTGATGGCTACACCA 244
Qy 88 CysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysAlaLeu 107
   ::::: ||||| ::::: |||||
Db 245 CTTGACGAAGGACAACTTCTAGGCATGCTCTTAAAGCTTATCAATGCCAAGAACACCATG 304
Qy 108 AspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAsp 127
   ::::: ||||| ::::: |||||
Db 305 GAAATAGGCGTCTTCACTGGTACTCTTCTTCCAGCTTCCCTGCCCTCTCTCTGAC 364
Qy 128 GlyArgValValThrCysGluValAlaAspAlaGlnProProGluLeuGlyArgProLeuTrp 147
   ::::: ||||| ::::: |||||
Db 365 GGAAGATCTTAGCTATGATGTTAAACCGGAATATTATGAATTGGGTTGCCCGTATT 424
Qy 148 ArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu 167
   ::::: ||||| ::::: |||||
Db 425 GAAAGGCTGGAGTGGCTCACAGATTGACTTCAGAGAAGGACCCGCTCTCTCTCTT 484
Qy 168 AspGluLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAla 186
   ::::: ||||| ::::: |||||
Db 485 GACGTTCTCATTAAGACGAAAGAAATAAGGAGCTTTGATTTCACTATGTTGGTATT 544
Qy 187 AspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206
   ::::: ||||| ::::: |||||
Db 545 GATAAGGACAATTACTTGAACCTACCAAGAGGGTGAATGAGCTTGTGAAGCTTGGGGA 604
Qy 207 IleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAsp 226
   ::::: ||||| ::::: |||||
Db 605 TTGATCGGCTACGATAACACCCCTATGGAATGGTGGTGGTGGCCGCCACCCGATGCTCT 664
Qy 227 ValAla-----AlaGluCysValArgAsnLeuAsnGluArgIleArg 240
   ::::: ||||| ::::: |||||
Db 665 CTCATGGATTGTTAAGTATTATCCGATTATTGTTATGAGCTCAACAGCTCTTGCA 724
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
   ::::: ||||| ::::: |||||
Db 725 CTTGATTCAAGGTCGAGATTGTCAGCTTCCGTTGGTGGTGGATTAACCTGTGCCGC 784
Qy 261 LysIle 262
   ::::: |||||
Db 785 CGCATC 790

RESULT 7
US-09-452-239-25
; Sequence 25, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafaleki, Antoni J.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: Glycine max
US-09-452-239-25
Alignment Scores:
Pred. No.: 2 54e-35 Length: 1023
Score: 32.50 Matches: 88
Percent Similarity: 58.11% Conservatives: 41
Best Local Similarity: 39.64% Mismatches: 84

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Query Match: 29.23% Indels: 9
DB: 3 Gaps: 3
US-10-017-407A-306 (1-262) x US-09-452-239-25 (1-1023)
Qy 50 GluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67
Db 132 CAGAGGATGCACTCTCAGTATATCTTAAACACAGTGTGTACCAAGAGAGCATGAG 191
Qy 68 AlaLeuArgSerLeuArgLeuThrLeuGluGlnProGlnGlyAspSerMetThr 87
   ::::: ||||| ::::: |||||
Db 192 AGCTTGAAGGAGCTACGAGAGTTGACGGAACACACCTTGGAACTGATGGCTACACCA 251
Qy 88 CysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysAlaLeu 107
   ::::: ||||| ::::: |||||
Db 252 CTTGACGAAGGACAACTTCTAGGCATGCTCTTAAAGCTTATCAATGCCAAGAACACCATG 311
Qy 108 AspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAsp 127
   ::::: ||||| ::::: |||||
Db 312 GAAATAGGCGTCTTCACTGGTACTCTTCCAGCTTCCCTGCCCTCTCTCTGAC 371
Qy 128 GlyArgValValThrCysGluValAlaAspAlaGlnProProGluLeuGlyArgProLeuTrp 147
   ::::: ||||| ::::: |||||
Db 372 GGAAGATCTTAGCTATGATGTTAAACCGGAATATTATGAATTGGGTTGCCCGTATT 431
Qy 148 ArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu 167
   ::::: ||||| ::::: |||||
Db 432 GAAAGGCTGGAGTGGCTCACAGATTGACTTCAGAGAAGGACCCGCTCTCTCTCTT 491
Qy 168 AspGluLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAla 186
   ::::: ||||| ::::: |||||
Db 492 GACGTTCTCATTAAGACGAAAGAAATAAGGAGCTTTGATTTCACTATGTTGGTATT 551
Qy 187 AspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206
   ::::: ||||| ::::: |||||
Db 552 GATAAGGACAATTACTTGAACCTACCAAGAGGGTGAATGAGCTTGTGAAGCTTGGGGA 611
Qy 207 IleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAsp 226
   ::::: ||||| ::::: |||||
Db 612 TTGATCGGCTACGATAACACCCCTATGGAATGGTGGTGGTGGCCGCCACCCGATGCTCT 671
Qy 227 ValAla-----AlaGluCysValArgAsnLeuAsnGluArgIleArg 240
   ::::: ||||| ::::: |||||
Db 672 CTCATGGATTGTTAAGTATTATCCGATTATTGTTATGAGCTCAACAGCTCTTGCA 731
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
   ::::: ||||| ::::: |||||
Db 732 CTTGATTCAAGGTCGAGATTGTCAGCTTCCGTTGGTGGTGGATTAACCTGTGCCGC 791
Qy 261 LysIle 262
   ::::: |||||
Db 792 CGCATC 797

RESULT 8
US-09-452-239-13
; Sequence 13, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafaleki, Antoni J.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; TYPE: DNA
; ORGANISM: Oryza sativa

```

FEATURE:  
NAME/KEY: unsure  
LOCATION: (483)  
US-09-452-239-13

## Alignment Scores:

Pred. No.: 6.17e-35 Length: 997  
Score: 389.00 Matches: 87  
Percent Similarity: 57.47% Conservative: 40  
Best Local Similarity: 39.37% Mismatches: 82  
Query Match: 28.97% Indels: 12  
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x US-09-452-239-13 (1-997)

QY 54 LeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSer 71  
DB 151 CTGTCAAGTATGCTCTGGACACGAGCGGTGCTGCCACGGGACCGGAGTGCATGCGCGAT 210  
QY 72 LeuArgLeuLeuThrLeuGlnProGlnGlyArgSerMetMetThrCysGluGlnAla 91  
DB 211 CTGGCGCTCATCAGGACAGCAGCAGTGGGGGTTTCATGCTGCTGCGCGATGAGCGG 270  
QY 92 GlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysLeuAlaLeuAspLeuGlyThr 111  
DB 271 CAGCTGCTGGGATGCTGCTGAAGATGGCCGAGCGAGCAATCAGAGTGCGTGC 330  
QY 112 PheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValVal 131  
DB 331 TTCCCGGCTACTCGCTGCTGCGACGCGGCTGGCGCTGCCGAGACGGGAGGTGGT 390  
QY 132 ThrCysGluValAspAlaGlnProGlnLeuGlyArgProLeuTrpArgGlnAlaGlu 151  
DB 391 GCGATCGCCCGACAGGAGAGTACGAGATCGGGCGCGCTTCTTGAGAAAGCCGGG 450  
QY 152 AlaGluHisLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeu 171  
DB 451 GTGGCGCACAAAGTGGACTTCCCAAGGGGAAANGGCTGGAGAAGCTGGACGCTGCTC 510  
QY 172 -----AlaAlaGlyGluAlaGlyThrPheAspValAlaValAspAlaAsp 187  
DB 511 GCGGAGGAGCG 570  
QY 188 LysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyLe 207  
DB 571 AAGCCCACTACGTCAAGTACCACAGCAGCTGCTGACGTGGTGGCGCTCGCGCGCGAC 630  
QY 208 LeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspVal 227  
DB 631 ATCGGTGTACGACAAACACGCTGTGGCGCGCACCGTGGCGCTGCCGCGACACGCGCTG 690  
QY 228 Ala-----AlaGluCysValArgAsnLeuAsnGluArgileArgArg 241  
DB 691 TCGGACCTGGACCGGAGGTTCCTCGTCGCATCAGGGACCTCAACTCCAGGCTCCCGCC 750  
QY 242 AspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLys 261  
DB 751 GACCCCGCATCGAGCTGTGCCAACTCGCCATCGCGACCGGATCACCATCTGCGCGCGC 810  
QY 262 Ile 262  
DB 811 CTC 813

## RESULT 9

US-09-452-239-45  
Sequence 45, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Rafaleki, Antoni J.  
APPLICANT: Fader, Gary M.  
APPLICANT: Cahoon, Rebecca E.  
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase  
FILE REFERENCE: BB1284 US NA

CURRENT APPLICATION NUMBER: US/09/452,239  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 60/110,594  
EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 45  
LENGTH: 953  
TYPE: DNA  
ORGANISM: Triticum aestivum  
US-09-452-239-45

## Alignment Scores:

Pred. No.: 9.77e-35 Length: 953  
Score: 387.00 Matches: 105  
Percent Similarity: 55.51% Conservative: 46  
Best Local Similarity: 38.60% Mismatches: 104  
Query Match: 28.82% Indels: 18  
DB: 3 Gaps: 8

US-10-017-407A-306 (1-262) x US-09-452-239-45 (1-953)

QY 3 GlnProValPro-----ArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 6 CAACCCATTCTCTCTACTACTCTCGGCACAACCCAGCCCAACAGAACTAGCGGACGAGCC 65  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40  
DB 66 AT-GGCGCC-----CAACGGAGACAACCCGTGGCCACGCT-----CCACGGCGCAT 112  
QY 41 ArgArgGluGln-CysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSe 60  
DB 113 CGACAGACCAACAAGACGCTGCTCAAGAGCGACGCC---CTCTACACTTACTCTCGA 169  
QY 60 rArgSerMet-----ArgGluHisProAlaLeuArgSerLeuArgLeuLeuGlu 78  
DB 170 CACCACCGCTGTCCCGCGAGCAGAGTGCATGCGGACCTGCGCCTCATCACCGCAAA 229  
QY 78 uGlnProGlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAl 98  
DB 230 GCACCATGGGTGTACATGCAGTCTCTCGACAGCGCGAGCTGTGGGATGCTGAT 289  
QY 98 aArgLeuileGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLe 118  
DB 290 CAAGATGCGCGCGCCCAAGAGACGATCAGGTGGCGTGTTCACGGGCTACTCGCTGT 349  
QY 118 uAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGl 138  
DB 350 GGCCACCGCGCTGGCGCTCCCGGAGGACGGAAGGTGGTGGCCATCGACACCGCGCA 409  
QY 138 nProGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLe 158  
DB 410 GTGTACAGGTGGTGTCCCTTCATCGAAGGCGCGCATGGCGCACAAAGTGGACTT 469  
QY 158 uArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGlu---AlaGl 177  
DB 470 CGCGAGGCGCACCGCGCTGGCGCGCTCGACGAGCTCTCTCGTGGAGGACGCGCGCGC 529  
QY 177 yThrPheAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluAr 197  
DB 530 GAGCTACGACTTCGCGTTCGTGGACGCGGACAAAGCCCAACTACGTGCGCTACACGAGCA 589  
QY 197 gCysLeuGlnLeuLeuArgProGlyLysLeuAlaValLeuAlaValLeuTrpArgGlu 217  
DB 590 GCTGTGAAGTGTGTTCGCGCGCGCATCTATCTTACGACAAACACGCTCTGGGGCGG 649  
QY 217 yLysValLeuGlnPro-----ProLysGlyAspVal-----AlaAlaGluC 231  
DB 650 CACGTGCGCGTGGCG 709  
QY 231 sValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeuLeuPr 251  
DB 710 CTTCAGGACCTCAACGCGCAAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 769



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Db 486 TGCCACAAAGATTGACTTTCAGAGAGGGCCCTGCTCTGCCAGTTCTGGACGAACCTGCTTAA 545
Qy 172 aalaglygluala---GlyThrPheaspValalavalalaspAlaaspLysGluasnCy 191
Db 546 GAATGAGGACATGCGATCGTTCATTTGTTGTCGGATGCGGACAAAGACAACTA 605
Qy 191 sSerAlaTyrTrpGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValle 211
Db 606 TCTAACTACACAGCGTCTGATCGATCTGTTGAGGTTGAGGTTGATGTCATATGA 665
Qy 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValala----- 228
Db 666 CAACACCCCTGTGGAACGATCTGTGTGCTCCACCCGATGCTCCCTTCAGGAAATATGT 725
Qy 229 -----AlaGluCysValArgAsnLeuAsnGluArgGlyIleLeuAlaValle 245
Db 726 GAGATATTACAGAGATTTCGTGATGAGCTAACCAAGGCCCTTGTGTCGATCCCGCAT 785
Qy 245 lTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 786 TGAGATCAGCCAAATCCAGTGGTGACGGCGTCCACCTTTTCAGGCGGTGTC 837

RESULT 12
US-09-169-789-94
; Sequence 94, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 94
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-169-789-94

Alignment Scores:
Pred. No.: 1.4e-34 Length: 1012
Score: 386.00 Matches: 86
Percent Similarity: 57.56% Conservative: 51
Best Local Similarity: 36.13% Mismatches: 88
Query Match: 28.74% Indels: 13
DB: 4 Gaps: 4

US-10-017-407a-306 (1-262) x US-09-169-789-94 (1-1012)
Qy 35 CysProTrpTrpArgGlyArgArgGluGln-CysLeuLeuProProGluAspSerArgLe 54
Db 135 TGTCCGCCATCAAGAGTGGGACACAAAAGTCTTTTG-----CAGAGCGATGCCCT 185
Qy 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
Db 186 CTATCAGTATATTGGAAACGAGGCTGTACCTCTGTAGCCCGGACCCATGAAGAGCT 245
Qy 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAlaGl 92
Db 246 CGCGAAGTGAAGTCCCAAGCATCCCTGGAACTCTGATGCTTCTGCGATGAGGCTCA 305
Qy 92 nLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysIleAlaLeuAspLeuGlyThrPh 112
Db 306 ATTTCTGGCGCTCCCTGCTGAGCTATTAAACCCCAAGAACACCATGGAGATTGGGTGTA 365
Qy 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaLeuAspGlyArgValValTh 132
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Db 366 CACTGTTTACTCGTTCCTCAGCACAGCCCTTGTGATTCGCCGATGATGGAAGATTCTTACG 425
Qy 132 rCysGluValaspAlaGlnProProGluLeuGlyArgProLeuTrpArgGluAlaGluAl 152
Db 426 CATGACATCAACAGAGAACTATGATATCGATTGCTTATTATTGAGAAAGCAGGAGT 485
Qy 152 aGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172
Db 486 TCCCAACAGATTGACTTCAGAGAGGGCCCTGCTCTGCCAGTTCTGGACGAACCTGCTTAA 545
Qy 172 aalaglygluala---GlyThrPheaspValalaValValaspAlaaspLysGluasnCy 191
Db 546 GAATGAGGACATGCGATCGTTCGATTTTGTGTTGTTGATGCGGACAAAGACAACTA 605
Qy 191 sSerAlaTyrTrpGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValle 211
Db 606 TCTAACTACACAGCGTCTGATCGATCTGTGTAAGGTTGAGGTTGATGTCATATGA 665
Qy 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValala----- 228
Db 666 CAACACCCCTGTGGAACGATCTGTGTGCTCCACCCGATGCTCCCTTCAGGAAATATGT 725
Qy 229 -----AlaGluCysValArgAsnLeuAsnGluArgIleArgAspValArgVa 245
Db 726 GAGATATTACAGAGATTTCGTGATGAGCTAACCAAGGCCCTTGTGTCGATCCCGCAT 785
Qy 245 lTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 786 TGAGATCAGCCAAATCCAGTGGTGACGGCGTCCACCTTTTCAGGCGGTGTC 837

RESULT 13
US-08-713-000-6
; Sequence 6, Application US/08713000
; Patent No. 5850020
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Grierson, Alastair
; TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,000
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-713-000-6
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## Alignment Scores:

Pred. No.: 1,42e-34 Length: 1026  
 Score: 386.00 Matches: 86  
 Percent Similarity: 57.56% Conservative: 51  
 Best Local Similarity: 36.13% Mismatches: 88  
 Query Match: 28.74% Indels: 13  
 DB: 2 Gaps: 4

US-10-017-407A-306 (1-262) x US-08-713-000-6 (1-1026)

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QY 35 CysProProTArgGlyArgGluGln-CysLeuLeuProGluAspSerArgLe 54
DB 149 TGTCCGCCATCAGAAAGTGGACACAAAAGTCTTTG-----CAGAGCATCCCT 199
QY 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
DB 200 CTATCAGTATATATTGGAACGAGCGTGTACCCCTGTGAGCCGACCAATGAAGGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluGlnAlaGl 92
DB 260 CCGCGAAGTGAAGTCCCAAGCATCCTCGAACCTCATGACTACTTCTGCGCATGAGGTC 319
QY 92 nLeuLeuAlaAenLeuAlaArgLeuileGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112
DB 320 ATTCTGGGCCCTCCTCGTGAAGCTATTAAACGCAAGAACACCATGAGGATGGGTGTA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132
DB 380 CACTGGTACTCGCTCTCAGCACAGCCCTTGATTCGCCGATGATGGAAGATTTCTAGC 439
QY 132 rCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGl 152
DB 440 CATGGACATCAACAGAGAACTATGATATCGGATTCGCTATTATTGAGAAAGCAGGAGT 499
QY 152 aGluHisLysLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172
DB 500 TGCCCAACAAGATTGACTTCAGAGAGGCCCTCGTCTGCCAGTTCCTGCGAGAACTGCTTAA 559
QY 172 aAlaGlyGluAla---GlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCy 191
DB 560 GAATGAGGACATCGATGATCGTTTCGATTTGTGTTGTCGTCGATGCGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVal 211
DB 620 TCTAAACTACCAACAGCGTCTGATCATCTGTGAGAGTGTGAGGTCCTGATTCATATGA 679
QY 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAla----- 228
DB 680 CAACACCCCTGTGGAACGGATCTGTGTGCTCCACCCGATGCTCCCTCAGGAAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgGlyArgAspValArgVa 245
DB 740 GAGATATTACAGATTTCTGTGATGAGCTAAACAGAGCCCTTGTCTGATCCCGCAT 799
QY 245 lTyrIleSerLeuLeuProGluGlyAspGlyLeuThrLeuAlaPheLysIle 262
DB 800 TGAGATCAGCAAAATCCCATCGTGTGACGCGCGTCCACCCCTTGACGCGCGTGC 851

```

## RESULT 14

US-08-975-316-6  
 Sequence 6, Application US/08975316  
 Patent No. 5952486  
 GENERAL INFORMATION:  
 APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
 APPLICANT: and GRIERSON, Alastair W.  
 TITLE OF INVENTION: MATERIALS AND METHODS FOR  
 TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT  
 NUMBER OF SEQUENCES: 88  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Law Offices of Ann W. Speckman  
 STREET: 2601 Elliott Avenue, Suite 4185  
 CITY: Seattle  
 STATE: WA

COUNTRY: USA  
 ZIP: 98121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/975,316  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/713,000  
 FILING DATE: September 11, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SLEATH, Janet  
 REGISTRATION NUMBER: 37,007  
 REFERENCE/DOCKET NUMBER: 11000/1003C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-269-0565  
 TELEFAX: 206-269-0563  
 TELEX:

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1026 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-975-316-6

Alignment Scores:  
 Pred. No.: 1,42e-34 Length: 1026  
 Score: 386.00 Matches: 86  
 Percent Similarity: 57.56% Conservative: 51  
 Best Local Similarity: 36.13% Mismatches: 88  
 Query Match: 28.74% Indels: 13  
 DB: 2 Gaps: 4

US-10-017-407A-306 (1-262) x US-08-975-316-6 (1-1026)

```

QY 35 CysProProTArgGlyArgGluGln-CysLeuLeuProGluAspSerArgLe 54
DB 149 TGTCCGCCATCAGAAAGTGGACACAAAAGTCTTTG-----CAGAGCATCCCT 199
QY 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
DB 200 CTATCAGTATATATTGGAACGAGCGTGTACCCCTGTGAGCCGACCAATGAAGGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluGlnAlaGl 92
DB 260 CCGCGAAGTGAAGTCCCAAGCATCCTCGAACCTCATGACTACTTCTGCGCATGAGGTC 319
QY 92 nLeuLeuAlaAenLeuAlaArgLeuileGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112
DB 320 ATTCTGGGCCCTCCTGTGAGCTATTAAACGCAAGAACACCATGAGGATGGGTGTA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132
DB 380 CACTGGTACTCGCTCTCAGCACAGCCCTTGATTCGCCGATGATGGAAGATTTCTAGC 439
QY 132 rCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGl 152
DB 440 CATGGACATCAACAGAGAACTATGATATCGGATTCGCTATTATTGAGAAAGCAGGAGT 499
QY 152 aGluHisLysLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172
DB 500 TGCCCAACAAGATTGACTTCAGAGAGGCCCTCGTCTGCCAGTTCCTGCGAGAACTGCTTAA 559
QY 172 aAlaGlyGluAla---GlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCy 191
DB 560 GAATGAGGACATCGATGATCGTTTCGATTTGTGTTGTCGTCGATGCGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVal 211

```

```
Db 620 TCTAAACTACCAACGCTCTGATCGATCTGGTGAAGGTTGGAGGTCCTGATTCATATCA 679
QY 211 uargValLeuTTPArgGlyLysValLeuGlnProPolysGlyAspValAla----- 228
Db 680 CAACACCCCTGTGAACGGATCTGTGTGGCTCCACCCGATGCTCCCTGAGGAAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgGileArgAspValArgVa 245
Db 740 GAGATATTACAGAGATTTCGTGATGAGCTAAACAAGGCCCTTGTCTGATCCCGCAT 799
QY 245 lTyrileSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 800 TGAGATCAGCAAAATCCAGTCGGTGACGCGCTCACCCCTTTGACGCGGTGC 851
```

## RESULT 15

```
US-09-211-710-6
; Sequence 6, Application US/09211710A
; Patent No. 6204434
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Grierson, Alastair
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003C3
; CURRENT APPLICATION NUMBER: US/09/211,710A
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-6
```

## Alignment Scores:

```
Pred. No.: 1,42e-34 Length: 1026
Score: 386.00 Matches: 86
Percent Similarity: 57.56% Conservative: 51
Best Local Similarity: 36.13% Mismatches: 88
Query Match: 28.74% Indels: 13
DB: 3 Gaps: 4
```

US-10-017-407A-306 (1-262) x US-09-211-710-6 (1-1026)

```
QY 35 CysProTrpArgGlyArgGluGln-CysLeuLeuProGluAspSerArgLe 54
Db 149 TGTCCGCCATCAAGAGTGGGACACAAAAGTCTTTTG-----CAGAGCGATGCCCT 199
QY 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
Db 200 CTATCAGTATATTTGGAACAGCGGTGTACCCTGTGAGCCCGAGCCCATGAAGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAlaGl 92
Db 260 CGCGAAGTGAAGTCCCAAGCATCCCTGGAACTCTGATGACTACTTCTGCCGATGAGGTCA 319
QY 92 nLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112
Db 320 ATTTCTGGGCGCTCTGCTGCTGATTAACCGCAAGAACACCATGGAGATTGGGGTGTA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132
Db 380 CACTGGTACTCGCTTCTCAGCAGACCCCTTGATGATGATGATGATGATGATGATGATGATG 439
QY 132 rCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGlua 152
Db 440 CATGGACATCAACAGAGAGAACTATGATATCGGATTCCTATTTATGAGAAAGCAGGAGT 499
QY 152 aGluHisLysIleAspLeuArgLeuLysProAlaLeuThrLeuAspGluLeuAl 172
Db 500 TGCCCAACAAGATTGCTTTCAGAGAGGCGCCCTCTCTGCGAGTTCTGGACGAAGCTCTTAA 559
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Search completed: April 20, 2005, 02:30:48  
Job time : 489 secs

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QY 172 aAlaGlyGluAla----GlyThrPheAspValAlaValValAspAlaAspLysGluAsnCy 191
Db 560 GAATGAGGACATGCATGATCGTTCGATTTTGTGTGATGCGGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValle 211
Db 620 TCTAAACTACCAACAGCGTCTGATCGATCTGTGAAGGTTGGAGGCTCTGATTCATATCA 679
QY 211 uArgValLeuTTPArgGlyLysValLeuGlnProPolysGlyAspValAla----- 228
Db 680 CAACACCCCTGTGAACGGATCTGTGTGGCTCCACCCGATGCTCCCTGAGGAAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgGileArgAspValArgVa 245
Db 740 GAGATATTACAGAGATTTCGTGATGAGCTAAACAAGGCCCTTGTCTGATCCCGCAT 799
QY 245 lTyrileSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 800 TGAGATCAGCAAAATCCAGTCGGTGACGCGCTCACCCCTTTGACGCGGTGC 851
```



```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: April 19, 2005, 22:32:16 ; Search time 586 Seconds
(Without alignments)
2646.710 Million cell updates/sec

US-10-017-407A-306
Title: 1343
Perfect score: 1343
Sequence: 1 MTPQVRLSPVPAALALGSA.....VRVYISLLPLGDLGLTAFKI 262
Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-O=/cgn2_1/USPTO.spool/US10017407/runat.19042005.142607.29831/app.query.fasta_1.455
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=1500 -DOCALIGN=200 -THR MAX=100 -THR MIN=0 -ALIGN=1500
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10017407 @CGN 1 1 644 @runat.19042005.142607.29831 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database: N Geneseq 16Dec04:*
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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
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7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID ABA05420 standard; cDNA; 789 BP.
DE Human O-methyltransferase family member 25692 coding sequence.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 2
ID ADQ87466 standard; cDNA; 927 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4343.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 3
ID AAZ98166 standard; cDNA; 985 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0

DE Human signal peptide containing protein HSPP-58 cDNA SEQ ID NO:192.
PN WO20000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 4
ID ADO42272 standard; cDNA; 988 BP.
DE Human NOVX polynucleotide #61.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE-) AGEE M L.
PA (ALSO-) ALSOBROOK J P.
PA (ANDE-) ANDERSON D W.
PA (BERG-) BERGHS C.
PA (BOLD-) BOLDOG F L.
PA (BURG-) BURGESS C B.
PA (CATT-) CATTERTON E.
PA (DIPI-) DIPIPPO V A.
PA (EDIN-) EDINGER S R.
PA (EISE-) EISEN A.
PA (ELLE-) ELLERMAN K.
PA (GANG-) GANGOLLI E A.
PA (GERL-) GERLACH V.
PA (GORM-) GORMAN L.
PA (ROTH-) ROTHBERG B G.
PA (GUOX-) GUO X S.
PA (HERR-) HERRMANN J L.
PA (HALV-) HALVORSEN Y.
PA (JIMW-) JI W.
PA (KEKU-) KERUA R.
PA (KHRA-) KHRAMTSOV N V.
PA (LARO-) LAROCHELLE W J.
PA (LEPL-) LEPLEY D M.
PA (LILL-) LI L.
PA (MACD-) MACDOUGALL J R.
PA (MILL-) MILLER C E.
PA (ORTT-) ORT T.
PA (PADI-) PADIGARU M.
PA (PATT-) PATTURAJAN M.
PA (PENA-) PENA C E A.
PA (PEYM-) PEYMAN J A.
PA (RIEG-) RIEGER D K.
PA (ROTH-) ROTHENBERG M E.
PA (SHEN-) SHENOY S G.
PA (SMIT-) SMITHSON G.
PA (SPAD-) SPADERNA S K.
PA (SPYT-) SPYTEK K A.
PA (STON-) STONE D J.
PA (TAUP-) TAUPIER R J.
PA (VERN-) VERNET C A M.
PA (VOSS-) VOSS E Z.
PA (ZHON-) ZHONG M.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 5
ID AAA37107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 6
ID AAF54419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 7
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 8
ID ACD68458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US20030731130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 9
ID ACHO4560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 10
ID ACD68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US20030731129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 11
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 12
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 13
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ADD70343 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ADD38464 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ADD39420 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ADE20207 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ADE50118 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADE21676 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 23  
ID ADF30101 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 24  
ID ADF55994 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 25  
ID ADH9498 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 26  
ID ADJ37302 standard; cDNA; 989 BP.  
DE Human tumour therapy associated PRO1558 cDNA.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 27  
ID ADE96678 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 28  
ID ADF25989 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 29  
ID ADF24888 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 30  
ID ADF29624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 31

ID ADE97155 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 32  
ID ADH03193 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 33  
ID ADH04147 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 34  
ID ADH03670 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 35  
ID ADG88226 standard; cDNA; 989 BP.  
DE Human PRO polypeptide cDNA #11.  
PN US2003170228-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 36  
ID ADH04624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 37  
ID ADH61625 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 38  
ID ADL94824 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 39  
ID ADO42276 standard; cDNA; 989 BP.

```
DE Human NOVX polynucleotide #63.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERE/) HEREMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG W.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 40
ID ABA05419 standard; cDNA; 1037 BP.
DE Human O-methyltransferase family member 25692 encoding cDNA.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 41
ID ABQ61039 standard; cDNA; 1100 BP.
DE Human PRO1558 protein encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 42
ID AAH33455 standard; cDNA; 967 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 98.85%
Query Match: 98.59%
Indels: 0
Mismatch: 3
Indel: 0
RESULT 43
ID AAC76634 standard; cDNA; 812 BP.
DE Human ORFX RF2189 polynucleotide sequence SEQ ID NO:4377.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.14%
Best Local Similarity: 99.14%
Query Match: 87.79%
Indels: 0
Conservative: 0
Mismatch: 2
Indel: 0
RESULT 44
ID AAD56372 standard; DNA; 876 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
Indels: 46
Conservative: 0
Mismatch: 1
Indel: 46
RESULT 45
ID AAD56361 standard; DNA; 885 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
Indels: 46
Conservative: 0
Mismatch: 1
Indel: 46
RESULT 46
ID ADO42274 standard; cDNA; 787 BP.
DE Human NOVX polynucleotide #62.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
Percent Similarity: 98.85%
Best Local Similarity: 98.59%
Query Match: 87.79%
Indels: 0
Conservative: 0
Mismatch: 2
Indel: 0
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PA (VERN/) VERNET C A M.  
PA (VONS/) VOSS E Z.  
PA (ZHON/) ZHONG M.  
Percent Similarity: 70.23%  
Best Local Similarity: 70.23%  
Query Match: 65.82%  
Indels: 78  
RESULT 47  
ID ADD34178 standard; DNA; 770 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.  
PN WO2003020220-A2.  
PD 13-MAR-2003.  
PA (UYEM-) UNIV EMORY.  
Percent Similarity: 92.49%  
Best Local Similarity: 84.97%  
Query Match: 56.22%  
Indels: 0  
RESULT 48  
ID ACH35890 standard; cDNA; 458 BP.  
DE Human endothelial cell cDNA #4023.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 99.02%  
Best Local Similarity: 98.04%  
Query Match: 37.90%  
Indels: 0  
RESULT 49  
ID ACH35195 standard; cDNA; 474 BP.  
DE Human endothelial cell cDNA #3328.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 99.02%  
Best Local Similarity: 98.04%  
Query Match: 37.90%  
Indels: 0  
RESULT 50  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Percent Similarity: 50.49%  
Best Local Similarity: 39.09%  
Query Match: 33.73%  
Indels: 56  
RESULT 51  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Percent Similarity: 50.49%  
Best Local Similarity: 39.09%  
Query Match: 33.73%  
Indels: 56  
RESULT 52  
ID AAA81501 standard; DNA; 48275 BP.  
DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 53  
ID AAA81489 standard; DNA; 837096 BP.  
DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.

PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 54  
ID AAF21610 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 55  
ID ABZ40101 standard; DNA; 666 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 62.15%  
Best Local Similarity: 42.52%  
Query Match: 32.69%  
Indels: 10  
RESULT 56  
ID ADM80044 standard; DNA; 675 BP.  
DE Spiramycin biosynthesis orfs\*, SEQ ID 11.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Percent Similarity: 60.99%  
Best Local Similarity: 46.19%  
Query Match: 32.61%  
Indels: 8  
RESULT 57  
ID ADN97560 standard; DNA; 675 BP.  
DE S ambofaciens spiramycin biosynthetic gene ORF5\*.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Percent Similarity: 60.99%  
Best Local Similarity: 46.19%  
Query Match: 32.61%  
Indels: 8  
RESULT 58  
ID ABD04592 standard; DNA; 846 BP.  
DE Pseudomonas aeruginosa polynucleotide #3196.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 55.19%  
Best Local Similarity: 42.32%  
Query Match: 31.94%  
Indels: 26  
RESULT 59  
ID AAQ44449 standard; DNA; 2381 BP.  
DE 3-acylating enzyme coding sequence.  
PN JP06038750-A.  
PD 15-FEB-1994.  
PA (MEIJ ) MEIJI SEIKA KAISHA.  
Percent Similarity: 54.12%  
Best Local Similarity: 39.61%  
Query Match: 31.68%  
Indels: 24  
RESULT 60  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Percent Similarity: 54.12%  
Best Local Similarity: 39.61%  
Query Match: 31.68%  
Indels: 24  
RESULT 61

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ID AAX25215 standard; cDNA; 1218 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PN WO9910498-A2.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 56.59%
Best Local Similarity: 39.15%
Query Match: 30.75%
Conservative: 45
Mismatch: 97
Indel: 15
RESULT 62
ID AAD05742 standard; cDNA; 1218 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) cDNA.
PN WO200134817-A2.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 56.59%
Best Local Similarity: 39.15%
Query Match: 30.75%
Conservative: 45
Mismatch: 97
Indel: 15
RESULT 63
ID ADI39160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 54.25%
Best Local Similarity: 38.87%
Query Match: 30.60%
Conservative: 38
Mismatch: 92
Indel: 21
RESULT 64
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PN WO2003106653-A2.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 59.71%
Best Local Similarity: 42.72%
Query Match: 30.49%
Conservative: 35
Mismatch: 80
Indel: 3
RESULT 65
ID ABS63417 standard; cDNA; 980 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 57.26%
Best Local Similarity: 38.17%
Query Match: 30.19%
Conservative: 46
Mismatch: 93
Indel: 10
RESULT 66
ID ABS63407 standard; cDNA; 891 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 56.03%
Best Local Similarity: 38.91%
Query Match: 29.86%
Conservative: 44
Mismatch: 88
Indel: 25
RESULT 67
ID AAD19545 standard; cDNA; 744 BP.
DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.
PN WO200173090-A2.
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
Percent Similarity: 59.91%
Best Local Similarity: 36.49%
Query Match: 29.67%
Conservative: 52
Mismatch: 80
Indel: 9
RESULT 68
ID ADI30327 standard; cDNA; 744 BP.
DE Alfalfa harvest inducible cDNA sequence H12.
PN WO2004002216-A2.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Conservative: 41
Mismatch: 84
Indel: 9
PA (UYGU-) UNIV GUELPH.
Percent Similarity: 59.91%
Best Local Similarity: 36.49%
Query Match: 29.67%
Conservative: 52
Mismatch: 80
Indel: 9
RESULT 69
ID ADI30333 standard; DNA; 1906 BP.
DE Alfalfa harvest inducible H12 gene genomic DNA sequence.
PN WO2004002216-A2.
PA (UYGU-) UNIV GUELPH.
Percent Similarity: 59.91%
Best Local Similarity: 36.49%
Query Match: 29.67%
Conservative: 52
Mismatch: 80
Indel: 9
RESULT 70
ID ADA70823 standard; DNA; 783 BP.
DE Rice gene, SEQ ID 4146.
PN WO2003000898-A1.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 55.86%
Best Local Similarity: 37.89%
Query Match: 29.43%
Conservative: 46
Mismatch: 93
Indel: 20
RESULT 71
ID ABS63412 standard; cDNA; 1058 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 55.86%
Best Local Similarity: 37.89%
Query Match: 29.43%
Conservative: 46
Mismatch: 93
Indel: 20
RESULT 72
ID ABS63427 standard; cDNA; 1078 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 54.14%
Best Local Similarity: 38.35%
Query Match: 29.34%
Conservative: 42
Mismatch: 100
Indel: 23
RESULT 73
ID ADA71076 standard; DNA; 1338 BP.
DE Rice gene, SEQ ID 4399.
PN WO2003000898-A1.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 57.87%
Best Local Similarity: 40.74%
Query Match: 29.28%
Conservative: 37
Mismatch: 79
Indel: 12
RESULT 74
ID ABS63418 standard; cDNA; 962 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Conservative: 41
Mismatch: 84
Indel: 9
RESULT 75
ID ABS63419 standard; cDNA; 1023 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Conservative: 41
Mismatch: 84
Indel: 9

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Best Local Similarity: 39.64% Mismatches: 84  
Query Match: 29.23% Indels: 9  
RESULT 76  
ID ADC68436 standard; cDNA; 1051 BP.  
DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Percent Similarity: 56.43% Conservative: 42  
Best Local Similarity: 39.00% Mismatches: 87  
Query Match: 29.23% Indels: 18  
RESULT 77  
ID ADC68544 standard; cDNA; 1059 BP.  
DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Percent Similarity: 56.43% Conservative: 42  
Best Local Similarity: 39.00% Mismatches: 87  
Query Match: 29.23% Indels: 18  
RESULT 78  
ID ADN74200 standard; cDNA; 780 BP.  
DE Thale cress cDNA expressed in E2Fa/Dpa expressing plants SeqID 2095.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 79  
ID ADN73162 standard; cDNA; 780 BP.  
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 80  
ID AAC42559 standard; cDNA; 1033 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 81  
ID ABN98364 standard; cDNA; 1072 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAM/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRICK/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Percent Similarity: 58.85% Conservative: 48

Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 82  
ID AAC44172 standard; cDNA; 1180 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 83  
ID AAC45547 standard; cDNA; 1032 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 55.14% Conservative: 49  
Best Local Similarity: 34.98% Mismatches: 88  
Query Match: 29.00% Indels: 21  
RESULT 84  
ID ABS63413 standard; cDNA; 997 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 57.47% Conservative: 40  
Best Local Similarity: 39.37% Mismatches: 82  
Query Match: 28.97% Indels: 12  
RESULT 85  
ID ABS63429 standard; cDNA; 953 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 55.51% Conservative: 46  
Best Local Similarity: 38.60% Mismatches: 104  
Query Match: 28.82% Indels: 18  
RESULT 86  
ID ABS54115 standard; cDNA; 967 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Percent Similarity: 58.56% Conservative: 48  
Best Local Similarity: 36.94% Mismatches: 83  
Query Match: 28.78% Indels: 9  
RESULT 87  
ID ADA49212 standard; cDNA; 798 BP.  
DE Maize gene conferring disease resistance in plants.  
PN WO2003000906-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.56% Conservative: 48  
Best Local Similarity: 37.16% Mismatches: 91  
Query Match: 28.74% Indels: 25  
RESULT 88  
ID AAA68001 standard; cDNA; 1012 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 57.56% Conservative: 51  
Best Local Similarity: 36.13% Mismatches: 88  
Query Match: 28.74% Indels: 13  
RESULT 89  
ID ADD41751 standard; cDNA; 1012 BP.  
DE O-methyl transferase DNA #9.  
PN US2003131373-A1.  
PD 10-JUL-2003.

PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 90  
 ID AAV23912 standard; DNA; 1026 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 91  
 ID AAZ06875 standard; cDNA; 1026 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 1.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 92  
 ID AAA67913 standard; DNA; 1026 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 93  
 ID ADD41663 standard; DNA; 1026 BP.  
 DE O-methyl transferase DNA #1.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 94  
 ID ABS63425 standard; cDNA; 1118 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 95  
 ID ABS63408 standard; cDNA; 1146 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 96  
 ID AAX25208 standard; cDNA; 1160 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.

Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 97  
 ID ABS63415 standard; cDNA; 931 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 59.46%  
 Best Local Similarity: 36.04%  
 Query Match: 28.70%  
 RESULT 98  
 ID ADC8545 standard; cDNA; 1063 BP.  
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Percent Similarity: 54.85%  
 Best Local Similarity: 37.69%  
 Query Match: 28.70%  
 RESULT 99  
 ID ADA71075 standard; DNA; 783 BP.  
 DE Rice gene. SEQ ID 4398.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 52.73%  
 Best Local Similarity: 38.67%  
 Query Match: 28.59%  
 RESULT 100  
 ID AAX25210 standard; cDNA; 1003 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 52.55%  
 Best Local Similarity: 36.50%  
 Query Match: 28.56%  
 RESULT 101  
 ID ABS63409 standard; cDNA; 1057 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 52.55%  
 Best Local Similarity: 36.50%  
 Query Match: 28.56%  
 RESULT 102  
 ID ABS63416 standard; cDNA; 929 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 56.43%  
 Best Local Similarity: 36.93%  
 Query Match: 28.48%  
 RESULT 103  
 ID ACN60610 standard; cDNA; 617 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LTB3829-025-Q6-K6-F5, SEQ:15391.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.



Percent Similarity: 60.00% Conservative: 38  
 Best Local Similarity: 41.00% Mismatches: 79  
 Query Match: 28.44% Indels: 1  
 RESULT 104  
 ID ABS63428 standard; cDNA; 1049 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.15% Conservative: 46  
 Best Local Similarity: 38.24% Mismatches: 105  
 Query Match: 28.37% Indels: 18  
 RESULT 105  
 ID ABS54114 standard; DNA; 845 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Percent Similarity: 57.66% Conservative: 47  
 Best Local Similarity: 36.49% Mismatches: 85  
 Query Match: 28.26% Indels: 9  
 RESULT 106  
 ID ADA49019 standard; DNA; 1112 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 53.58% Conservative: 40  
 Best Local Similarity: 38.49% Mismatches: 103  
 Query Match: 28.22% Indels: 22  
 RESULT 107  
 ID AAX25209 standard; cDNA; 944 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9310498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 52.42% Conservative: 42  
 Best Local Similarity: 36.80% Mismatches: 114  
 Query Match: 28.15% Indels: 15  
 RESULT 108  
 ID ABN87108 standard; cDNA; 1113 BP.  
 DE Lolium perenne LpCCoAMTA nucleotide sequence SEQ ID NO:1.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 56.02% Conservative: 44  
 Best Local Similarity: 37.76% Mismatches: 88  
 Query Match: 28.11% Indels: 18  
 RESULT 109  
 ID ADR5554 standard; cDNA; 1233 BP.  
 DE Cotton cDNA sequence, SEQ ID 6335.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Percent Similarity: 56.91% Conservative: 53  
 Best Local Similarity: 35.37% Mismatches: 88  
 Query Match: 28.07% Indels: 18  
 RESULT 110  
 ID ABN87245 standard; cDNA; 1161 BP.  
 DE Lolium perenne CCoAMT1 cDNA sequence SEQ ID NO:168.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 56.41% Conservative: 43  
 Best Local Similarity: 38.03% Mismatches: 88  
 Query Match: 28.03% Indels: 14  
 RESULT 111  
 ID AAO32259 standard; cDNA; 1258 BP.  
 DE Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).  
 PN DE4117747-A.  
 PD 03-DEC-1992.  
 PA (FARB) BAYER AG.  
 Percent Similarity: 57.21% Conservative: 45  
 Best Local Similarity: 36.94% Mismatches: 86  
 Query Match: 28.03% Indels: 9  
 RESULT 112  
 ID ABS63410 standard; cDNA; 923 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 53.10% Conservative: 41  
 Best Local Similarity: 37.21% Mismatches: 109  
 Query Match: 28.00% Indels: 13  
 RESULT 113  
 ID ABN87246 standard; cDNA; 1199 BP.  
 DE Lolium perenne CCoAMT2 cDNA sequence SEQ ID NO:170.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 56.36% Conservative: 42  
 Best Local Similarity: 38.56% Mismatches: 85  
 Query Match: 27.89% Indels: 18  
 RESULT 114  
 ID ABS54112 standard; DNA; 870 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Percent Similarity: 58.11% Conservative: 50  
 Best Local Similarity: 35.59% Mismatches: 84  
 Query Match: 27.81% Indels: 9  
 RESULT 115  
 ID ABS54113 standard; DNA; 811 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAMT-2) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Percent Similarity: 58.72% Conservative: 49  
 Best Local Similarity: 36.24% Mismatches: 81  
 Query Match: 27.74% Indels: 9  
 RESULT 116  
 ID AAC45004 standard; DNA; 917 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Percent Similarity: 56.64% Conservative: 40  
 Best Local Similarity: 38.94% Mismatches: 86  
 Query Match: 27.48% Indels: 12  
 RESULT 117  
 ID ADR73686 standard; DNA; 1252 BP.  
 DE Rice promoter putative caffeoyl CoA3O methyltransferase CDS.  
 PN WO2004070039-A2.  
 PD 19-AUG-2004.  
 PA (CROP-) CROPDISEIGN NV.  
 Percent Similarity: 57.47% Conservative: 40  
 Best Local Similarity: 39.37% Mismatches: 82  
 Query Match: 27.48% Indels: 13  
 RESULT 118  
 ID ABS63424 standard; cDNA; 1018 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 50.55% Conservative: 42

Best Local Similarity: 35.06% Mismatches: 84  
Query Match: 27.44% Indels: 50  
RESULT 119  
ID ADA48371 standard; DNA; 835 BP.  
DE Rice gene conferring disease resistance in plants.  
PN WO200300906-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 56.76% Conservative: 46  
Best Local Similarity: 39.00% Mismatches: 89  
Query Match: 27.36% Indels: 24  
RESULT 120  
ID ADR62522 standard; cDNA; 995 BP.  
DE Cotton cDNA sequence, SEQ ID 3303.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Percent Similarity: 58.30% Conservative: 49  
Best Local Similarity: 36.32% Mismatches: 83  
Query Match: 27.29% Indels: 10  
RESULT 121  
ID ABR94134 standard; DNA; 326 BP.  
DE Gene #632 used to diagnose liver cancer.  
PN WO200223103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 98.65% Conservative: 0  
Best Local Similarity: 98.65% Mismatches: 0  
Query Match: 27.25% Indels: 1  
RESULT 122  
ID ABR87118 standard; cDNA; 1103 BP.  
DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:12.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.23% Conservative: 50  
Best Local Similarity: 35.00% Mismatches: 100  
Query Match: 26.99% Indels: 19  
RESULT 123  
ID AB214595 standard; DNA; 729 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
PN WO200218655-A2.  
PD 28-FEB-2002.  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 56.28% Conservative: 37  
Best Local Similarity: 39.07% Mismatches: 84  
Query Match: 26.81% Indels: 10  
RESULT 124  
ID AAC42096 standard; DNA; 1186 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 60.66% Conservative: 48  
Best Local Similarity: 37.91% Mismatches: 76  
Query Match: 26.58% Indels: 7  
RESULT 125  
ID ADH02852 standard; cDNA; 1006 BP.  
DE Torenia TMT5.nt cDNA #SEQ ID 11.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 56.58% Conservative: 46  
Best Local Similarity: 36.40% Mismatches: 84  
Query Match: 26.40% Indels: 15  
RESULT 126  
ID ABS63420 standard; cDNA; 912 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.

PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAPALSKI J A.  
Percent Similarity: 53.71% Conservative: 39  
Best Local Similarity: 36.68% Mismatches: 96  
Query Match: 26.36% Indels: 10  
RESULT 127  
ID ADK69931 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #10.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 48.57% Conservative: 45  
Best Local Similarity: 32.50% Mismatches: 71  
Query Match: 26.32% Indels: 73  
RESULT 128  
ID ADK69906 standard; DNA; 1180 BP.  
DE Maize F4 CCoAOMT2 gene, seq id 3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 41.83% Conservative: 45  
Best Local Similarity: 29.36% Mismatches: 98  
Query Match: 26.28% Indels: 112  
RESULT 129  
ID ADK69932 standard; DNA; 1199 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #5.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 42.90% Conservative: 45  
Best Local Similarity: 30.11% Mismatches: 97  
Query Match: 26.21% Indels: 104  
RESULT 130  
ID ADK69927 standard; DNA; 1178 BP.  
DE Maize W64A CCoAOMT2 gene deletion mutant #2.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 48.39% Conservative: 44  
Best Local Similarity: 32.62% Mismatches: 72  
Query Match: 26.14% Indels: 72  
RESULT 131  
ID ADK69925 standard; DNA; 1196 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 46.67% Conservative: 38  
Best Local Similarity: 33.33% Mismatches: 74  
Query Match: 26.14% Indels: 78  
RESULT 132  
ID ADK69918 standard; DNA; 1172 BP.  
DE Maize W64A CCoAOMT2 gene deletion mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 48.21% Conservative: 44  
Best Local Similarity: 32.50% Mismatches: 72  
Query Match: 26.10% Indels: 73  
RESULT 133  
ID ADK69919 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Percent Similarity: 48.21% Conservative: 44  
Best Local Similarity: 32.50% Mismatches: 72  
Query Match: 26.10% Indels: 73  
RESULT 134  
ID ADK69920 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #2.  
PN FR2833615-A1.

PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 135  
 ID ADK69928 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #7.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 136  
 ID ADK69923 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #5.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 137  
 ID ADK69904 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene, seq id 1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 138  
 ID ADK69922 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 139  
 ID ADK69924 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #6.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 140  
 ID ADK69929 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #8.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 141  
 ID ADK69921 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 142  
 ID ADK69930 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #9.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.

PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 143  
 ID ADK69917 standard; DNA; 1186 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 144  
 ID ADH02845 standard; cDNA; 888 BP.  
 DE Petunia E20 cDNA #SEQ ID 4.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39% Conservative: 40  
 Best Local Similarity: 37.66% Mismatches: 88  
 Query Match: 25.99% Indels: 21  
 RESULT 145  
 ID ADH02842 standard; cDNA; 969 BP.  
 DE Petunia dife cDNA #SEQ ID 1.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39% Conservative: 40  
 Best Local Similarity: 37.66% Mismatches: 88  
 Query Match: 25.99% Indels: 21  
 RESULT 146  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 Percent Similarity: 51.97% Conservative: 31  
 Best Local Similarity: 38.43% Mismatches: 104  
 Query Match: 25.91% Indels: 6  
 RESULT 147  
 ID ADK69926 standard; DNA; 1199 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 47.20% Conservative: 44  
 Best Local Similarity: 31.82% Mismatches: 72  
 Query Match: 25.87% Indels: 79  
 RESULT 148  
 ID ABS63422 standard; cDNA; 982 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAPALSKI J A.  
 Percent Similarity: 55.14% Conservative: 37  
 Best Local Similarity: 37.85% Mismatches: 86  
 Query Match: 25.39% Indels: 10  
 RESULT 149  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Percent Similarity: 52.63% Conservative: 28  
 Best Local Similarity: 40.35% Mismatches: 98  
 Query Match: 25.32% Indels: 10  
 RESULT 150  
 ID ADH02867 standard; cDNA; 1079 BP.  
 DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 57.59% Conservative: 47

Best Local Similarity: 36.61% Mismatches: 84  
Query Match: 25.28% Indels: 11  
RESULT 151  
ID ABN87110 standard; cDNA; 758 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:4.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 51.82% Conservative: 42  
Best Local Similarity: 34.82% Mismatches: 86  
Query Match: 25.17% Indels: 33  
RESULT 152  
ID ABN87115 standard; cDNA; 793 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:9.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 55.56% Conservative: 40  
Best Local Similarity: 37.04% Mismatches: 76  
Query Match: 24.91% Indels: 20  
RESULT 153  
ID ABN87126 standard; cDNA; 689 BP.  
DE Lolium perenne LpCCoAMTC nucleotide sequence SEQ ID NO:21.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 55.94% Conservative: 30  
Best Local Similarity: 41.09% Mismatches: 72  
Query Match: 24.80% Indels: 17  
RESULT 154  
ID ABN87112 standard; cDNA; 765 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:6.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 58.33% Conservative: 37  
Best Local Similarity: 39.06% Mismatches: 72  
Query Match: 24.46% Indels: 8  
RESULT 155  
ID ADH02847 standard; cDNA; 1077 BP.  
DE Petunia E33 cDNA #SEQ ID 5.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 56.70% Conservative: 46  
Best Local Similarity: 36.16% Mismatches: 86  
Query Match: 24.42% Indels: 11  
RESULT 156  
ID ADH02884 standard; cDNA; 943 BP.  
DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 57.47% Conservative: 48  
Best Local Similarity: 35.75% Mismatches: 82  
Query Match: 24.35% Indels: 12  
RESULT 157  
ID ADH02882 standard; cDNA; 841 BP.  
DE Fuchsia FMT (3282) cDNA #SEQ ID 41.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 58.82% Conservative: 44  
Best Local Similarity: 37.25% Mismatches: 74  
Query Match: 24.20% Indels: 10  
RESULT 158  
ID AAC47161 standard; DNA; 738 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.  
PN EP1033405-A2.

PD 06-SEP-2000.  
Percent Similarity: 56.42% Conservative: 44  
Best Local Similarity: 36.24% Mismatches: 85  
Query Match: 24.13% Indels: 10  
RESULT 159  
ID AAC47930 standard; DNA; 833 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 56.42% Conservative: 44  
Best Local Similarity: 36.24% Mismatches: 85  
Query Match: 24.13% Indels: 10  
RESULT 160  
ID ABN87111 standard; cDNA; 774 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:5.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 57.81% Conservative: 37  
Best Local Similarity: 38.54% Mismatches: 73  
Query Match: 24.09% Indels: 8  
RESULT 161  
ID ABN87113 standard; cDNA; 777 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:7.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.63% Conservative: 40  
Best Local Similarity: 36.11% Mismatches: 78  
Query Match: 24.01% Indels: 20  
RESULT 162  
ID ABN87114 standard; cDNA; 792 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:8.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.63% Conservative: 40  
Best Local Similarity: 36.11% Mismatches: 78  
Query Match: 23.94% Indels: 20  
RESULT 163  
ID ABN87122 standard; cDNA; 789 BP.  
DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 52.77% Conservative: 37  
Best Local Similarity: 37.02% Mismatches: 94  
Query Match: 23.90% Indels: 18  
RESULT 164  
ID ADR65555 standard; cDNA; 749 BP.  
DE Cotton cDNA sequence, SEQ ID 6336.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Percent Similarity: 55.67% Conservative: 44  
Best Local Similarity: 33.99% Mismatches: 74  
Query Match: 23.83% Indels: 16  
RESULT 165  
ID ABN87121 standard; cDNA; 773 BP.  
DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.25% Conservative: 33  
Best Local Similarity: 38.68% Mismatches: 86  
Query Match: 23.45% Indels: 12

RESULT 166  
ID ADS72763 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1360.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 23.38%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0

RESULT 167  
ID ABZ13934 standard; cDNA; 699 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84  
Indel: 15

RESULT 168  
ID ADG87603 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.  
PN WO20022675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84  
Indel: 15

RESULT 169  
ID ADG87604 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.  
PN WO20022675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84  
Indel: 15

RESULT 170  
ID ADA67907 standard; cDNA; 699 BP.  
DE Arabidopsis thaliana gene, SEQ ID 151.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84  
Indel: 15

RESULT 171  
ID ADS72855 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1452.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 98.39%  
Best Local Similarity: 98.39%  
Query Match: 23.01%  
Indels: 0  
Conservative: 0  
Mismatch: 1  
Indel: 0

RESULT 172  
ID AAL61190 standard; cDNA; 504 BP.  
DE Actinomyces pretiosum O-methyltransferase gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.

Percent Similarity: 57.32%  
Best Local Similarity: 43.29%  
Query Match: 22.30%  
Indels: 3  
Conservative: 23  
Mismatch: 67  
Indel: 3

RESULT 173  
ID AAV23875 standard; cDNA; 1075 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99  
Indel: 23

RESULT 174  
ID AAZ06878 standard; cDNA; 1075 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 4.  
PN US952486-A.  
PD 14-SEP-1999.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99  
Indel: 23

RESULT 175  
ID AAA67962 standard; cDNA; 1075 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99  
Indel: 23

RESULT 176  
ID ADD41712 standard; cDNA; 1075 BP.  
DE O-methyl transferase DNA #8.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99  
Indel: 23

RESULT 177  
ID AAX28142 standard; cDNA; 3072 BP.  
DE CCoAOMT promoter, PtCCoAOMT2.  
PN WO9909188-A2.  
PD 23-FEB-1999.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 43.80%  
Best Local Similarity: 27.91%  
Query Match: 22.19%  
Indels: 82  
Conservative: 41  
Mismatch: 63  
Indel: 82

RESULT 178  
ID ACL23248 standard; cDNA; 509 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #12339.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Percent Similarity: 57.23%  
Best Local Similarity: 39.76%  
Query Match: 22.15%  
Indels: 7  
Conservative: 29  
Mismatch: 64  
Indel: 7

RESULT 179  
ID AAQ14978 standard; cDNA; 1810 BP.  
DE AGYA Gene.  
PN EP459525-A.  
PD 04-DEC-1991.  
PA (SAOC) MERCIAN CORP.  
Percent Similarity: 49.76%  
Best Local Similarity: 39.02%  
Query Match: 21.89%  
Indels: 34  
Conservative: 22  
Mismatch: 69  
Indel: 34

RESULT 180  
ID AAV23874 standard; cDNA; 1074 BP.  
DE Plant OMT enzyme DNA sequence.

PN W09811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 53.15% Conservative: 46  
 Best Local Similarity: 32.43% Mismatches: 92  
 Indels: 12  
 Query Match:  
 RESULT 181  
 ID AAZ06877 standard; cDNA; 1074 BP.  
 DE Fine O-methyl transferase (OMT) partial cDNA 3.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 53.15% Conservative: 46  
 Best Local Similarity: 32.43% Mismatches: 92  
 Indels: 12  
 Query Match:  
 RESULT 182  
 ID AAA67961 standard; DNA; 1074 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
 PN W0200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 53.15% Conservative: 46  
 Best Local Similarity: 32.43% Mismatches: 92  
 Indels: 12  
 Query Match:  
 RESULT 183  
 ID ADD41711 standard; DNA; 1074 BP.  
 DE O-methyl transferase DNA #7.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK-) BLOKSBERG L N.  
 PA (HAVU-) HAVUKKALA I.  
 Percent Similarity: 53.15% Conservative: 46  
 Best Local Similarity: 32.43% Mismatches: 92  
 Indels: 12  
 Query Match:  
 RESULT 184  
 ID ABN87120 standard; cDNA; 693 BP.  
 DE Lollium perenne LpCoAMTB partial nucleotide sequence SEQ ID NO:15.  
 PN W0200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 54.15% Conservative: 32  
 Best Local Similarity: 38.54% Mismatches: 81  
 Indels: 14  
 Query Match:  
 RESULT 185  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
 Percent Similarity: 47.60% Conservative: 39  
 Best Local Similarity: 33.21% Mismatches: 111  
 Indels: 31  
 Query Match:  
 RESULT 186  
 ID AAZ60809 standard; DNA; 2983 BP.  
 DE Nucleotide sequence of promoter of caffeoyl-CoA-O-methyltransferase.  
 PN W0200006752-A1.  
 PD 10-FEB-2000.  
 PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 Percent Similarity: 43.63% Conservative: 41  
 Best Local Similarity: 27.80% Mismatches: 63  
 Indels: 83  
 Query Match:  
 RESULT 187  
 ID ABN99073 standard; DNA; 792 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.  
 PN US2002023281-A1.  
 PD 21-FEB-2002.  
 PA (GORL-) GORLACH J.  
 PA (ANYI-) AN Y.  
 PA (HAMT-) HAMILTON C M.  
 PA (PRIC-) PRICE J L.  
 PA (RAIN-) RAINES T M.  
 PA (YUYV-) YU Y.

PA (RAME-) RAMEAKA J G.  
 PA (PAGE-) PAGE A.  
 PA (MATH-) MATHAW A V.  
 PA (LEDF-) LEDFORD B L.  
 PA (WOES-) WOESSNER J P.  
 PA (HAAS-) HAAS W D.  
 PA (GARC-) GARCIA C A.  
 PA (KRIC-) KRICKER M.  
 PA (SLAT-) SLATER T.  
 PA (DAVI-) DAVIS K R.  
 PA (ALLE-) ALLEN K.  
 PA (HOFF-) HOFFMAN N.  
 PA (HURB-) HURBAN P.  
 Percent Similarity: 56.35% Conservative: 40  
 Best Local Similarity: 34.25% Mismatches: 68  
 Indels: 11  
 Query Match:  
 RESULT 188  
 ID ACN55288 standard; cDNA; 546 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-K6-D4, SEQ:10069.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK-) DEIKMAN J.  
 PA (FENG-) FENG P C C.  
 PA (FINC-) FINCHER K L.  
 PA (ZIEG-) ZIEGLER T E.  
 Percent Similarity: 58.48% Conservative: 42  
 Best Local Similarity: 33.92% Mismatches: 64  
 Indels: 7  
 Query Match:  
 RESULT 189  
 ID AAX28141 standard; DNA; 3800 BP.  
 DE CCoAMT promoter, PtCCoAMT1.  
 PN W09909188-A2.  
 PD 25-FEB-1999.  
 PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 Percent Similarity: 40.79% Conservative: 43  
 Best Local Similarity: 25.27% Mismatches: 63  
 Indels: 101  
 Query Match:  
 RESULT 190  
 ID AAZ60808 standard; DNA; 3800 BP.  
 DE Nucleotide sequence of promoter of caffeoyl-CoA-O-methyltransferase.  
 PN W0200006752-A1.  
 PD 10-FEB-2000.  
 PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 Percent Similarity: 40.79% Conservative: 43  
 Best Local Similarity: 25.27% Mismatches: 63  
 Indels: 101  
 Query Match:  
 RESULT 191  
 ID ABKG2368 standard; cDNA; 343 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #275.  
 PN W0200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 60.00% Conservative: 5  
 Best Local Similarity: 55.65% Mismatches: 6  
 Indels: 40  
 Query Match:  
 RESULT 192  
 ID ADB55662 standard; DNA; 343 BP.  
 DE Toxicity-related gene, SEQ ID 688.  
 PN W02003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 60.00% Conservative: 5  
 Best Local Similarity: 55.65% Mismatches: 6  
 Indels: 40  
 Query Match:  
 RESULT 193  
 ID ABT40596 standard; DNA; 343 BP.  
 DE Toxicity modelling related rat gene SEQ ID No 298.  
 PN W0200295000-A2.  
 PD 28-NOV-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 60.00% Conservative: 5  
 Best Local Similarity: 55.65% Mismatches: 6  
 Indels: 40  
 Query Match:  
 RESULT 194  
 ID ABB99073 standard; DNA; 792 BP.  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.  
 PN US2002023281-A1.  
 PD 21-FEB-2002.  
 PA (GORL-) GORLACH J.  
 PA (ANYI-) AN Y.  
 PA (HAMT-) HAMILTON C M.  
 PA (PRIC-) PRICE J L.  
 PA (RAIN-) RAINES T M.  
 PA (YUYV-) YU Y.

RESULT 194  
 ID ADH02862 standard; cDNA; 780 BP.  
 DE Fuchsia FMT cDNA #SEQ ID 21.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITPL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 57.50%  
 Best Local Similarity: 38.12%  
 Query Match: 19.81%  
 RESULT 195  
 ID ABD00975 standard; DNA; 675 BP.  
 DE Klebsiella pneumoniae polynucleotide seqid 6750.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENE-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 53.33%  
 Best Local Similarity: 35.56%  
 Query Match: 19.21%  
 RESULT 196  
 ID ADD34177 standard; DNA; 407 BP.  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
 PN WO2003020220-A2.  
 PD 13-MAR-2003.  
 PA (UYEM-) UNIV EMORY.  
 Percent Similarity: 85.71%  
 Best Local Similarity: 79.37%  
 Query Match: 18.69%  
 RESULT 197  
 ID AAV23845 standard; DNA; 760 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.96%  
 Best Local Similarity: 37.31%  
 Query Match: 16.72%  
 RESULT 198  
 ID AAZ06846 standard; cDNA; 760 BP.  
 DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.96%  
 Best Local Similarity: 37.31%  
 Query Match: 16.72%  
 RESULT 199  
 ID AAA69584 standard; cDNA; 760 BP.  
 DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.96%  
 Best Local Similarity: 37.31%  
 Query Match: 16.72%  
 RESULT 200  
 ID AAA67932 standard; DNA; 760 BP.  
 DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.96%  
 Best Local Similarity: 37.31%  
 Query Match: 16.72%  
 RESULT 201  
 ID ADD41682 standard; DNA; 760 BP.  
 DE O-methyl transferase DNA #5.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.

PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 58.96%  
 Best Local Similarity: 37.31%  
 Query Match: 16.72%  
 RESULT 202  
 ID ABS63430 standard; cDNA; 534 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (RAFA/) RAFALESKI J A.  
 Percent Similarity: 58.71%  
 Best Local Similarity: 36.13%  
 Query Match: 16.68%  
 RESULT 203  
 ID ABN87119 standard; cDNA; 628 BP.  
 DE Lolium perenne LpCCOAMTB partial nucleotide sequence SEQ ID NO:14.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 51.93%  
 Best Local Similarity: 35.36%  
 Query Match: 16.46%  
 RESULT 204  
 ID ACL23249 standard; DNA; 542 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13240.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Percent Similarity: 55.70%  
 Best Local Similarity: 37.97%  
 Query Match: 15.82%  
 RESULT 205  
 ID ABS63423 standard; cDNA; 528 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALESKI J A.  
 Percent Similarity: 59.52%  
 Best Local Similarity: 38.10%  
 Query Match: 15.41%  
 RESULT 206  
 Percent Similarity: 54.29%  
 Best Local Similarity: 33.14%  
 Query Match: 15.08%  
 RESULT 207  
 Percent Similarity: 54.29%  
 Best Local Similarity: 33.14%  
 Query Match: 15.08%  
 RESULT 208  
 ID AAA68101 standard; DNA; 399 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 62.93%  
 Best Local Similarity: 39.66%  
 Query Match: 15.04%  
 RESULT 209  
 ID ADD41851 standard; DNA; 399 BP.  
 DE Caffeoyl CoA methyl transferase DNA #2.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 62.93%  
 Best Local Similarity: 39.66%  
 Query Match: 15.04%

RESULT 210  
ID ADA31006 standard; DNA; 588 BP.  
DE DNA encoding Acinetobacter baumannii protein #2293.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 50.24%  
Best Local Similarity: 33.66%  
Query Match: 15.00%  
Conservative: 34  
Mismatch: 65  
Indels: 37

RESULT 211  
ID ACN56145 standard; cDNA; 525 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D4, SEQ:10926.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Percent Similarity: 57.02%  
Best Local Similarity: 33.88%  
Query Match: 14.48%  
Conservative: 28  
Mismatch: 45  
Indels: 7

RESULT 212  
ID ABN87109 standard; cDNA; 557 BP.  
DE Lolium perenne LpCoAMTA partial nucleotide sequence SEQ ID NO:3.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.35%  
Best Local Similarity: 34.06%  
Query Match: 14.30%  
Conservative: 28  
Mismatch: 52  
Indels: 11

RESULT 213  
ID AAS96694 standard; DNA; 8580 BP.  
DE Arabidopsis DMT4 (1DMT4) DNA.  
PN WO200180626-A1.  
PD 01-NOV-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 39.59%  
Best Local Similarity: 25.89%  
Query Match: 14.11%  
Conservative: 27  
Mismatch: 51  
Indels: 69

RESULT 214  
ID ADM39547 standard; DNA; 8580 BP.  
DE DMT polynucleotide #9.  
PN US2003135890-A1.  
PD 17-JUL-2003.  
PA (FISC/) FISCHER R.  
PA (CHOI/) CHOI Y.  
PA (HANN/) HANNON M.  
PA (OKAM/) OKAMURO J.  
PA (TATA/) TATARINOVA T.  
Percent Similarity: 39.59%  
Best Local Similarity: 25.89%  
Query Match: 14.11%  
Conservative: 27  
Mismatch: 51  
Indels: 69

RESULT 215  
ID AAG68012 standard; DNA; 594 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.17%  
Best Local Similarity: 36.89%  
Query Match: 13.63%  
Conservative: 25  
Mismatch: 38  
Indels: 2

RESULT 216  
ID ADD41762 standard; DNA; 594 BP.  
DE O-methyl transferase DNA #11.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 61.17%  
Best Local Similarity: 36.89%  
Query Match: 13.63%  
Conservative: 25  
Mismatch: 38  
Indels: 2

RESULT 217  
ID ADB06101 standard; DNA; 798 BP.  
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:41.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Percent Similarity: 47.98%  
Best Local Similarity: 32.32%  
Query Match: 13.55%  
Conservative: 31  
Mismatch: 72  
Indels: 31

RESULT 218  
ID ADB12064 standard; DNA; 1754382 BP.  
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Percent Similarity: 47.98%  
Best Local Similarity: 32.32%  
Query Match: 13.55%  
Conservative: 31  
Mismatch: 72  
Indels: 31

RESULT 219  
ID ABS63421 standard; cDNA; 505 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAPALSKI J A.  
Percent Similarity: 51.92%  
Best Local Similarity: 32.69%  
Query Match: 13.51%  
Conservative: 30  
Mismatch: 56  
Indels: 19

RESULT 220  
ID AAV23843 standard; DNA; 607 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22%  
Best Local Similarity: 37.76%  
Query Match: 13.40%  
Conservative: 23  
Mismatch: 36  
Indels: 2

RESULT 221  
ID AAZ06844 standard; cDNA; 607 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.  
PN US9592486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22%  
Best Local Similarity: 37.76%  
Query Match: 13.40%  
Conservative: 23  
Mismatch: 36  
Indels: 2

RESULT 222  
ID AAA69594 standard; cDNA; 607 BP.  
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22%  
Best Local Similarity: 37.76%  
Query Match: 13.40%  
Conservative: 23  
Mismatch: 36  
Indels: 2

RESULT 223  
ID AAA67930 standard; DNA; 607 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22%  
Best Local Similarity: 37.76%  
Query Match: 13.40%  
Conservative: 23  
Mismatch: 36  
Indels: 2

RESULT 224  
ID ADD41680 standard; DNA; 607 BP.  
DE O-methyl transferase DNA #3.  
PN US2003131373-A1.



PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 61.22%  
 Best Local Similarity: 37.76%  
 Mismatches: 36  
 Indels: 2  
 Query Match:  
 RESULT 225  
 ID AAS59516 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 45.54%  
 Best Local Similarity: 28.57%  
 Mismatches: 91  
 Indels: 32  
 Query Match:  
 RESULT 226  
 ID ACF64445 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes DNA contig sequence #11.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 45.54%  
 Best Local Similarity: 28.57%  
 Mismatches: 91  
 Indels: 32  
 Query Match:  
 RESULT 227  
 ID ADA48866 standard; DNA; 584 BP.  
 DE Banana gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 46.67%  
 Best Local Similarity: 33.33%  
 Mismatches: 38  
 Indels: 34  
 Query Match:  
 RESULT 228  
 ID ABS63411 standard; cDNA; 510 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 54.93%  
 Best Local Similarity: 33.92%  
 Mismatches: 45  
 Indels: 20  
 Query Match:  
 RESULT 229  
 ID ABS63426 standard; cDNA; 600 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 48.84%  
 Best Local Similarity: 36.63%  
 Mismatches: 57  
 Indels: 32  
 Query Match:  
 RESULT 230  
 ID AAA31496 standard; DNA; 451 BP.  
 DE Plant microsatellite marker #457.  
 PN WO9967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 59.18%  
 Best Local Similarity: 37.76%  
 Mismatches: 38  
 Indels: 2  
 Query Match:  
 RESULT 231  
 ID AAA68102 standard; DNA; 296 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 62.89%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 232  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 62.89%  
 Best Local Similarity: 39.18%  
 Mismatches: 32  
 Indels: 4  
 Query Match:  
 RESULT 233  
 ID ABQ81846 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC. PROD NESTLE SA.  
 Percent Similarity: 42.31%  
 Best Local Similarity: 27.31%  
 Mismatches: 137  
 Indels: 13  
 Query Match:  
 RESULT 234  
 ID AAV23873 standard; DNA; 562 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 235  
 ID AAZ06876 standard; cDNA; 562 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 2.  
 PN US9592486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 236  
 ID AAA69580 standard; cDNA; 562 BP.  
 DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 237  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 238  
 ID ADD41710 standard; DNA; 562 BP.  
 DE O-methyl transferase DNA #6.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 239  
 ID ADP95323 standard; cDNA; 447 BP.

Best Local Similarity: 39.18%  
 Mismatches: 32  
 Indels: 4  
 Query Match:  
 RESULT 232  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 62.89%  
 Best Local Similarity: 39.18%  
 Mismatches: 32  
 Indels: 4  
 Query Match:  
 RESULT 233  
 ID ABQ81846 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC. PROD NESTLE SA.  
 Percent Similarity: 42.31%  
 Best Local Similarity: 27.31%  
 Mismatches: 137  
 Indels: 13  
 Query Match:  
 RESULT 234  
 ID AAV23873 standard; DNA; 562 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 235  
 ID AAZ06876 standard; cDNA; 562 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 2.  
 PN US9592486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 236  
 ID AAA69580 standard; cDNA; 562 BP.  
 DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 237  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 238  
 ID ADD41710 standard; DNA; 562 BP.  
 DE O-methyl transferase DNA #6.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 239  
 ID ADP95323 standard; cDNA; 447 BP.

DE Cotton expressed sequence tag, EST, #4334.  
 PN US2004123338-A1.  
 PD 24-JUN-2004.  
 PA (FINC/) FINCHER K L.  
 Percent Similarity: 60.42% Conservative: 22  
 Best Local Similarity: 37.50% Mismatches: 36  
 Query Match: 12.66% Indels: 2  
 RESULT 240  
 ID ABX09141 standard; DNA; 75216 BP.  
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv230.  
 PN WO200274903-A2.  
 PD 26-SEP-2002.  
 PA (INSP ) INST PASTEUR.  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 241  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 242  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 243  
 ID ABQ68900 standard; DNA; 1289 BP.  
 DE Listeria monocytogenes 4b contig DNA sequence #1666.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Percent Similarity: 43.91% Conservative: 36  
 Best Local Similarity: 27.10% Mismatches: 96  
 Query Match: 12.58% Indels: 24  
 RESULT 244  
 Percent Similarity: 44.95% Conservative: 37  
 Best Local Similarity: 27.98% Mismatches: 88  
 Query Match: 12.58% Indels: 32  
 RESULT 245  
 ID ABQ70732 standard; DNA; 2233 BP.  
 DE Listeria monocytogenes 4b contig DNA sequence #674.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Percent Similarity: 43.93% Conservative: 36  
 Best Local Similarity: 27.10% Mismatches: 96  
 Query Match: 12.51% Indels: 24  
 RESULT 246  
 ID AA68100 standard; DNA; 399 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 61.86% Conservative: 21  
 Best Local Similarity: 40.21% Mismatches: 27  
 Query Match: 12.21% Indels: 11  
 RESULT 247  
 ID ADD41850 standard; DNA; 399 BP.  
 DE Caffeoyl CoA methyl transferase DNA #1.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 61.86% Conservative: 21  
 Best Local Similarity: 40.21% Mismatches: 27  
 Query Match: 12.21% Indels: 11  
 RESULT 248  
 Percent Similarity: 41.84% Conservative: 37  
 Best Local Similarity: 26.36% Mismatches: 93  
 Query Match: 12.21% Indels: 46  
 RESULT 249

Percent Similarity: 41.84% Conservative: 37  
 Best Local Similarity: 26.36% Mismatches: 93  
 Query Match: 12.21% Indels: 46  
 RESULT 250  
 ID ADA31376 standard; DNA; 702 BP.  
 DE DNA encoding Acinetobacter baumannii protein #2663.  
 PN US6562958-B1.  
 PD 13-MAY-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 42.92% Conservative: 37  
 Best Local Similarity: 26.03% Mismatches: 104  
 Query Match: 12.10% Indels: 21  
 RESULT 251  
 Percent Similarity: 51.18% Conservative: 38  
 Best Local Similarity: 28.82% Mismatches: 72  
 Query Match: 12.10% Indels: 11  
 RESULT 252  
 ID ABX62366 standard; DNA; 415 BP.  
 DE Arabidopsis thaliana expressed sequence related polynucleotide #481.  
 PN US2002040490-A1.  
 PD 04-APR-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.  
 Percent Similarity: 54.10% Conservative: 26  
 Best Local Similarity: 32.79% Mismatches: 45  
 Query Match: 11.88% Indels: 11  
 RESULT 253  
 ID ADB74386 standard; DNA; 38675 BP.  
 DE Mycobacterium leprae DNA #20.  
 PN US6583266-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 40.42% Conservative: 43  
 Best Local Similarity: 25.44% Mismatches: 128  
 Query Match: 11.76% Indels: 44  
 RESULT 254  
 ID ADH82166 standard; DNA; 801 BP.  
 DE Enterococcus faecalis polynucleotide #51.  
 PN US6617156-B1.  
 PD 09-SEP-2003.  
 PA (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 Percent Similarity: 41.38% Conservative: 37  
 Best Local Similarity: 25.43% Mismatches: 112  
 Query Match: 11.69% Indels: 24  
 RESULT 255  
 ID AAX13116 standard; DNA; 19024 BP.  
 DE Enterococcus faecalis genome contig SEQ ID NO:179.  
 PN WO9850555-A2.  
 PD 12-NOV-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 41.38% Conservative: 37  
 Best Local Similarity: 25.43% Mismatches: 112  
 Query Match: 11.62% Indels: 24  
 RESULT 256  
 ID ABS98911 standard; DNA; 19024 BP.

DE Enterococcus faecalis contig sequence #179.  
 PN US2002120116-A1.  
 PD 29-AUG-2002.  
 PA (KUNS/) KUNSCH C A.  
 PA (DILL/) DILLON P J.  
 PA (BARA/) BARASH S.  
 Percent Similarity: 41.38%  
 Best Local Similarity: 25.43%  
 Query Match: 11.62%  
 RESULT 257  
 Conservative: 37  
 Mismatches: 112  
 Indels: 24  
 ID ABS63414 standard; cDNA; 508 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 51.28%  
 Best Local Similarity: 37.61%  
 Query Match: 11.13%  
 RESULT 258  
 Conservative: 16  
 Mismatches: 39  
 Indels: 19  
 ID ACL23251 standard; DNA; 422 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13242.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Percent Similarity: 58.02%  
 Best Local Similarity: 39.51%  
 Query Match: 10.87%  
 RESULT 259  
 ID AAF08409 standard; cDNA; 645 BP.  
 DE Fusarium venenatum EST SEQ ID NO:932.  
 PN WO200056762-A2.  
 PD 28-SEP-2000.  
 PA (NOVO) NOVO NORDISK INC.  
 PA (NOVO) NOVO NORDISK AS.  
 Percent Similarity: 48.35%  
 Best Local Similarity: 26.92%  
 Query Match: 10.46%  
 RESULT 260  
 ID ADR65553 standard; cDNA; 409 BP.  
 DE Cotton cDNA sequence, SEQ ID 6334.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Percent Similarity: 54.00%  
 Best Local Similarity: 35.00%  
 Query Match: 10.13%  
 RESULT 261  
 ID ABN69362 standard; DNA; 705 BP.  
 DE Streptococcus polynucleotide SEQ ID NO 6637.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 44.06%  
 Best Local Similarity: 25.25%  
 Query Match: 10.13%  
 RESULT 262  
 ID ABX72177 standard; cDNA; 894 BP.  
 DE Human NOVX polynucleotide #8.  
 PN WO200281498-A2.  
 PD 17-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 29.17%  
 Query Match: 9.53%  
 RESULT 263  
 ID AAD13478 standard; DNA; 2316 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding DNA.  
 PN WO200157220-A2.

PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 39.54%  
 Best Local Similarity: 31.56%  
 Query Match: 9.53%  
 RESULT 264  
 ID ABK74977 standard; DNA; 534 BP.  
 DE Bacillus licheniformis genomic sequence tag (GST) #2268.  
 PN WO200229113-A2.  
 PD 11-APR-2002.  
 PA (NOVO) NOVOZYMES BIOTECH INC.  
 PA (NOVO) NOVOZYMES AS.  
 Percent Similarity: 44.81%  
 Best Local Similarity: 25.68%  
 Query Match: 9.42%  
 RESULT 265  
 ID AAD13476 standard; cDNA; 777 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #1.  
 PN WO200157220-A2.  
 PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 RESULT 266  
 ID AAD33497 standard; cDNA; 777 BP.  
 DE Human drug metabolising enzyme (DME-18) cDNA.  
 PN WO200212467-A2.  
 PD 14-FEB-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 RESULT 267  
 ID ABX72178 standard; cDNA; 897 BP.  
 DE Human NOVX polynucleotide #9.  
 PN WO200281498-A2.  
 PD 17-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 RESULT 268  
 ID ABN69361 standard; DNA; 705 BP.  
 DE Streptococcus polynucleotide SEQ ID NO 6635.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 43.28%  
 Best Local Similarity: 23.95%  
 Query Match: 9.34%  
 RESULT 269  
 Percent Similarity: 43.28%  
 Best Local Similarity: 23.95%  
 Query Match: 9.34%  
 RESULT 270  
 ID ADS65765 standard; cDNA; 242 BP.  
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 781.  
 PN US2003237110-A9.  
 PD 25-DEC-2003.  
 PA (INCY-) INCYTE PHARM INC.  
 Percent Similarity: 53.85%  
 Best Local Similarity: 37.18%  
 Query Match: 9.27%  
 RESULT 271  
 ID ABN87123 standard; cDNA; 532 BP.  
 DE Lolium perenne LpCCOAM7b partial nucleotide sequence, SEQ ID NO:18.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 52.69%  
 Conservative: 19

Best Local Similarity: 32.26% Mismatches: 38  
 Query Match: 9.23% Indels: 7  
 RESULT 272  
 ID ABN87124 standard; cDNA; 532 BP.  
 DE Lolium perenne LpCCoMTB partial nucleotide sequence SEQ ID NO:19.  
 PN WO20026994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 52.69% Conservative: 19  
 Best Local Similarity: 32.26% Mismatches: 38  
 Query Match: 9.23% Indels: 7  
 RESULT 273  
 ID ADC92983 standard; DNA; 498 BP.  
 DE E. faecium DNA sequence SEQ ID 2610.  
 PN US6583275-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 45.78% Conservative: 29  
 Best Local Similarity: 28.31% Mismatches: 74  
 Query Match: 9.16% Indels: 16  
 RESULT 274  
 ID ABN91349 standard; DNA; 699 BP.  
 DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:812.  
 PN US6380370-B1.  
 PD 30-APR-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 44.83% Conservative: 38  
 Best Local Similarity: 22.99% Mismatches: 86  
 Query Match: 9.16% Indels: 10  
 RESULT 275  
 ID AAH54424 standard; DNA; 3673 BP.  
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3788.  
 PN WO200134809-A2.  
 PD 17-MAY-2001.  
 PA (GLAX) GLAXO GROUP LTD.  
 Percent Similarity: 44.83% Conservative: 38  
 Best Local Similarity: 22.99% Mismatches: 86  
 Query Match: 9.16% Indels: 10  
 RESULT 276  
 ID AAA31117 standard; DNA; 402 BP.  
 DE Plant microsatellite marker #78.  
 PN WO9967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 57.32% Conservative: 15  
 Best Local Similarity: 39.02% Mismatches: 32  
 Query Match: 9.08% Indels: 3  
 RESULT 277  
 ID ABX06678 standard; DNA; 711 BP.  
 DE S. pneumoniae type 4 strain coding region #966.  
 PN WO200277021-A2.  
 PD 03-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 278  
 ID ADR92174 standard; DNA; 726 BP.  
 DE Novel S. pneumoniae DNA sequence, SEQ ID 809.  
 PN US6800744-B1.  
 PD 05-OCT-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 279  
 ID AAV52241 standard; DNA; 11309 BP.  
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:108.  
 PN WO9818931-A2.  
 PD 07-MAY-1998.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 280  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 281  
 ID AAZ54186 standard; DNA; 918 BP.  
 DE Neisseria gonorrhoeae ORF 695 partial DNA sequence SEQ ID NO:2321.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.00% Conservative: 17  
 Best Local Similarity: 35.71% Mismatches: 18  
 Query Match: 8.94% Indels: 10  
 RESULT 282  
 ID AAZ54188 standard; DNA; 921 BP.  
 DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2325.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.61% Conservative: 16  
 Best Local Similarity: 36.36% Mismatches: 24  
 Query Match: 8.94% Indels: 2  
 RESULT 283  
 ID ABX17318 standard; cDNA; 2712 BP.  
 DE Human cancer promoting protein pP7517.  
 PN CN1351082-A.  
 PD 29-MAY-2002.  
 PA (SHAN-) SHANGHAI INST ONCOLOGY.  
 Percent Similarity: 40.19% Conservative: 25  
 Best Local Similarity: 28.50% Mismatches: 81  
 Query Match: 8.90% Indels: 47  
 RESULT 284  
 ID ACN44729 standard; cDNA; 1253 BP.  
 DE Mouse mRNA sequence mCT7005.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 33.56% Conservative: 40  
 Best Local Similarity: 20.13% Mismatches: 111  
 Query Match: 8.82% Indels: 87  
 RESULT 285  
 ID AAD13477 standard; cDNA; 507 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #2.  
 PN WO200157220-A2.  
 PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 45.52% Conservative: 17  
 Best Local Similarity: 32.84% Mismatches: 53  
 Query Match: 8.79% Indels: 20  
 RESULT 286  
 ID AAZ54187 standard; DNA; 918 BP.  
 DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2323.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.61% Conservative: 16  
 Best Local Similarity: 36.36% Mismatches: 24  
 Query Match: 8.79% Indels: 2  
 RESULT 287  
 ID AAH66205 standard; DNA; 639 BP.  
 DE C. glutamicum coding sequence fragment SEQ ID NO: 1240.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.70% Conservative: 28  
 Best Local Similarity: 25.63% Mismatches: 82

Query Match: 8.56% Indels: 38  
 RESULT 288  
 ID ACA00413 standard; DNA; 639 BP.  
 DE C. glutamicum derived ORF SEQ ID 404.  
 PN DE10128510-A1.  
 PD 19-DEC-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 289  
 ID ADD13690 standard; DNA; 769 BP.  
 DE C. glutamicum homeostasis and adaptation associated DNA SEQ ID 91.  
 PN WO2003040290-A2.  
 PD 15-MAY-2003.  
 PA (BADI ) BASF AG.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 290  
 ID AAH68527 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 7062.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KIOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 291  
 ID ACF72506 standard; DNA; 636 BP.  
 DE Staphylococcus aureus DNA #186.  
 PN WO200294868-A2.  
 PD 28-NOV-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 42.01%  
 Best Local Similarity: 21.92%  
 Query Match: 8.49%  
 Indels: 28  
 RESULT 292  
 ID ABL12193 standard; cDNA; 5514 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 36.09%  
 Best Local Similarity: 25.19%  
 Query Match: 8.45%  
 Indels: 100  
 RESULT 293  
 ID AAC89765 standard; cDNA; 178 BP.  
 DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
 PN WO200073324-A2.  
 PD 07-DEC-2000.  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 8.41%  
 Indels: 0  
 RESULT 296  
 ID ABN87116 standard; cDNA; 457 BP.  
 DE Lolium perenne LpCCoAWta partial nucleotide sequence SEQ ID NO:10.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 54.93%  
 Best Local Similarity: 35.21%  
 Query Match: 8.41%  
 Indels: 6

RESULT 297  
 ID AAD35115 standard; DNA; 2086 BP.  
 DE Corynebacterium glutamicum sigE gene.  
 PN WO200218428-A2.  
 PD 07-MAR-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 39.80%  
 Best Local Similarity: 25.51%  
 Query Match: 8.34%  
 Indels: 38  
 RESULT 298  
 ID ABQ90300 standard; DNA; 4029 BP.  
 DE M. capsulatus gene #285 for DNA array.  
 PN WO200253655-A2.  
 PD 18-JUL-2002.  
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.  
 Percent Similarity: 37.63%  
 Best Local Similarity: 25.44%  
 Query Match: 8.30%  
 Indels: 83  
 RESULT 299  
 ID AAH53823 standard; DNA; 495 BP.  
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3039.  
 PN WO200134809-A2.  
 PD 17-MAY-2001.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Percent Similarity: 44.24%  
 Best Local Similarity: 22.42%  
 Query Match: 8.27%  
 Indels: 10  
 RESULT 300  
 ID ADB74275 standard; DNA; 38494 BP.  
 DE Mycobacterium leprae DNA #2.  
 PN US6583266-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 50.00%  
 Best Local Similarity: 33.33%  
 Query Match: 8.27%  
 Indels: 0  
 RESULT 301  
 ID AAA68082 standard; DNA; 236 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:175.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 54.55%  
 Best Local Similarity: 29.87%  
 Query Match: 8.19%  
 Indels: 8  
 RESULT 302  
 ID ADD41832 standard; DNA; 236 BP.  
 DE O-methyl transferase DNA #16.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 54.55%  
 Best Local Similarity: 29.87%  
 Query Match: 8.19%  
 Indels: 8  
 RESULT 303  
 ID ADS59333 standard; cDNA; 624 BP.  
 DE Bacterial polynucleotide #11320.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 37.20%  
 Best Local Similarity: 21.74%  
 Query Match: 8.12%  
 Indels: 50  
 RESULT 304  
 ID AAQ13306 standard; DNA; 1107 BP.  
 DE Human catechol-O-methyltransferase gene.

PN W09111513-A.  
 PD 08-AUG-1991.  
 PA (ORIN ) ORION YHYMAE OY.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.08% Indels: 45  
 RESULT 305  
 ID ACN40883 standard; cDNA; 1289 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA226561, SEQ ID NO:5956.  
 PN W02004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.08% Indels: 45  
 RESULT 306  
 ID ADP45594 standard; DNA; 133100 BP.  
 DE Human NUMA1/FLJ20625/LOC220074 region gDNA.  
 Percent Similarity: 41.83% Conservative: 28  
 Best Local Similarity: 28.37% Mismatches: 81  
 Query Match: 8.04% Indels: 41  
 RESULT 307  
 ID ABZ83278 standard; cDNA; 1024 BP.  
 DE Toxicologically relevant human nucleotide sequence #437.  
 PN W02003016500-A2.  
 PD 27-FEB-2003.  
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 308  
 ID ADE84973 standard; DNA; 1206 BP.  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
 PN W02003038129-A2.  
 PD 08-MAY-2003.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 309  
 ID ADQ85986 standard; cDNA; 1291 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2858.  
 PN W02004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 310  
 ID ACN44731 standard; cDNA; 1311 BP.  
 DE Human mRNA sequence hCT1955643.  
 PN W02003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 311  
 ID ABX63642 standard; cDNA; 1327 BP.  
 DE Human cDNA #642 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 312  
 ID ADS69859 standard; cDNA; 253 BP.  
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4875.  
 PN US2003237110-A9.  
 PD 25-DEC-2003.

PA (INCY-) INCYTE PHARM INC.  
 Percent Similarity: 52.44% Conservative: 9  
 Best Local Similarity: 41.46% Mismatches: 34  
 Query Match: 7.97% Indels: 5  
 RESULT 313  
 ID ABZ51068 standard; cDNA; 836 BP.  
 DE Aspergillus oryzae polynucleotide SEQ ID NO 181.  
 PN W0200279476-A1.  
 PD 10-OCT-2002.  
 PA (NARE-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (NORQ ) NAT FOOD RES INST MIN AGRIC.  
 Percent Similarity: 40.96% Conservative: 21  
 Best Local Similarity: 28.31% Mismatches: 57  
 Query Match: 7.97% Indels: 41  
 RESULT 314  
 ID AAC77872 standard; cDNA; 1350 BP.  
 DE Human cancer associated gene sequence SEQ ID NO:266.  
 PN W0200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.84% Conservative: 38  
 Best Local Similarity: 24.70% Mismatches: 116  
 Query Match: 7.89% Indels: 35  
 RESULT 315  
 ID AA31195 standard; DNA; 356 BP.  
 DE Plant microsatellite marker #156.  
 PN W09967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 52.87% Conservative: 16  
 Best Local Similarity: 34.48% Mismatches: 33  
 Query Match: 7.82% Indels: 9  
 RESULT 316  
 ID AAD35116 standard; DNA; 457 BP.  
 DE Corynebacterium glutamicum sigE gene upstream region DNA.  
 PN W0200218428-A2.  
 PD 07-MAR-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 44.37% Conservative: 26  
 Best Local Similarity: 26.06% Mismatches: 59  
 Query Match: 7.82% Indels: 20  
 RESULT 317  
 ID ACS51621 standard; DNA; 834 BP.  
 DE Prokaryotic essential gene #33278.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.11% Conservative: 33  
 Best Local Similarity: 26.57% Mismatches: 95  
 Query Match: 7.71% Indels: 82  
 RESULT 318  
 ID ADB58045 standard; DNA; 1531 BP.  
 DE Toxicity-related gene, SEQ ID 3071.  
 PN W02003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Query Match: 7.71% Indels: 31  
 RESULT 319  
 ID ADB52519 standard; DNA; 1531 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
 PN W02003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Query Match: 7.71% Indels: 31  
 RESULT 320  
 ID ACN40884 standard; cDNA; 1067 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326926, SEQ ID NO:5958.

PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 40.51%  
 Best Local Similarity: 24.05%  
 Mismatches: 110  
 Indels: 31  
 Query Match: 7.67%  
 RESULT 321  
 ID ADK5023 standard; DNA; 64492 BP.  
 DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
 PN US2004053274-A1.  
 PD 18-MAR-2004.  
 PA (TOKD ) TOKYO INST TECHNOLOGY.  
 Percent Similarity: 30.15%  
 Best Local Similarity: 22.77%  
 Mismatches: 85  
 Indels: 142  
 Query Match: 7.67%  
 RESULT 322  
 ID AAQ13305 standard; DNA; 1591 BP.  
 DE Rat catechol-O-methyltransferase gene.  
 PN WO9111513-A.  
 PD 08-AUG-1991.  
 PA (ORIN ) ORION YHTWAE OY.  
 Percent Similarity: 43.19%  
 Best Local Similarity: 23.94%  
 Mismatches: 92  
 Indels: 31  
 Query Match: 7.63%  
 RESULT 323  
 ID AQ67408 standard; cDNA; 3003 BP.  
 DE Novel human cDNA sequence #2381.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 37.29%  
 Best Local Similarity: 27.12%  
 Mismatches: 66  
 Indels: 45  
 Query Match: 7.63%  
 RESULT 324  
 ID AAS81954 standard; cDNA; 4083 BP.  
 DE DNA encoding novel human diagnostic protein #19758.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 37.29%  
 Best Local Similarity: 27.12%  
 Mismatches: 66  
 Indels: 45  
 Query Match: 7.63%  
 RESULT 325  
 ID AAQ88760 standard; DNA; 1813 BP.  
 DE Human ubiquitous nuclear receptor protein DNA.  
 PN WO9513373-A1.  
 PD 18-MAY-1995.  
 PA (ARCH-) ARCH DEV CORP.  
 Percent Similarity: 34.41%  
 Best Local Similarity: 25.59%  
 Mismatches: 122  
 Indels: 101  
 Query Match: 7.59%  
 RESULT 326  
 ID AAT79634 standard; DNA; 1898 BP.  
 DE DNA encoding human ubiquitous nuclear receptor polypeptide.  
 PN US539616-A.  
 PD 17-JUN-1997.  
 PA (ARCH-) ARCH DEV CORP.  
 Percent Similarity: 34.21%  
 Best Local Similarity: 25.73%  
 Mismatches: 120  
 Indels: 105  
 Query Match: 7.59%  
 RESULT 327  
 ID AAT7617 standard; cDNA to mRNA; 1688 BP.  
 DE Steroid hormone receptor analogue ECDN small mol. variant cDNA.  
 PN WO9609324-A1.  
 PD 28-MAR-1996.  
 PA (CANC-) CANCER INST.  
 PA (EISA ) EISAI CO LTD.  
 Percent Similarity: 37.41%  
 Best Local Similarity: 25.90%  
 Mismatches: 106  
 Indels: 68  
 Query Match: 7.56%  
 RESULT 328  
 ID ACC85541 standard; DNA; 2505 BP.  
 DE T thermophilus strain GK24 DNA polymerase gene SEQ ID NO: 1.  
 PN WO200304830b-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.73%  
 Best Local Similarity: 26.19%  
 Mismatches: 31  
 Indels: 78  
 Query Match: 7.56%  
 RESULT 329  
 ID ACC85544 standard; DNA; 2505 BP.  
 DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 4.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.73%  
 Best Local Similarity: 26.19%  
 Mismatches: 31  
 Indels: 78  
 Query Match: 7.56%  
 RESULT 330  
 ID ABZ11775 standard; cDNA; 1564 BP.  
 DE Human polynucleotide SEQ ID NO 657.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 31.96%  
 Best Local Similarity: 24.63%  
 Mismatches: 25  
 Indels: 108  
 Query Match: 7.52%  
 RESULT 331  
 ID ADM4293 standard; cDNA; 1786 BP.  
 DE Novel human arginine-rich protein cDNA #657.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Percent Similarity: 31.96%  
 Best Local Similarity: 24.63%  
 Mismatches: 25  
 Indels: 108  
 Query Match: 7.52%  
 RESULT 332  
 ID ADC30127 standard; cDNA; 3298 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:209.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 37.09%  
 Best Local Similarity: 28.17%  
 Mismatches: 19  
 Indels: 55  
 Query Match: 7.52%  
 RESULT 333  
 ID ACF36088 standard; DNA; 1815 BP.  
 DE Human LXR beta polypeptide encoding DNA.  
 PN WO2003059884-A1.  
 PD 24-JUL-2003.  
 PA (XCEP-) X-CEPTOR THERAPEUTICS INC.  
 Percent Similarity: 37.68%  
 Best Local Similarity: 27.90%  
 Mismatches: 27  
 Indels: 64  
 Query Match: 7.48%  
 RESULT 334  
 ID ACF04414 standard; DNA; 1815 BP.  
 DE Human liver X receptor LXR beta coding sequence.  
 PN WO2003060078-A2.  
 PD 24-JUL-2003.  
 PA (XCEP-) X-CEPTOR THERAPEUTICS INC.  
 Percent Similarity: 37.68%  
 Best Local Similarity: 27.90%  
 Mismatches: 27  
 Indels: 64  
 Query Match: 7.48%  
 RESULT 335  
 ID ADQ83721 standard; cDNA; 1986 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #535.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 37.68%  
 Best Local Similarity: 27.90%  
 Mismatches: 27  
 Indels: 64  
 Query Match: 7.48%

RESULT 336  
ID ADQ87023 standard; cDNA; 1986 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3899.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 337  
ID ACN40662 standard; cDNA; 1986 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326744, SEQ ID NO:5578.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 338  
ID ADL12925 standard; cDNA; 1987 BP.  
DE Human steroid-induced C3A liver cell cDNA #654.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 339  
ID ADQ89943 standard; DNA; 7531 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #187.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 340  
ID AAT88206 standard; cDNA; 8460 BP.  
DE cDNA for protein (OA-519) cross-reactive with hpr gene product.  
PN US5665874-A.  
PD 09-SEP-1997.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 341  
ID ACC49471 standard; cDNA; 8460 BP.  
DE Human fatty acid synthase encoding cDNA.  
PN WO2003023355-A2.  
PD 20-MAR-2003.  
PA (BURN-) BURNHAM INST.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 342  
ID ACA64923 standard; DNA; 8460 BP.  
DE Human breast carcinoma fatty acid synthase DNA corresponding to U29344.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHARRAY GMBH.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 343  
ID ACF63393 standard; DNA; 8460 BP.  
DE Human fatty acid synthase gene SEQ ID NO:115.  
PN WO2003006478-A1.  
PD 23-JAN-2003.  
PA (OLIG-) OLIGOS ETC INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%

Query Match: 7.45%  
Indels: 134  
RESULT 344  
ID ADO21281 standard; cDNA; 8460 BP.  
DE DNA encoding human fatty acid synthase.  
PN US2004077570-A1.  
PD 22-APR-2004.  
PA (FREI/) FREIER S M.  
PA (DOB/) DOBIE K W.  
PA (BHAM/) BHANOT S.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 345  
ID ADP13456 standard; DNA; 8460 BP.  
DE Renal cell carcinoma differentially expressed gene #192.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 346  
ID ADQ89779 standard; DNA; 8460 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #105.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 347  
ID AAV74506 standard; DNA; 13715 BP.  
DE Staphylococcus aureus contig SEQ ID #195.  
PN EP786519-A2.  
PD 30-JUL-1997.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 39.27%  
Best Local Similarity: 21.46%  
Conservative: 39  
Mismatches: 105  
Indels: 28  
Query Match: 7.45%  
RESULT 348  
ID ABD07304 standard; DNA; 2469 BP.  
DE Pseudomonas aeruginosa polynucleotide #5908.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.37%  
Best Local Similarity: 27.40%  
Conservative: 28  
Mismatches: 107  
Indels: 69  
Query Match: 7.41%  
RESULT 349  
ID ABD11218 standard; DNA; 636 BP.  
DE Pseudomonas aeruginosa polynucleotide #9822.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 43.88%  
Best Local Similarity: 28.78%  
Conservative: 21  
Mismatches: 58  
Indels: 20  
Query Match: 7.37%  
RESULT 350  
ID ABD11311 standard; DNA; 1275 BP.  
DE Pseudomonas aeruginosa polynucleotide #9915.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 43.88%  
Best Local Similarity: 28.78%  
Conservative: 21  
Mismatches: 58  
Indels: 20  
Query Match: 7.37%  
RESULT 351



ID ABD11556 standard; DNA; 1443 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10160.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 43.88% Conservative: 21  
 Best Local Similarity: 28.78% Mismatches: 58  
 Query Match: 7.37% Indels: 20  
 RESULT 352  
 ID AAQ24322 standard; DNA; 1635 BP.  
 DE Mutant thermostable DNA polymerase p205A292.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 353  
 ID AAQ24321 standard; DNA; 1899 BP.  
 DE Mutant thermostable DNA polymerase p205d2-203.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 354  
 ID ABK84201 standard; cDNA; 2010 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #772.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 355  
 ID ADJ14181 standard; DNA; 2010 BP.  
 DE DNA encoding human liver X receptor LXR beta.  
 PN US2004018560-A1.  
 PD 29-JAN-2004.  
 PA (BLED/) BLEDSE R K.  
 PA (MILL/) MILLER A.  
 PA (MOOR/) MOORE J T.  
 PA (MOOR/) MOORE L.  
 PA (WILL/) WILLIAMS S P.  
 PA (WISE/) WISELY G B.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 356  
 ID ADMA1245 standard; DNA; 2010 BP.  
 DE Human liver X receptor beta gene.  
 PN EPI398032-A1.  
 PD 17-MAR-2004.  
 PA (PHEN-) PHENEX PHARM AG.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 357  
 ID AAQ63134 standard; cDNA; 2030 BP.  
 DE Human recombinant steroid hormone receptor NERI cDNA.  
 PN WO9407916-A1.  
 PD 14-APR-1994.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 358  
 ID AAT18996 standard; DNA; 2030 BP.  
 DE Human steroid receptor NER gene.  
 PN WO9613519-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MERCK & CO INC.

PA (MEDI-) MEDICAL COLLEGE PENNSYLVANIA.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 359  
 ID AAT30031 standard; DNA; 2030 BP.  
 DE NER receptor potentiator DNA.  
 PN WO9613257-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 360  
 ID AAQ24320 standard; DNA; 2043 BP.  
 DE Mutant thermostable DNA polymerase p205d2-155.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 361  
 ID AAQ24013 standard; DNA; 2277 BP.  
 DE Mutant thermostable DNA polymerase p205d2-77.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 362  
 ID AAQ24012 standard; DNA; 2370 BP.  
 DE Mutant thermostable DNA polymerase p205d2-46.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 363  
 ID AAQ24011 standard; DNA; 2505 BP.  
 DE Mutant thermostable DNA polymerase from Thermus species Z05.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 364  
 ID ADG64486 standard; DNA; 2685 BP.  
 DE Chimeric thermostable DNA polymerase CS8 encoding DNA SEQ ID NO:171.  
 PN EPI350841-A2.  
 PD 08-OCT-2003.  
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 365  
 ID ADG64462 standard; DNA; 2685 BP.  
 DE Chimeric thermostable DNA polymerase CS7 encoding DNA SEQ ID NO:147.  
 PN EPI350841-A2.  
 PD 08-OCT-2003.  
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 366  
 ID ADA13364 standard; cDNA; 2877 BP.  
 DE Human intracellular signalling molecule INTSIG-1 cDNA, SEQ ID NO:46.



Query Match: 7.33% Indels: 51  
 RESULT 381  
 ID AAX07131 standard; DNA; 3147 BP.  
 DE Staphylococcus aureus mutant P14B25 virulence gene.  
 PN WO9901473-A2.  
 PD 14-JAN-1999.  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 382  
 ID AAS52328 standard; DNA; 3147 BP.  
 DE E. coli DNA for cellular proliferation protein #50.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 383  
 ID AAH81417 standard; DNA; 3147 BP.  
 DE Escherichia coli protein encoding nucleotide sequence SEQ ID NO:216.  
 PN WO200148209-A2.  
 PD 05-JUL-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 384  
 ID ACA32390 standard; DNA; 3147 BP.  
 DE Prokaryotic essential gene #14047.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 385  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.48% Mismatches: 85  
 Query Match: 7.33% Indels: 52  
 RESULT 386  
 ID ACA44128 standard; DNA; 828 BP.  
 DE Prokaryotic essential gene #25785.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.36% Conservative: 16  
 Best Local Similarity: 30.04% Mismatches: 79  
 Query Match: 7.30% Indels: 84  
 RESULT 387  
 ID ABD01505 standard; DNA; 1713 BP.  
 DE Pseudomonas aeruginosa polynucleotide #109.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.16% Conservative: 26  
 Best Local Similarity: 26.57% Mismatches: 73  
 Query Match: 7.30% Indels: 101  
 RESULT 388  
 ID AAH16078 standard; cDNA; 1782 BP.  
 DE Human cDNA sequence SEQ ID NO:14776.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 31.67% Conservative: 24  
 Best Local Similarity: 24.63% Mismatches: 125  
 Query Match: 7.30% Indels: 108  
 RESULT 389  
 ID ACC78000 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.

PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.37% Conservative: 34  
 Best Local Similarity: 25.61% Mismatches: 115  
 Query Match: 7.30% Indels: 68  
 RESULT 390  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Percent Similarity: 32.34% Conservative: 36  
 Best Local Similarity: 21.66% Mismatches: 79  
 Query Match: 7.30% Indels: 149  
 RESULT 391  
 ID ABD10747 standard; DNA; 657 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9351.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.50% Conservative: 23  
 Best Local Similarity: 28.32% Mismatches: 83  
 Query Match: 7.26% Indels: 56  
 RESULT 392  
 ID AAZ91260 standard; DNA; 1632 BP.  
 DE Acetohydroxyacid synthase nucleotide sequence SEQ ID NO:14.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 38.33% Conservative: 34  
 Best Local Similarity: 26.48% Mismatches: 124  
 Query Match: 7.26% Indels: 53  
 RESULT 393  
 ID AAT27616 standard; cDNA to mRNA; 1979 BP.  
 DE Human foetal lung steroid hormone receptor analogue ECDN cDNA.  
 PN WO9609324-A1.  
 PD 28-MAR-1996.  
 PA (CANC-) CANCER INST.  
 PA (EISA) EISAI CO LTD.  
 Percent Similarity: 37.77% Conservative: 26  
 Best Local Similarity: 28.42% Mismatches: 105  
 Query Match: 7.26% Indels: 68  
 RESULT 394  
 ID ABD13152 standard; DNA; 2232 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11756.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.11% Conservative: 28  
 Best Local Similarity: 28.32% Mismatches: 112  
 Query Match: 7.26% Indels: 67  
 RESULT 395  
 ID ABD13005 standard; DNA; 2274 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11609.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.11% Conservative: 28  
 Best Local Similarity: 28.32% Mismatches: 112  
 Query Match: 7.26% Indels: 67  
 RESULT 396  
 ID ACC85543 standard; DNA; 2505 BP.  
 DE T. thermophilus strain lb21 DNA polymerase gene SEQ ID NO: 3.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 37.33% Conservative: 34  
 Best Local Similarity: 25.68% Mismatches: 111  
 Query Match: 7.26% Indels: 74  
 RESULT 397  
 ID ACC85542 standard; DNA; 2505 BP.  
 DE T. thermophilus strain RQ-1 DNA polymerase gene SEQ ID NO: 2.

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PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
RESULT 398
ID ACC85547 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 7.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
RESULT 399
ID ACC85545 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 5.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
RESULT 400
ID ACC85550 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 10.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
RESULT 401
ID ACC85546 standard; DNA; 2505 BP.
DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 6.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 37.33%
Best Local Similarity: 25.68%
Query Match: 7.26%
RESULT 402
ID ABD13232 standard; DNA; 2613 BP.
DE Pseudomonas aeruginosa polynucleotide #11836.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.11%
Best Local Similarity: 28.32%
Query Match: 7.26%
RESULT 403
ID ACC77974 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
RESULT 404
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.34%
Query Match: 7.26%
RESULT 405
ID AA291253 standard; DNA; 24494 BP.
DE Bacterium 2412.1 fumonisin-catabolising gene cluster.
PN WO200004159-A2.

PD 27-JAN-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 38.33%
Best Local Similarity: 26.48%
Query Match: 7.26%
RESULT 406
ID AAQ46806 standard; DNA; 29879 BP.
DE eryA region of S. erythraea chromosome.
PN WO9313663-A1.
PD 22-JUL-1993.
PA (ABBO-) ABBOTT LAB.
Percent Similarity: 33.03%
Best Local Similarity: 24.62%
Query Match: 7.26%
RESULT 407
ID ABD11655 standard; DNA; 1086 BP.
DE Pseudomonas aeruginosa polynucleotide #10259.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
RESULT 408
ID ABD11993 standard; DNA; 1101 BP.
DE Pseudomonas aeruginosa polynucleotide #10597.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
RESULT 409
ID ACA5703 standard; DNA; 1104 BP.
DE Prokaryotic essential gene #27360.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 44.22%
Best Local Similarity: 26.63%
Query Match: 7.22%
RESULT 410
ID AAA81453 standard; DNA; 36471 BP.
DE N. meningitidis partial DNA sequence gnm_1 SEQ ID NO:1.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
RESULT 411
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
RESULT 412
ID AAF21611 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
RESULT 413
ID ABD13494 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #12098.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%

Conservative: 34
Mismatches: 124
Indels: 53
Conservative: 28
Mismatches: 93
Indels: 130
Conservative: 40
Mismatches: 122
Indels: 49
Conservative: 35
Mismatches: 72
Indels: 39
Conservative: 36
Mismatches: 103
Indels: 92
Conservative: 36
Mismatches: 103
Indels: 92
Conservative: 36
Mismatches: 103
Indels: 92
Conservative: 24
Mismatches: 93
Indels: 71
```

RESULT 414  
 ID ABD13569 standard; DNA; 984 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12173.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.43% Conservative: 24  
 Best Local Similarity: 25.98% Mismatches: 93  
 Query Match: 7.19% Indels: 71

RESULT 415  
 ID ABD13816 standard; DNA; 1254 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12420.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.03% Conservative: 23  
 Best Local Similarity: 27.57% Mismatches: 125  
 Query Match: 7.19% Indels: 50

RESULT 416  
 ID ACC77992 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.19% Indels: 74

RESULT 417  
 ID ABD07318 standard; DNA; 3135 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5922.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.17% Conservative: 27  
 Best Local Similarity: 27.14% Mismatches: 101  
 Query Match: 7.15% Indels: 68

RESULT 418  
 ID ADC59447 standard; DNA; 15534 BP.  
 DE Human epiplakin-encoding cDNA.  
 PN JP2003047469-A.  
 PD 18-FEB-2003.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 419  
 ID ADJ75047 standard; DNA; 15534 BP.  
 DE Marker gene SEQ ID NO:299.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 420  
 ID ACF12853 standard; cDNA; 15952 BP.  
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:51.  
 PN WO2002101075-A2.  
 PD 19-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 421  
 ID ABD09003 standard; DNA; 852 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7607.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.39% Conservative: 20  
 Best Local Similarity: 27.27% Mismatches: 71  
 Query Match: 7.11% Indels: 29

RESULT 422

ID ADS62025 standard; cDNA; 1272 BP.  
 DE Bacterial polynucleotide #14012.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.03% Conservative: 18  
 Best Local Similarity: 30.34% Mismatches: 114  
 Query Match: 7.11% Indels: 33

RESULT 423  
 ID ABD05329 standard; DNA; 1452 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3933.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89% Conservative: 34  
 Best Local Similarity: 26.30% Mismatches: 95  
 Query Match: 7.11% Indels: 70

RESULT 424  
 ID AAT27255 standard; DNA; 1794 BP.  
 DE DNA polymerase I exonuclease-free fragment.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74

RESULT 425  
 ID AAT32327 standard; DNA; 1794 BP.  
 DE Thermus flavus DNA polymerase I exonuclease free fragment.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74

RESULT 426  
 ID ADN96193 standard; cDNA; 1837 BP.  
 DE Human NOVX polynucleotide #124.  
 PN US2004067490-A1.  
 PD 08-APR-2004.  
 PA (ZHON/) ZHONG M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (SPYT/) SPYTEK K A.  
 PA (KEKU/) KEKUDA R.  
 PA (TAUP/) TRAUPIER R J.  
 PA (ANDE/) ANDERSON D W.  
 PA (VERN/) VERNET C A M.  
 PA (CATT/) CATTERTON E.  
 PA (MILL/) MILLER C E.  
 PA (SHEN/) SHENOY S G.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (TCHN/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (GUSE/) GUSEV V Y.  
 PA (MALY/) MALYANKAR U M.  
 PA (BURG/) BURGESS C E.  
 PA (GERL/) GERLACH V.  
 PA (CASM/) CASMAN S J.  
 PA (RIEG/) RIEGER D K.  
 PA (GROS/) GROSSE W M.  
 PA (SMIT/) SMITHSON G.  
 PA (PEYM/) PEYMAN J A.  
 PA (STAR/) STARLING G.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LARO/) LAROCHELLE W J.  
 PA (SHIM/) SHIMKETS R A.  
 PA (CRAB/) CRABTREE J.

PA (RAST/) RASTELLI L.  
 PA (VOSS/) VOSS E Z.  
 PA (BOLD/) BOLDOG F L.  
 PA (EDIN/) EDINGER S R.  
 PA (MILL/) MILLET I.  
 PA (MACD/) MACDOUGALL J R.  
 PA (ELLE/) ELLERMAN K.  
 PA (CHAP/) CHAPOVAL A.  
 Percent Similarity: 32.99%  
 Best Local Similarity: 24.40%  
 Query Match: 7.11%  
 Indels: 102  
 Conservative: 25  
 Mismatches: 93

RESULT 427  
 ID AAS54053 standard; DNA; 2553 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #184.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26%  
 Best Local Similarity: 27.47%  
 Query Match: 7.11%  
 Indels: 76  
 Conservative: 24  
 Mismatches: 99

RESULT 428  
 ID ACA42124 standard; DNA; 2553 BP.  
 DE Prokaryotic essential gene #23781.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26%  
 Best Local Similarity: 27.47%  
 Query Match: 7.11%  
 Indels: 76  
 Conservative: 24  
 Mismatches: 99

RESULT 429  
 ID AAZ48661 standard; DNA; 2942 BP.  
 DE L. mycophilus chitinase gene, N4-7 chia.  
 PN WO9555833-A2.  
 PD 04-NOV-1999.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 Percent Similarity: 35.89%  
 Best Local Similarity: 27.42%  
 Query Match: 7.11%  
 Indels: 68  
 Conservative: 21  
 Mismatches: 92

RESULT 430  
 ID AAT27254 standard; DNA; 3048 BP.  
 DE DNA polymerase I holoenzyme coding sequence.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.68%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 112

RESULT 431  
 ID ACC78014 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113

RESULT 432  
 ID ACC78011 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113

RESULT 433  
 ID ACC77998 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.68%  
 Query Match: 7.11%  
 Indels: 112  
 Conservative: 33  
 Mismatches: 112

Query Match: 7.11%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 95

RESULT 434  
 ID ABD05402 standard; DNA; 4284 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4006.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89%  
 Best Local Similarity: 26.30%  
 Query Match: 7.11%  
 Indels: 70  
 Conservative: 34  
 Mismatches: 95

RESULT 435  
 ID ABQ55289 standard; cDNA; 553 BP.  
 DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 45.69%  
 Best Local Similarity: 25.00%  
 Query Match: 7.07%  
 Indels: 4  
 Conservative: 24  
 Mismatches: 59

RESULT 436  
 ID AAH13983 standard; cDNA; 1416 BP.  
 DE Human cDNA sequence SEQ ID NO:11048.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 24.89%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 94

RESULT 437  
 ID ACA27231 standard; DNA; 1948 BP.  
 DE Prokaryotic essential gene #8888.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 29.66%  
 Best Local Similarity: 22.57%  
 Query Match: 7.07%  
 Indels: 172  
 Conservative: 27  
 Mismatches: 96

RESULT 438  
 ID ADA52678 standard; cDNA; 2597 BP.  
 DE Human coding sequence, SEQ ID 246.  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 24.89%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 94

RESULT 439  
 ID ADD69665 standard; cDNA; 3153 BP.  
 DE Human REMAP cDNA - SEQ ID 94.  
 PN WO2003048305-A2.  
 PD 12-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 39.81%  
 Best Local Similarity: 26.07%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 72

RESULT 440  
 ID ADD24914 standard; DNA; 4184 BP.  
 DE DNA encoding Escherichia coli intracellular protease #6.  
 PN US2003036176-A1.  
 PD 20-FEB-2003.  
 PA (BOME/) BOWER S G.  
 PA (RAMS/) RAMSEIER T M.  
 Percent Similarity: 36.84%  
 Best Local Similarity: 25.39%  
 Query Match: 7.07%  
 Indels: 97  
 Conservative: 37  
 Mismatches: 109

RESULT 441  
 ID ADQ85412 standard; cDNA; 4962 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2226.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 Query Match: 7.07%  
 Indels: 97  
 Conservative: 37  
 Mismatches: 109

PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 37.13% Conservative: 29  
 Best Local Similarity: 24.89% Mismatches: 94  
 Query Match: 7.07% Indels: 55  
 RESULT 442  
 ID AAF6431 standard; DNA; 349980 BP.  
 DE *Pyrococcus abyssi* genomic fragment #1.  
 PN FR2792651-A1.  
 PD 27-OCT-2000.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (IFRE-) IPREMER INST FR RECH EXPL MER.  
 Percent Similarity: 36.00% Conservative: 43  
 Best Local Similarity: 20.36% Mismatches: 100  
 Query Match: 7.07% Indels: 76  
 RESULT 443  
 ID AAQ14176 standard; cDNA; 2304 BP.  
 DE Clone pXR2C8 encoding insect steroid receptor XR2C.  
 PN WO9114695-A.  
 PD 03-OCT-1991.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 444  
 ID AAQ55374 standard; DNA; 2304 BP.  
 DE pXR2C8 DNA.  
 PN WO9401558-A2.  
 PD 20-JAN-1994.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 445  
 ID AAT76787 standard; DNA; 2304 BP.  
 DE Insect XR2C receptor coding sequence.  
 PN US5641652-A.  
 PD 24-JUN-1997.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 446  
 ID AAT99959 standard; DNA; 2304 BP.  
 DE D. melanogaster XR2C retinoid-like receptor DNA.  
 PN US568691-A.  
 PD 18-NOV-1997.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 447  
 ID ABL07559 standard; cDNA; 2483 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17159.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 448  
 ID ACC77970 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 449  
 ID ACC77978 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.

PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 450  
 ID ACC77991 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 451  
 ID ACC77984 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 452  
 ID ABL07558 standard; cDNA; 4483 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17156.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 453  
 ID ABL07492 standard; cDNA; 18737 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 16958.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 454  
 ID ABL07530 standard; cDNA; 18737 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17072.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 455  
 ID ACA43915 standard; DNA; 717 BP.  
 DE *Prokaryotic essential gene* #25572.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.08% Conservative: 22  
 Best Local Similarity: 25.84% Mismatches: 84  
 Query Match: 7.00% Indels: 93  
 RESULT 456  
 ID AAS65542 standard; cDNA; 825 BP.  
 DE DNA encoding novel human diagnostic protein #1346.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 44.79% Conservative: 11  
 Best Local Similarity: 33.33% Mismatches: 33  
 Query Match: 7.00% Indels: 20  
 RESULT 457  
 ID AAQ80524 standard; DNA; 1410 BP.  
 DE Oxidoreducing avermectin DNA from *S. avermetilis* ATCC31271.  
 PN JP06189774-A.  
 PD 12-JUL-1994.  
 PA (KITA ) KITASATO KENKYUSHO SH.

Percent Similarity: 35.48% Conservative: 32  
 Best Local Similarity: 24.01% Mismatches: 104  
 Query Match: 7.00% Indels: 76  
 RESULT 458  
 ID ABD13438 standard; DNA; 1527 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12042.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.62% Conservative: 23  
 Best Local Similarity: 26.67% Mismatches: 78  
 Query Match: 7.00% Indels: 53  
 RESULT 459  
 ID ABD01627 standard; DNA; 1962 BP.  
 DE Pseudomonas aeruginosa polynucleotide #231.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.64% Conservative: 24  
 Best Local Similarity: 28.42% Mismatches: 118  
 Query Match: 7.00% Indels: 67  
 RESULT 460  
 ID ABD13335 standard; DNA; 2313 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11939.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.62% Conservative: 23  
 Best Local Similarity: 26.67% Mismatches: 78  
 Query Match: 7.00% Indels: 53  
 RESULT 461  
 ID ADQ22115 standard; DNA; 4618 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4935.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 37.33% Conservative: 22  
 Best Local Similarity: 27.19% Mismatches: 79  
 Query Match: 7.00% Indels: 57  
 RESULT 462  
 ID ADR44308 standard; DNA; 9576 BP.  
 DE Mosquito leucine-rich repeat protein gene sequence SEQ ID NO:54.  
 PN EP1452183-A1.  
 PD 01-SEP-2004.  
 PA (EMBL-) EMBL.  
 Percent Similarity: 36.54% Conservative: 45  
 Best Local Similarity: 22.12% Mismatches: 99  
 Query Match: 7.00% Indels: 99  
 RESULT 463  
 ID ABD10637 standard; DNA; 1233 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9241.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.86% Conservative: 26  
 Best Local Similarity: 24.65% Mismatches: 100  
 Query Match: 6.96% Indels: 147  
 RESULT 464  
 ID ABD10108 standard; DNA; 1980 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8712.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 30.93% Conservative: 17  
 Best Local Similarity: 25.09% Mismatches: 78  
 Query Match: 6.96% Indels: 123  
 RESULT 465  
 ID ACC85548 standard; DNA; 2505 BP.  
 DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 8.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.30% Conservative: 31

Best Local Similarity: 25.68% Mismatches: 114  
 Query Match: 6.96% Indels: 74  
 RESULT 466  
 ID ACC85552 standard; DNA; 2505 BP.  
 DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 12.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 6.96% Indels: 74  
 RESULT 467  
 ID ACC85549 standard; DNA; 2505 BP.  
 DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 9.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 6.96% Indels: 74  
 RESULT 468  
 ID ACC85551 standard; DNA; 2505 BP.  
 DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 11.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.30% Conservative: 31  
 Best Local Similarity: 25.68% Mismatches: 114  
 Query Match: 6.96% Indels: 74  
 RESULT 469  
 ID ACC78001 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 470  
 ID ACC78002 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 471  
 ID ACC77983 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 472  
 ID ACC77987 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 473  
 ID ACC77996 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74



Query Match: 6.96% Indels: 74  
 RESULT 474  
 ID ACC78013 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 6.96%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113  
 Indels: 74  
 RESULT 475  
 ID AAV62176 standard; DNA; 117213 BP.  
 DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.96%  
 Indels: 86  
 Conservative: 22  
 Mismatches: 109  
 Indels: 86  
 RESULT 476  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.96%  
 Indels: 86  
 Conservative: 22  
 Mismatches: 109  
 Indels: 86  
 RESULT 477  
 ID ABD03356 standard; DNA; 1701 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1960.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 478  
 ID ABD10467 standard; DNA; 1848 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9071.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.06%  
 Best Local Similarity: 25.95%  
 Query Match: 6.92%  
 Indels: 110  
 Conservative: 16  
 Mismatches: 68  
 Indels: 110  
 RESULT 479  
 ID AAV39834 standard; cDNA; 1898 BP.  
 DE Mouse protein phosphatase 2A subunit encoding cDNA.  
 PN WO9824915-A1.  
 PD 11-JUN-1998.  
 PA (VEHE-) VER HET NEDERLANDS KANKER INST.  
 PA (PROL-) PROLIFIX LTD.  
 Percent Similarity: 36.02%  
 Best Local Similarity: 28.39%  
 Query Match: 6.92%  
 Indels: 70  
 Conservative: 18  
 Mismatches: 81  
 Indels: 70  
 RESULT 480  
 ID ADS58106 standard; cDNA; 1908 BP.  
 DE Bacterial polynucleotide #10093.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Percent Similarity: 39.93%  
 Best Local Similarity: 26.12%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 37  
 Mismatches: 87  
 Indels: 75  
 RESULT 481  
 ID AAV39835 standard; cDNA; 1988 BP.  
 DE Mouse protein phosphatase 2A subunit variant encoding cDNA.  
 PN WO9824915-A1.  
 PD 11-JUN-1998.  
 PA (VEHE-) VER HET NEDERLANDS KANKER INST.  
 PA (PROL-) PROLIFIX LTD.

Percent Similarity: 36.02%  
 Best Local Similarity: 28.39%  
 Query Match: 6.92%  
 Indels: 70  
 Conservative: 18  
 Mismatches: 81  
 Indels: 70  
 RESULT 482  
 ID ABD03306 standard; DNA; 2169 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1910.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 483  
 ID ABA97187 standard; DNA; 2326 BP.  
 DE Goat lactoferrin-associated DNA.  
 PN KR98043944-A.  
 PD 05-SEP-1998.  
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.  
 Percent Similarity: 37.01%  
 Best Local Similarity: 27.05%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 28  
 Mismatches: 103  
 Indels: 75  
 RESULT 484  
 ID ABD03441 standard; DNA; 2946 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2045.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 485  
 ID AAQ3954 standard; DNA; 3221 BP.  
 DE Heat stable DNA polymerase coding sequence.  
 PN JP05317058-A.  
 PD 03-DEC-1993.  
 PA (TOYM) TOYOBO KK.  
 Percent Similarity: 35.64%  
 Best Local Similarity: 23.27%  
 Query Match: 6.92%  
 Indels: 77  
 Conservative: 34  
 Mismatches: 101  
 Indels: 77  
 RESULT 486  
 ID ACC77985 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 487  
 ID ACC77994 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 488  
 ID ACC77979 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 489  
 ID ADR06764 standard; cDNA; 3470 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 270.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 40.00%  
 Indels: 16  
 Conservative: 16

Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 490  
ID ABZ11703 standard; cDNA; 3744 BP.  
DE Human polynucleotide SEQ ID NO 585.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYPSE-) HYSPO INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 491  
ID ADM44221 standard; cDNA; 3744 BP.  
DE Novel human arginine-rich protein cDNA #585.  
PN US2004053250-A1.  
PD 18-MAR-2004. Y T.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 492  
ID ADR24447 standard; DNA; 4018 BP.  
DE Breast cancer prognosis marker #308.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 493  
ID ABQ83861 standard; DNA; 5032 BP.  
DE Human MDT-3 encoding cDNA SEQ ID NO:26.  
PN WO200278420-A2.  
PD 10-OCT-2002.  
PA (INCV-) INCVTE GENOMICS INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 494  
ID ABV77879 standard; DNA; 5591 BP.  
DE Hypoxia-induced protein coding sequence #7.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 495  
ID ADI82477 standard; DNA; 5592 BP.  
DE Human modifier of p21 (MF21) gene sequence SeqID43.  
PN WO2004005486-A2.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 496  
ID ADQ86758 standard; cDNA; 5592 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3633.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 497  
ID ADQ84279 standard; cDNA; 5592 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1093.

PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 498  
ID ACN40426 standard; cDNA; 5592 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326541, SEQ ID NO:5197.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 499  
ID ADP24535 standard; cDNA; 5595 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1713.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 500  
ID ADI23894 standard; DNA; 7788 BP.  
DE Streptomyces fradiae A541 locus ORF3.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 36.24% Conservative: 33  
Best Local Similarity: 24.74% Mismatches: 114  
Query Match: 6.92% Indels: 70  
RESULT 501  
ID ADI23892 standard; DNA; 37360 BP.  
DE Streptomyces fradiae A541 locus contig 2.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 36.24% Conservative: 33  
Best Local Similarity: 24.74% Mismatches: 114  
Query Match: 6.92% Indels: 70  
RESULT 502  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 89  
RESULT 503  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 504  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 505  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 506  
ID ADI22710 standard; DNA; 1052 BP.  
DE S. pristinaeae spiralis papM gene C658T mutant.  
PN WO2004003012-A2.  
PD 08-JAN-2004.  
PA (AVET-) AVENTIS PHARMA SA.  
Percent Similarity: 32.23% Conservative: 26  
Best Local Similarity: 22.71% Mismatches: 120  
Query Match: 6.89% Indels: 65  
RESULT 507  
ID ADI22712 standard; DNA; 1052 BP.  
DE S. pristinaeae spiralis papM gene C658T/G828A mutant.  
PN WO2004003012-A2.

PD 08-JAN-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
Percent Similarity: 32.23% Conservative: 26  
Best Local Similarity: 22.71% Mismatches: 120  
Query Match: 6.89% Indels: 65  
RESULT 508  
ID ABD01646 standard; DNA; 1200 BP.  
DE Pseudomonas aeruginosa polynucleotide #250.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.17% Conservative: 23  
Best Local Similarity: 28.01% Mismatches: 114  
Query Match: 6.89% Indels: 66  
RESULT 509  
ID ABD05045 standard; DNA; 1311 BP.  
DE Pseudomonas aeruginosa polynucleotide #3649.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 37.06% Conservative: 33  
Best Local Similarity: 25.52% Mismatches: 95  
Query Match: 6.89% Indels: 86  
RESULT 510  
ID ADK56578 standard; DNA; 1828 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #3961.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DMC ) DOW CHEM CO.  
Percent Similarity: 34.20% Conservative: 38  
Best Local Similarity: 21.82% Mismatches: 102  
Query Match: 6.89% Indels: 100  
RESULT 511  
ID ADI93034 standard; DNA; 2433 BP.  
DE Thermus sp polymerase nuclease domain chimera N1C4 DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 512  
ID ADI93026 standard; DNA; 2445 BP.  
DE Thermus sp polymerase chimera S26 (K69E) DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 513  
ID ADI93022 standard; DNA; 2445 BP.  
DE Thermus sp polymerase chimera S26 (FT) DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 514  
ID ADI93028 standard; DNA; 2445 BP.  
DE Thermus sp polymerase chimera S26 (FT/K69E) DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 515  
ID ADI93018 standard; DNA; 2445 BP.  
DE Thermus sp polymerase chimera S26 DNA.  
PN WO200190337-A2.

PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 516  
ID ADI93036 standard; DNA; 2493 BP.  
DE Thermus sp polymerase nuclease domain chimera N2C3 DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 517  
ID ADI93032 standard; DNA; 2499 BP.  
DE Thermus sp polymerase nuclease domain chimera N1A12 DNA.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 518  
ID ADI92870 standard; DNA; 2508 BP.  
DE Construct TthAKK A518L DNA SEQ ID 423.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 519  
ID ADI92852 standard; DNA; 2508 BP.  
DE Construct TthAKK E425V DNA SEQ ID 405.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 520  
ID ADI92858 standard; DNA; 2508 BP.  
DE Construct TthAKK A504F DNA SEQ ID 411.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 521  
ID ADI92862 standard; DNA; 2508 BP.  
DE Construct TthAKK A504F DNA SEQ ID 415.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 522  
ID ADI92864 standard; DNA; 2508 BP.  
DE Construct TthAKK A504S DNA SEQ ID 417.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 523  
ID ADI92866 standard; DNA; 2508 BP.  
DE Construct TthAKK S517G DNA SEQ ID 419.  
PN WO200190337-A2.  
PD 29-NOV-2001.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 524  
 ID ADI92856 standard; DNA; 2508 BP.  
 DE Construct TthAKK L422F/W430C DNA SEQ ID 409.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 525  
 ID ADI92886 standard; DNA; 2508 BP.  
 DE Construct TthAKK T508P DNA SEQ ID 439.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 526  
 ID ADI92848 standard; DNA; 2508 BP.  
 DE Construct TthAKK L429V DNA SEQ ID 401.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 527  
 ID ADI92873 standard; DNA; 2508 BP.  
 DE Construct TthAKK A518R DNA SEQ ID 426.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 528  
 ID ADI92878 standard; DNA; 2508 BP.  
 DE Construct TthAKK A504K DNA SEQ ID 431.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 529  
 ID ADI92854 standard; DNA; 2508 BP.  
 DE Construct TthAKK L422N/E425V DNA SEQ ID 407.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 530  
 ID AAV53995 standard; DNA; 2511 BP.  
 DE Nucleotide sequence of the structure specific endonuclease 2.  
 PN WO9823774-A1.  
 PD 04-JUN-1998.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 531  
 ID ABS68749 standard; DNA; 2511 BP.  
 DE DNA encoding thermus thermophilus mutant DNA polymerase #2.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34

Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 532  
 ID ADES3076 standard; DNA; 2511 BP.  
 DE FEN-1 related DNA used within the scope of the invention, #231.  
 PN WO200270755-A2.  
 PD 12-SEP-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 533  
 ID ADI92709 standard; DNA; 2511 BP.  
 DE T. thermophilus polymerase Tth mutant SEQ ID 262.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 534  
 ID ADI92946 standard; DNA; 2514 BP.  
 DE Construct Tsc(KG9B)TthAKK DNA SEQ ID 499.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 535  
 ID ADI92922 standard; DNA; 2514 BP.  
 DE Construct Tsc(1-167)TthAKK DNA SEQ ID 475.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 536  
 ID ADI92580 standard; DNA; 2514 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 133.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 537  
 ID ADI92901 standard; DNA; 2514 BP.  
 DE Construct Tsc(FT)TthAKK DNA SEQ ID 454.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 538  
 ID ADI92956 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-B/M2 DNA SEQ ID 509.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 539  
 ID ADI92964 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-D/M5 DNA SEQ ID 517.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 540  
 ID ADI92964 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-D/M5 DNA SEQ ID 517.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34

Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 540  
 ID ADI92980 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-H/M9 DNA SEQ ID 533.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 541  
 ID ADI92575 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 128.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 542  
 ID ADI92960 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-C/M3 DNA SEQ ID 513.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 543  
 ID ADI92972 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-F/M7 DNA SEQ ID 525.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 544  
 ID ADI92516 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 69.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 545  
 ID ADI92942 standard; DNA; 2517 BP.  
 DE Construct Taq(K69E)ThAKK DNA SEQ ID 495.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 546  
 ID ADI92984 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-I/M10 DNA SEQ ID 537.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 547  
 ID ADI92948 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK) DNA SEQ ID 501.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111

Query Match: 6.89% Indels: 74  
 RESULT 548  
 ID ADI92968 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-E/M6 DNA SEQ ID 521.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 549  
 ID ADI92931 standard; DNA; 2517 BP.  
 DE Construct Taq(FT)ThAKK DNA SEQ ID 484.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 550  
 ID ADI92976 standard; DNA; 2517 BP.  
 DE Construct TaqEFT-Tth(AKK)-G/M8 DNA SEQ ID 529.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 551  
 ID ADI93020 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase chimera S36 DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 552  
 ID ADI92952 standard; DNA; 2520 BP.  
 DE Construct TaqEFT-Tth(AKK)-A/M1 DNA SEQ ID 505.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 553  
 ID ADI92669 standard; DNA; 2520 BP.  
 DE HCMV associated DNA SEQ ID 222.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 554  
 ID ADI93030 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase nuclease domain chimera N3D7 DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 555  
 ID ADI92990 standard; DNA; 2520 BP.  
 DE Construct TaqEFT-Tth(AKK)-MI-10 DNA SEQ ID 543.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 556  
 ID ADI92990 standard; DNA; 2520 BP.  
 DE Construct TaqEFT-Tth(AKK)-MI-10 DNA SEQ ID 543.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74

RESULT 556  
 ID ADI92988 standard; DNA; 2520 BP.  
 DE Construct TscTthAKK(MI-9 DNA SEQ ID 541).  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 557  
 ID ADI93024 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase chimera S36(FT) DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 558  
 ID ABS68757 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #4.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 559  
 ID ABS68759 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #5.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 560  
 ID ABS68751 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 561  
 ID ABS68755 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 562  
 ID ADI93005 standard; DNA; 2526 BP.  
 DE T. thermophilusTthAKK DNA fragment.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 563  
 ID ADI92565 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 118.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 564  
 ID ADI92714 standard; DNA; 2526 BP.

ID ADI92902 standard; DNA; 2526 BP.  
 DE Construct Tsc(167-333)TthAKK DNA SEQ ID 455.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 565  
 ID ADI92838 standard; DNA; 2526 BP.  
 DE Construct TthAKK(N221H/R224Q) DNA SEQ ID 391.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 566  
 ID ADI92564 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 117.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 567  
 ID ADI92566 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 119.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 568  
 ID ADI92830 standard; DNA; 2526 BP.  
 DE Construct TthAKK(P255L) DNA SEQ ID 383.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 569  
 ID ADI92842 standard; DNA; 2526 BP.  
 DE Construct TthAKK(R251H) DNA SEQ ID 395.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 570  
 ID ADI92899 standard; DNA; 2526 BP.  
 DE Construct Tth(K69E)AKK DNA SEQ ID 452.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 571  
 ID ADI92579 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 132.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 572  
 ID ADI92714 standard; DNA; 2526 BP.

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DE T. thermophilus Tth DN HT DNA SEQ ID 267.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 573
ID ADI92944 standard; DNA; 2526 BP.
DE Construct Tfi(K69E)/TthAKK DNA SEQ ID 497.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 574
ID ADI92826 standard; DNA; 2526 BP.
DE Construct TthAKK(N417K/L418K) DNA SEQ ID 379.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 575
ID ADI92918 standard; DNA; 2526 BP.
DE Construct Tsc(111-334)/TthAKK DNA SEQ ID 471.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 576
ID ADI92796 standard; DNA; 2526 BP.
DE Mutant Tsc construct mutagenic primer SEQ ID 349.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 577
ID ADI92822 standard; DNA; 2526 BP.
DE Construct TthAKK(P195K) DNA SEQ ID 375.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 578
ID ADI92906 standard; DNA; 2526 BP.
DE Construct Tsc(167-334)/TthAKK DNA SEQ ID 459.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 579
ID ADI92550 standard; DNA; 2526 BP.
DE Synthetic 5' nuclease DNA SEQ ID 103.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 580
ID ADI92551 standard; DNA; 2526 BP.
DE Synthetic 5' nuclease DNA SEQ ID 104.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 581
ID ADI92720 standard; DNA; 2526 BP.
DE T. thermophilus Tth DN RX HT DNA SEQ ID 273.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 582
ID ADI92820 standard; DNA; 2526 BP.
DE Construct TthAKK(P195A) DNA SEQ ID 373.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 583
ID ADI92846 standard; DNA; 2526 BP.
DE Construct TthAKK(F311Y) DNA SEQ ID 387.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 584
ID ADI92834 standard; DNA; 2526 BP.
DE Construct TthAKK(F311Y) DNA SEQ ID 387.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 585
ID ADI92910 standard; DNA; 2532 BP.
DE Construct Tfi(222-334)/TthAKK DNA SEQ ID 463.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 586
ID ADI92914 standard; DNA; 2532 BP.
DE Construct Tfi(167-334)/TthAKK DNA SEQ ID 467.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 587
ID ADI93010 standard; DNA; 2619 BP.
DE Construct Afu328-Tth296(AKK) DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 588
ID ADI93006 standard; DNA; 2643 BP.
DE Construct Afu336-Tth296(AKK) DNA.
PN WO200190337-A2.

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PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 589  
ID ADI92928 standard; DNA; 3135 BP.  
DE Construct TthAKK-alpha peptide DNA SEQ ID 481.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 590  
ID ACC77865 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 591  
ID ACC77880 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 592  
ID ACC77960 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 593  
ID ACC77936 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 37.89% Conservative: 36  
Best Local Similarity: 25.26% Mismatches: 119  
Query Match: 6.89% Indels: 60  
RESULT 594  
ID ACC77975 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 595  
ID ACC78006 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 596  
ID ACC77873 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.

PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 597  
ID ACC77961 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 598  
ID ACC77990 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 599  
ID ACC77809 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 600  
ID ACC77999 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 601  
ID ACC77993 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 602  
ID ACC77883 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 603  
ID ACC77966 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 604  
ID ACC78012 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.



Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 605  
 ID ACC77935 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.89% Conservative: 36  
 Best Local Similarity: 25.26% Mismatches: 119  
 Query Match: 6.89% Indels: 60  
 RESULT 606  
 ID ACC78003 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 607  
 ID ACC77976 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 608  
 ID ADS57429 standard; cDNA; 813 BP.  
 DE Bacterial polynucleotide #9416.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.68% Conservative: 32  
 Best Local Similarity: 25.51% Mismatches: 93  
 Query Match: 6.85% Indels: 56  
 RESULT 609  
 ID AAF26352 standard; DNA; 1035 BP.  
 DE P. putida oxygenase encoding DNA ORF04472.  
 PN WO200107629-A2.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MEH.  
 PA (DKFZ) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Percent Similarity: 33.21% Conservative: 22  
 Best Local Similarity: 24.91% Mismatches: 100  
 Query Match: 6.85% Indels: 77  
 RESULT 610  
 ID ACA31567 standard; DNA; 1130 BP.  
 DE Prokaryotic essential gene #13224.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.62% Conservative: 27  
 Best Local Similarity: 24.76% Mismatches: 89  
 Query Match: 6.85% Indels: 42  
 RESULT 611  
 ID AAS72289 standard; cDNA; 1390 BP.  
 DE DNA encoding novel human diagnostic protein #8093.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.03% Conservative: 21  
 Best Local Similarity: 23.83% Mismatches: 75

Query Match: 6.85% Indels: 100  
 RESULT 612  
 ID ABD14414 standard; DNA; 1407 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13018.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.41% Conservative: 31  
 Best Local Similarity: 28.15% Mismatches: 96  
 Query Match: 6.85% Indels: 90  
 RESULT 613  
 ID ADO07762 standard; cDNA; 1932 BP.  
 DE Fly polynucleotide #43.  
 PN US2004071700-A1.  
 PD 15-APR-2004.  
 PA (LIFE-) LIFE SCI DEV CORP.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 614  
 ID AAS94512 standard; cDNA; 2305 BP.  
 DE DNA encoding novel human diagnostic protein #30316.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 31.54% Conservative: 19  
 Best Local Similarity: 23.65% Mismatches: 94  
 Query Match: 6.85% Indels: 71  
 RESULT 615  
 ID ABL08195 standard; cDNA; 2396 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19067.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 616  
 ID ABL20321 standard; DNA; 2590 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12436.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 617  
 ID ABL20331 standard; DNA; 2894 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12466.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 618  
 ID ACC77995 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99% Conservative: 34  
 Best Local Similarity: 25.34% Mismatches: 112  
 Query Match: 6.85% Indels: 74  
 RESULT 619  
 ID AAS84829 standard; cDNA; 3451 BP.  
 DE DNA encoding novel human diagnostic protein #20633.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 42.95% Conservative: 25  
 Best Local Similarity: 26.92% Mismatches: 58  
 Query Match: 6.85% Indels: 32

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RESULT 620
ID ADR06934 standard; cDNA; 5008 BP.
DE Full length human cDNA useful for treating neurological disease Seq 440.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.21% Conservative: 26
Best Local Similarity: 27.57% Mismatches: 95
Query Match: 6.85% Indels: 98
RESULT 621
ID ACA44278 standard; DNA; 1116 BP.
DE Prokaryotic essential gene #25935.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.45% Conservative: 31
Best Local Similarity: 25.10% Mismatches: 76
Query Match: 6.81% Indels: 81
RESULT 622
ID ABD08133 standard; DNA; 1197 BP.
DE Pseudomonas aeruginosa polynucleotide #6737.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 623
ID ABD08348 standard; DNA; 1272 BP.
DE Pseudomonas aeruginosa polynucleotide #6952.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 624
ID ABZ38701 standard; DNA; 1560 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 1991.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 38.21% Conservative: 33
Best Local Similarity: 24.80% Mismatches: 91
Query Match: 6.81% Indels: 61
RESULT 625
ID AAQ24328 standard; DNA; 1635 BP.
DE Mutant thermostable DNA polymerase pTHA292.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 626
ID AAQ24327 standard; DNA; 1899 BP.
DE Mutant thermostable DNA polymerase pTHD2-203.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 627
ID AAQ24326 standard; DNA; 2043 BP.
DE Mutant thermostable DNA polymerase pTHD2-155.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 628
ID AAV53994 standard; DNA; 2511 BP.
DE AAV53994 standard; DNA; 2511 BP.

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ID ACA42740 standard; DNA; 2253 BP.
DE Prokaryotic essential gene #24397.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.85% Conservative: 27
Best Local Similarity: 27.09% Mismatches: 101
Query Match: 6.81% Indels: 55
RESULT 629
ID AAQ24325 standard; DNA; 2277 BP.
DE Mutant thermostable DNA polymerase pTHD2-77.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 630
ID ABD08178 standard; DNA; 2346 BP.
DE Pseudomonas aeruginosa polynucleotide #6782.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 631
ID AAQ24324 standard; DNA; 2370 BP.
DE Mutant thermostable DNA polymerase pTHD2-46.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 632
ID AD192526 standard; DNA; 2499 BP.
DE Synthetic 5' nuclease DNA SEQ ID 79.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 633
ID AAQ24323 standard; DNA; 2505 BP.
DE Mutant thermostable DNA polymerase from Thermus thermophilus.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 634
ID AAV53993 standard; DNA; 2505 BP.
DE Nucleotide sequence of the nucleic acid 6.
PN WO9823774-A1.
PD 04-JUN-1998.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 635
ID AD192602 standard; DNA; 2505 BP.
DE T. thermophilus polymerase DNA SEQ ID 155.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 636
ID AAV53994 standard; DNA; 2511 BP.

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DE Nucleotide sequence of the structure specific endonuclease 1.  
 PN WO9823774-A1.  
 PD 04-JUN-1998.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 637  
 ID ABS68747 standard; DNA; 2511 BP.  
 DE Thermus thermophilus DNA polymerase, PCR primer #4.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 638  
 ID ADI92691 standard; DNA; 2511 BP.  
 DE T. thermophilus modified Tth polymerase DNA SEQ ID 244.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 639  
 ID AAQ12748 standard; DNA; 2640 BP.  
 DE T. thermophilus DNA polymerase I.  
 PN WO9109950-A.  
 PD 11-JUL-1991.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 640  
 ID AAH14004 standard; cDNA; 2653 BP.  
 DE Human cDNA sequence SEQ ID NO:11090.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST..  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 641  
 ID AAD45690 standard; DNA; 2653 BP.  
 DE Human LBDS4 DNA.  
 PN WO200270560-A2.  
 PD 12-SEP-2002.  
 PA (INPH-) INPHARMATICA LTD.  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 642  
 ID ADS99994 standard; DNA; 2669 BP.  
 DE Human therapeutic DNA - SEQ ID 231.  
 PN WO2004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 643  
 ID AAA30241 standard; DNA; 2943 BP.  
 DE Chimaeric Pfu/T. thermophilus DNA polymerase coding sequence.  
 PN GB2344591-A.  
 PD 14-JUN-2000.  
 PA (BIOL-) BIOLINE LTD.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 644  
 ID ABD11116 standard; DNA; 3006 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9720.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.97% Conservative: 28  
 Best Local Similarity: 22.45% Mismatches: 80  
 Query Match: 6.81% Indels: 120  
 RESULT 645  
 ID ACC78016 standard; DNA; 3210 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 646  
 ID AAQ6261 standard; DNA; 3221 BP.  
 DE Thermus thermophilus thermostable DNA polymerase genomic DNA.  
 PN JP07163343-A.  
 PD 27-JUN-1995.  
 PA (TOYM) TOYOCO KK.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 647  
 ID ACC77892 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 648  
 ID ACC77919 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 649  
 ID ACC77962 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 650  
 ID ACC77972 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 651  
 ID ACC77874 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 652  
 ID ACC77915 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.

PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 661			
ID	ACC77920 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 662			
ID	ACC77977 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 663			
ID	ACC77872 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 664			
ID	ACC77879 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 665			
ID	ACC77984 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 666			
ID	ACC77911 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 667			
ID	ACC77937 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 668			
ID	ACC77967 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 669			
ID	ACC77967 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
FN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		



RESULT 693	ID	ACC77940 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 694	ID	ACC77878 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 695	ID	ACC77882 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 696	ID	ACC77899 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 697	ID	ACC77905 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 698	ID	ACC77932 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 699	ID	ACC77963 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 700	ID	ACC77963 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 701	ID	ACC78008 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	WO2003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74

[illegible]





PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
RESULT 734  
ID ABD13665 standard; DNA; 3660 BP.  
DE Pseudomonas aeruginosa polynucleotide #12269.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.90%  
Best Local Similarity: 26.92%  
Query Match: 6.81%  
RESULT 735  
ID ADD4868 standard; DNA; 5352 BP.  
DE Rat gene M34384, SEQ ID NO 14397.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Percent Similarity: 36.32%  
Best Local Similarity: 28.25%  
Query Match: 6.81%  
RESULT 736  
ID ACA35857 standard; DNA; 846 BP.  
DE Prokaryotic essential gene #17514.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.74%  
Best Local Similarity: 26.02%  
Query Match: 6.78%  
RESULT 737  
ID ACH97285 standard; DNA; 906 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 3080.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.25%  
Best Local Similarity: 24.26%  
Query Match: 6.78%  
RESULT 738  
ID ABD14669 standard; DNA; 966 BP.  
DE Pseudomonas aeruginosa polynucleotide #13273.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.55%  
Best Local Similarity: 28.43%  
Query Match: 6.78%  
RESULT 739  
ID ABD08723 standard; DNA; 1083 BP.  
DE Pseudomonas aeruginosa polynucleotide #7327.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.72%  
Best Local Similarity: 27.73%  
Query Match: 6.78%  
RESULT 740  
ID ABD16105 standard; DNA; 1200 BP.  
DE Pseudomonas aeruginosa polynucleotide #14709.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
RESULT 741  
ID ABD16436 standard; DNA; 1290 BP.  
DE Pseudomonas aeruginosa polynucleotide #15040.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
RESULT 742  
ID ABD15673 standard; DNA; 1299 BP.  
DE Pseudomonas aeruginosa polynucleotide #14277.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.00%  
Best Local Similarity: 27.31%  
Query Match: 6.78%  
RESULT 743  
ID ABD14522 standard; DNA; 1428 BP.  
DE Pseudomonas aeruginosa polynucleotide #13126.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86%  
Best Local Similarity: 30.86%  
Query Match: 6.78%  
RESULT 744  
ID ABD16317 standard; DNA; 1449 BP.  
DE Pseudomonas aeruginosa polynucleotide #14921.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
RESULT 745  
ID ACF39359 standard; DNA; 1509 BP.  
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:96.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
RESULT 746  
ID ABD14362 standard; DNA; 1515 BP.  
DE Pseudomonas aeruginosa polynucleotide #12966.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86%  
Best Local Similarity: 30.86%  
Query Match: 6.78%  
RESULT 747  
ID ACA53421 standard; DNA; 1590 BP.  
DE Prokaryotic essential gene #35078.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 34.89%  
Best Local Similarity: 24.82%  
Query Match: 6.78%  
RESULT 748  
ID ABD15703 standard; DNA; 1824 BP.  
DE Pseudomonas aeruginosa polynucleotide #14307.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.00%  
Best Local Similarity: 27.31%  
Query Match: 6.78%  
RESULT 749  
ID AAN70306 standard; DNA; 1906 BP.  
DE Sequence encoding bovine mullerian inhibiting substance (MIS)-like  
DE polypeptide and the promoter region based on genomic/cDNA fusion.  
PN EP221761-A.  
PD 13-MAY-1987.

PA (BIOJ ) BIOGEN NV.			
PA (GEO ) GEN HOSPITAL CORP.			
Percent Similarity: 32.72%	Conservative: 25		
Best Local Similarity: 25.00%	Mismatches: 111		
Query Match: 6.78%	Indels: 107		
RESULT 750			
ID AAF60989 standard; DNA; 2085 BP.			
DE P. putida KT2440-associated DNA ORF01994.			
PN DE1935088-A1.			
PD 01-FEB-2001.			
PA (TIGR-) TIGR INST GENOMIC RES.			
PA (QUIA-) QUIAGEN GMBH.			
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.			
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.			
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.			
Percent Similarity: 34.39%	Conservative: 22		
Best Local Similarity: 26.67%	Mismatches: 116		
Query Match: 6.78%	Indels: 71		
RESULT 751			
ID ABS51351 standard; cDNA; 2299 BP.			
DE cDNA encoding human secretory protein #49.			
PN WO200257304-A2.			
PD 25-JUL-2002.			
PA (INCY-) INCYTE GENOMICS INC.			
Percent Similarity: 37.30%	Conservative: 32		
Best Local Similarity: 24.18%	Mismatches: 77		
Query Match: 6.78%	Indels: 76		
RESULT 752			
ID AAZ34073 standard; cDNA; 2748 BP.			
DE Human PRO846 nucleotide sequence.			
PN WO9946281-A2.			
PD 16-SEP-1999.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 753			
ID AAA99905 standard; cDNA; 2749 BP.			
DE cDNA encoding human protein PRO846.			
PN WO200053757-A2.			
PD 14-SEP-2000.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 754			
ID AAA88517 standard; cDNA; 2749 BP.			
DE Human PRO846 cDNA clone DNA44196-1353.			
PN WO200053760-A2.			
PD 14-SEP-2000.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 755			
ID AAC78503 standard; cDNA; 2749 BP.			
DE Human PRO846 (UNQ422) nucleotide sequence SEQ ID NO:215.			
PN WO200053756-A2.			
PD 14-SEP-2000.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 756			
ID AAS21436 standard; cDNA; 2749 BP.			
DE Human cDNA sequence encoding for PRO846 polypeptide.			
PN WO200140466-A2.			
PD 07-JUN-2001.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 757			
ID ACA71805 standard; cDNA; 2749 BP.			
DE Human secreted and transmembrane polypeptide PRO846 cDNA.			
PN US200217553-A1.			
PD 28-NOV-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 758			
ID ABL88101 standard; cDNA; 2749 BP.			
DE Human PRO846 cDNA sequence SEQ ID NO:59.			
PN WO200200690-A2.			
PD 03-JAN-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 759			
ID ABL95590 standard; cDNA; 2749 BP.			
DE Human angiogenesis related cDNA PRO846 SEQ ID NO: 59.			
PN WO200208284-A2.			
PD 31-JAN-2002.			
PA (GETH ) GENENTECH INC.			
PA (BAKE/) BAKER K P.			
PA (FERR/) FERRARA N.			
PA (GERB/) GERBER H.			
PA (GERR/) GERRITSEN M E.			
PA (GODD/) GODDARD A.			
PA (GODO/) GODOWSKI P J.			
PA (GURN/) GURNEY A L.			
PA (HILL/) HILLAN K J.			
PA (MARS/) MARSTERS S A.			
PA (PANJ/) PAN J.			
PA (PAON/) PRONI N F.			
PA (STEP/) STEPHAN J F.			
PA (WATA/) WATANABE C K.			
PA (WILL/) WILLIAMS P M.			
PA (WOOD/) WOOD W I.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 760			
ID ACA63641 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2002192706-A1.			
PD 19-DEC-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 761			
ID ACA4520 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003003531-A1.			
PD 02-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 762			
ID ACA03795 standard; cDNA; 2749 BP.			
DE cDNA encoding human PRO polypeptide #193.			
PN US2003036180-A1.			
PD 20-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 763			
ID ACA71805 standard; cDNA; 2749 BP.			
DE Human secreted and transmembrane polypeptide PRO846 cDNA.			
PN US200217553-A1.			
PD 28-NOV-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		

PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 764  
 ID ABX89333 standard; cDNA; 2749 BP.  
 DE DNA encoding novel secreted and transmembrane protein PRO846.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 765  
 ID ABX92445 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2002169284-A1.  
 PD 14-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 766  
 ID ABX80979 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein cDNA, #183.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 767  
 ID ACD4488 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 768  
 ID ACD41987 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #193.  
 PN US2003036179-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 769  
 ID ACA66186 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003004102-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 770  
 ID ABX79659 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein cDNA, #183.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 771  
 ID ACA93680 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003022187-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 772  
 ID ABX81362 standard; DNA; 2749 BP.  
 DE Human secreted or transmembrane protein related PCR primer #149.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 773  
 ID ACA04216 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 385.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 774  
 ID ACA93178 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003017476-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 775  
 ID ABX17262 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 776  
 ID ACA68117 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 777  
 ID ACA88566 standard; cDNA; 2749 BP.  
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.  
 PN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 778  
 ID ACD82073 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2003017981-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 779  
 ID ADA45904 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003022328-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 780  
 ID ADA76335 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.

Query Match: 6.78%  
 Indels: 100  
 RESULT 772  
 ID ABX81362 standard; DNA; 2749 BP.  
 DE Human secreted or transmembrane protein related PCR primer #149.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 773  
 ID ACA04216 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 385.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 774  
 ID ACA93178 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003017476-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 775  
 ID ABX17262 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 776  
 ID ACA68117 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 777  
 ID ACA88566 standard; cDNA; 2749 BP.  
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.  
 PN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 778  
 ID ACD82073 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2003017981-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 779  
 ID ADA45904 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003022328-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 780  
 ID ADA76335 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.

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PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 30.08%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 781
ID ADA18985 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 782
ID ADA61608 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 783
ID ADB19393 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 784
ID ADB27934 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 785
ID ADA86413 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 786
ID ADB15977 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 787
ID ADA38027 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003082997-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 788
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 789
ID ADA21713 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 790
ID ADA10500 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 791
ID ADA67558 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 792
ID ADB30565 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 793
ID ADA85861 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 794
ID ADA18044 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 795
ID ADA97073 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 796
ID ADA79377 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 797
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
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Query Match: 6.78% Indels: 100
RESULT 797
ID ADA87516 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087345-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 798
ID ADB16718 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087349-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 799
ID ADA28152 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003054359-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 800
ID ADA31810 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082694-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 801
ID ADB14873 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087351-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 802
ID ADA24754 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050241-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 803
ID ADB18834 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003073211-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 804
ID ADA94049 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077722-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 805
ID ADA82268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.

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ID ADB19945 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082691-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 806
ID ADB13257 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082710-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 807
ID ACD98616 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003044945-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 808
ID ACD29787 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050240-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 809
ID ADA12415 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003055216-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 810
ID ADA94732 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059832-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 811
ID ADA74511 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068798-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 812
ID ADB24744 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077713-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 813
ID ADA82268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.

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PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 814  
ID ADA75231 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 815  
ID ADA85309 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 816  
ID ADA84757 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 817  
ID ADB330013 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 818  
ID ADA80541 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 819  
ID ADA75783 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 820  
ID ADA38957 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 821  
ID ADA47008 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003073210-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 822  
ID ADB25304 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide SEQ ID NO 385.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 823  
ID ADA93480 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 824  
ID ADB31117 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 825  
ID ADA93078 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 826  
ID ADA61045 standard; cDNA; 2749 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 827  
ID ADB24192 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide SEQ ID NO 385.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 828  
ID ADA96521 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 838	ID ADA88068 standard; cDNA; 2749 BP.	DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN	US2003082700-A1.	
PD	01-MAY-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 839	ID ADA46456 standard; cDNA; 2749 BP.	
DE	Novel human secreted and transmembrane protein PRO846 cDNA.	
PN	US2003054516-A1.	
PD	20-MAR-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 840	ID ADB28486 standard; cDNA; 2749 BP.	
DE	cDNA encoding human PRO polypeptide #193.	
PN	US2003082699-A1.	
PD	01-MAY-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 841	ID ADB29038 standard; cDNA; 2749 BP.	
DE	cDNA encoding human PRO polypeptide #193.	
PN	US2003082706-A1.	
PD	01-MAY-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 842	ID ACH65634 standard; cDNA; 2749 BP.	
DE	Human cDNA encoding secreted/transmembrane protein PRO846.	
PN	US2003044806-A1.	
PD	06-MAR-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 843	ID ADA76990 standard; cDNA; 2749 BP.	
DE	Human PRO polynucleotide #193.	
PN	US2003059909-A1.	
PD	27-MAR-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 844	ID ADA22639 standard; cDNA; 2749 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO846.	
PN	US2003040473-A1.	
PD	27-FEB-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 845	ID ADA86620 standard; cDNA; 2749 BP.	
DE	Novel human secreted and transmembrane protein PRO846 cDNA.	
PN	US2003073213-A1.	
PD	17-APR-2003.	
PA (GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative: 25
Best Local Similarity:	19.92%	Mismatches: 72
Query Match:	6.78%	Indels: 100
RESULT 846	ID ADA97625 standard; cDNA; 2749 BP.	
DE	Human PRO polynucleotide #193.	

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PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 847
ID ADB27382 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 848
ID ADB22315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 849
ID ACD39624 standard; cDNA; 2749 BP.
DE Human PRO 846 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 850
ID ADA6805 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #147.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 851
ID ADA39498 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 852
ID ADA67006 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 853
ID ADB22867 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 854
ID ADB23640 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 855
ID ADA92362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 856
ID ADB15425 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 857
ID ADB38677 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 858
ID ADB96524 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 859
ID ADB38125 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 860
ID ADB66597 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 861
ID ADB89677 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 862
ID ADB30409 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 863
ID ADB39510 standard; cDNA; 2749 BP.

```



DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082764-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 864  
 ID ADB73721 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide sequence #46.  
 PN US2003045462-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 865  
 ID ADB73721 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082697-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 866  
 ID ADB86740 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082697-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 867  
 ID ADB7345 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082696-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 868  
 ID ADB7345 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082696-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 869  
 ID ADB34502 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US200307717-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 870  
 ID ADB35606 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US200307719-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 871  
 ID ADB33950 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.

PN US200307716-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 872  
 ID ADB35054 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US200307718-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 873  
 ID ADB36158 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US200307720-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 874  
 ID ADB46553 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082692-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 875  
 ID ADC43863 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003054986-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 876  
 ID ADC57996 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003027754-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 877  
 ID ADC55360 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003045463-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 878  
 ID ADC12227 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003049681-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 879  
 ID ADC1623 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003049684-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%

Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 880  
 ID ADC63587 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003054405-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 881  
 ID ADC66687 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003060406-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 882  
 ID ADC56649 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003064375-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 883  
 ID ADC68811 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003064407-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 884  
 ID ADC62871 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003068648-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 885  
 ID ADC67936 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003069178-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 886  
 ID ADC11694 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003069403-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 887  
 ID ADC41256 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003072745-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 888

ID ADC67311 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003073131-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 889  
 ID ADC62247 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003073624-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 890  
 ID ADC41880 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003104998-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 891  
 ID ADC50426 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092106-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 892  
 ID ADC71973 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092107-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 893  
 ID ADC59952 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092109-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 894  
 ID ADC52959 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087365-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 895  
 ID ADC57313 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087366-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 896  
 ID ADC60504 standard; cDNA; 2749 BP.

DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087367-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 897  
 ID ADC50979 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087361-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 898  
 ID ADC65506 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003087362-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 899  
 ID ADC54604 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087363-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 900  
 ID ADC53565 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087364-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 901  
 ID ADC59088 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087359-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 902  
 ID ADC55965 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087360-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 903  
 ID ADC58536 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087346-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 904  
 ID ADC14816 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.

PN US2003082546-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 905  
 ID ADD08348 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US200308623-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 906  
 ID ADD03210 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092104-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 907  
 ID ADC90202 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087348-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 908  
 ID ADC82173 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003083461-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 909  
 ID ADC69621 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003194770-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 910  
 ID ADC48510 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194773-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 911  
 ID ADD10039 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194776-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 912  
 ID ADD07815 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002193299-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 913  
 ID ADC14816 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.

Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 913  
 ID ADD04614 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087354-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 914  
 ID ADC82706 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003059833-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 915  
 ID ADC80570 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092103-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 916  
 ID ADD11077 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194774-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 917  
 ID ADD10348 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
 PN US2003105011-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 918  
 ID ADC47958 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194771-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 919  
 ID ADD08886 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003073090-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 920  
 ID ADC80018 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087358-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 921

ID ADD07135 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002193300-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 922  
 ID ADD11308 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
 PN US2003105013-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 923  
 ID ADD09487 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194775-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 924  
 ID ADC83382 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003059783-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 925  
 ID ADD41200 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203438-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 926  
 ID ADD52339 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003194769-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 927  
 ID ADD53079 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003194792-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 928  
 ID ADD53631 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203437-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 929  
 ID ADD55489 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.

Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 938			
ID ADD92519 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003199030-A1.			
PD 23-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 939			
ID ADD91415 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003199055-A1.			
PD 23-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 940			
ID ADE04029 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003199057-A1.			
PD 23-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 941			
ID ADE31904 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane protein PRO846.			
PN US2003068647-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 942			
ID ADE27039 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003087304-A1.			
PD 08-MAY-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 943			
ID ADE32326 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003194765-A1.			
PD 16-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 944			
ID ADE22258 standard; cDNA; 2749 BP.			
DE cDNA encoding human PRO polypeptide #193.			
PN US2003199056-A1.			
PD 23-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 945			
ID ADD79482 standard; cDNA; 2749 BP.			
DE cDNA encoding human PRO polypeptide #193.			
PN US2003203428-A1.			
PD 30-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100

RESULT 946  
ID ADE35303 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 947  
ID ADE16417 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 948  
ID ADD73032 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 949  
ID ADE42018 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 950  
ID ADE17835 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 951  
ID ADD91967 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 952  
ID ADE33430 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 953  
ID ADE33982 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 954  
ID ADD78928 standard; cDNA; 2749 BP.

ID ADD80034 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 955  
ID ADD93071 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 956  
ID ADD72390 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 957  
ID ADE19491 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 958  
ID ADE18939 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 959  
ID ADE43135 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 960  
ID ADD95924 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 961  
ID ADE22810 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 962  
ID ADD78928 standard; cDNA; 2749 BP.

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DE cDNA encoding human PRO polypeptide #193.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 963
ID ADE26506 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 964
ID ADE32878 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 965
ID ADE32878 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 966
ID ADE17041 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 967
ID ADD80586 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 968
ID ADD89614 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 969
ID ADE40898 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 970
ID ADE04697 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199034-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 971
ID ADE32826 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 972
ID ADF47055 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 973
ID ADF67443 standard; cDNA; 2749 BP.
DE Human PRO846 nucleotide sequence SEQ ID NO:516.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 974
ID ADG21535 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 975
ID ADG23176 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 976
ID ADF97511 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 977
ID ADG80575 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 978
ID ADG52812 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003216561-A1.
PD 20-NOV-2003.
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PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 979			
ID ADG60132 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO846.			
PN US2003206915-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 980			
ID ADG80023 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003207372-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 981			
ID ADH55315 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207381-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 982			
ID ADH55867 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207379-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 983			
ID ADI35697 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #147.			
PN US2003050457-A1.			
PD 13-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 984			
ID ADI60892 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane protein, PRO846.			
PN US200307700-A1.			
PD 24-APR-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 985			
ID ADI64086 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207385-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 986			
ID ADI65035 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207386-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 987			
ID ADH81948 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207388-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 988			
ID ADI00190 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003049682-A1.			
PD 13-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 989			
ID ADH81396 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003207377-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 990			
ID ABX78063 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #147.			
PN US2003027163-A1.			
PD 06-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 991			
ID ABX80475 standard; cDNA; 2749 BP.			
DE Human secreted or transmembrane protein related PCR primer #149.			
PN US2002132252-A1.			
PD 19-SEP-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 992			
ID ACA69381 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane protein PRO846.			
PN US2003032023-A1.			
PD 13-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 993			
ID ACD24045 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003032156-A1.			
PD 13-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 994			
ID ABX90452 standard; cDNA; 2749 BP.			
DE Human secreted/transmembrane protein cDNA, #183.			
PN US2002160384-A1.			
PD 31-OCT-2002.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 30.08%	Conservative: 25		
Best Local Similarity: 19.92%	Mismatches: 72		
Query Match: 6.78%	Indels: 100		
RESULT 995			
ID ACD42606 standard; cDNA; 2749 BP.			



DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 996  
ID ABX64298 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 997  
ID ACA67186 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 998  
ID ADM2565 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 999  
ID ADN15964 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1000  
ID ADN16593 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1001  
ID ADN15412 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1002  
ID ADN14860 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1003  
ID AD163534 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.

PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1004  
ID ADC81122 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1005  
ID ADD76570 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1006  
ID ADD87934 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1007  
ID ADD86338 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1008  
ID ADE75786 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1009  
ID ADE48549 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1010  
ID ADE41309 standard; cDNA; 2749 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 1011  
ID ADE23362 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003092108-A1.

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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 30.08%
Conservative: 25
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1012
ID ADE231914 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1013
ID ADE24557 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1014
ID ADD87382 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1015
ID ADE89248 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1016
ID ADE18387 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1017
ID ADE88696 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1018
ID ADE89650 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1019
ID ADF61290 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1020
ID ADE39982 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1021
ID ADF45778 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1022
ID ADE94716 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1023
ID ADE91127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1024
ID ADF35642 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%

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Query Match: 6.78% Indels: 100
RESULT 1025
ID ADE95268 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1026
ID ADE93378 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1027
ID ADE93378 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1028
ID ADF40606 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1029
ID ADF33550 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1030
ID ADF33533 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1031
ID ADF34959 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1032
ID ADF27000 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1033
ID ADF27636 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1034
ID ADE92274 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1035
ID ADE90575 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1036
ID ADF41230 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1037
ID ADF32909 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1038
ID ADE25275 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1039
ID ADF26376 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1040
ID ADF34165 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1041
ID ADF34165 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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ID ADF46402 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1042  
ID ADE91722 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1043  
ID ADG11892 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1044  
ID ADG02301 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1045  
ID ADG22087 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1046  
ID ADG20157 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1047  
ID ADF98063 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1048  
ID ADG4280 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1049  
ID ADF98634 standard; cDNA; 2749 BP.

DE Human PRO polynucleotide #193.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1050  
ID ADG03465 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1051  
ID ADF99186 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1052  
ID ADG16771 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1053  
ID ADG05230 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1054  
ID ADG19497 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1055  
ID ADG13334 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1056  
ID ADG08391 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 1057  
ID ADG15561 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.

PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1058  
ID ADF96959 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1059  
ID ADG06144 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1060  
ID ADG23728 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1061  
ID ADG04017 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1062  
ID ADG24918 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1063  
ID ADG07215 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1064  
ID ADG07767 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1065  
ID ADG55262 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003194778-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1066  
ID ADG60926 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1067  
ID ADG62030 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1068  
ID ADG82231 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1069  
ID ADG57470 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1070  
ID ADG56918 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1071  
ID ADG55814 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1072  
ID ADG58574 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
RESULT 1073  
ID ADG70940 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.

Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1082			
ID	ADG49764 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003215905-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1083			
ID	ADG51636 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003215908-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1084			
ID	ADG52430 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207414-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1085			
ID	ADG54158 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207416-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1086			
ID	ADG49140 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003216305-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1087			
ID	ADG81127 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
PN	US2003194793-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1088			
ID	ADG56366 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207366-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1089			
ID	ADH12632 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207378-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1090			
ID	ADH12632 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207378-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100

Query Match: 6.78% Indels: 100  
 RESULT 1090  
 ID ADG48516 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003216560-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1091  
 ID ADH21255 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003224358-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1092  
 ID ADG61478 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207429-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1093  
 ID ADH20295 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003219856-A1.  
 PD 27-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1094  
 ID ADH28565 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003022331-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1095  
 ID ADG54710 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207367-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1096  
 ID ADG59750 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207369-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1097  
 ID ADG51012 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1098  
 ID ADG51012 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1099  
 ID ADH43492 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #30.  
 PN US2003224984-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1100  
 ID ADG58956 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005657-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1101  
 ID ADI81174 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003207361-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1102  
 ID ADH25437 standard; cDNA; 2749 BP.  
 DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:215.  
 PN EP1386931-A1.  
 PD 04-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1103  
 ID ADG09917 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004005548-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1104  
 ID ADI15388 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207382-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1105  
 ID ADG09265 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004005547-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1106  
 ID ADI14720 standard; cDNA; 2749 BP.

DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207383-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1107  
 ID ADI18315 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207349-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1108  
 ID ADJ63596 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004039164-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1109  
 ID ADJ77491 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2004038336-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1110  
 ID ADK82837 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #30.  
 PN US2004043927-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1111  
 ID ADJ65613 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004038335-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1112  
 ID ADM27749 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004048333-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1113  
 ID ADM17214 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1114  
 ID ADL07048 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.

PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1115  
 ID ADM24273 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004058424-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1116  
 ID ADM28335 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004077064-A1.  
 PD 22-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1117  
 ID ADI95817 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003077659-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1118  
 ID ADI96369 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1119  
 ID ACC77620 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.78%  
 RESULT 1120  
 ID ACC77632 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.78%  
 RESULT 1121  
 ID ADS55878 standard; cDNA; 3459 BP.  
 DE Bacterial polynucleotide #7865.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 36.92%  
 Best Local Similarity: 27.31%  
 Query Match: 6.78%



RESULT 1122  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 83  
Indels: 32

RESULT 1123  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 83  
Indels: 32

RESULT 1124  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 83  
Indels: 32

RESULT 1125  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 83  
Indels: 32

ID ADJ40534 standard; cDNA; 1611 BP.  
DE Plant cDNA #1534.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVANT N.  
PA (RICK/) RICKS D.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 38.91%  
Best Local Similarity: 28.87%  
Query Match: 6.74%  
Conservative: 24  
Mismatch: 87  
Indels: 60

RESULT 1127  
ID ADO57711 standard; DNA; 1950 BP.  
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide gene #81.  
PN WO2004045499-A2.  
PD 03-JUN-2004.  
PA (UYFL ) UNIV FLORIDA.  
Percent Similarity: 37.25%  
Best Local Similarity: 23.08%  
Query Match: 6.74%  
Conservative: 35  
Mismatch: 127  
Indels: 28

RESULT 1128  
ID ABD14922 standard; DNA; 2496 BP.  
DE Pseudomonas aeruginosa polynucleotide #13526.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91%  
Best Local Similarity: 26.25%  
Query Match: 6.74%  
Conservative: 25  
Mismatch: 90  
Indels: 77

RESULT 1129  
ID AD192549 standard; DNA; 2526 BP.  
DE Synthetic 5' nuclease DNA SEQ ID 102.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.30%  
Best Local Similarity: 25.00%  
Query Match: 6.74%  
Conservative: 33  
Mismatch: 114  
Indels: 74

RESULT 1130  
ID ABD15329 standard; DNA; 2622 BP.  
DE Pseudomonas aeruginosa polynucleotide #13933.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91%  
Best Local Similarity: 26.25%  
Query Match: 6.74%  
Conservative: 25  
Mismatch: 90  
Indels: 77

RESULT 1131  
ID ABD15222 standard; DNA; 2685 BP.

DE Pseudomonas aeruginosa polynucleotide #13826.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91%  
Best Local Similarity: 26.25%  
Query Match: 6.74%  
Conservative: 25  
Mismatch: 90  
Indels: 77

RESULT 1132  
ID AAV02312 standard; cDNA; 3065 BP.  
DE C16N gene for promoting neuron survival and type 1 collagen production.  
PN WO9740150-A1.  
PD 30-OCT-1997.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Percent Similarity: 30.84%  
Best Local Similarity: 22.19%  
Query Match: 6.74%  
Conservative: 30  
Mismatch: 95  
Indels: 146

RESULT 1133  
ID ACC77988 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.74%  
Conservative: 33  
Mismatch: 113  
Indels: 74

RESULT 1134  
ID ACC77981 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.74%  
Conservative: 33  
Mismatch: 113  
Indels: 74

RESULT 1135  
ID ACC78005 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.74%  
Conservative: 33  
Mismatch: 113  
Indels: 74

RESULT 1136  
ID ACC77997 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.74%  
Conservative: 33  
Mismatch: 113  
Indels: 74

RESULT 1137  
ID AAZ40178 standard; cDNA; 3337 BP.  
DE Mouse C16N-2 coding sequence.  
PN JP11308995-A.  
PD 09-NOV-1999.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Percent Similarity: 30.84%  
Best Local Similarity: 22.19%  
Query Match: 6.74%  
Conservative: 30  
Mismatch: 95  
Indels: 146

RESULT 1138  
ID AAZ44729 standard; cDNA; 3337 BP.  
DE Murine C16N-2 cDNA.  
PN WO200001405-A1.  
PD 13-JAN-2000.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Percent Similarity: 30.84%  
Best Local Similarity: 22.19%  
Query Match: 6.74%  
Conservative: 30  
Mismatch: 95  
Indels: 146

RESULT 1139  
ID AAZ40177 standard; cDNA; 3674 BP.  
DE Mouse C16N-1 coding sequence.

PN JP11308995-A.  
 PD 09-NOV-1999.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Percent Similarity: 30.84%  
 Best Local Similarity: 22.19%  
 Query Match: 6.74%  
 RESULT 1140  
 ID AAZ44728 standard; cDNA; 3674 BP.  
 DE Murine C16N-1 cDNA.  
 PN WO200001403-A1.  
 PD 13-JAN-2000.  
 PA (SUMU ) SUMITOMO PHARM CO LTD.  
 Percent Similarity: 30.84%  
 Best Local Similarity: 22.19%  
 Query Match: 6.74%  
 RESULT 1141  
 ID AAD07024 standard; DNA; 5054 BP.  
 DE Pseudomonas putida PHA synthase DNA.  
 PN WO200123596-A2.  
 PD 05-APR-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Percent Similarity: 39.16%  
 Best Local Similarity: 25.86%  
 Query Match: 6.74%  
 RESULT 1142  
 ID ABA17139 standard; DNA; 32179 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 9470.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.89%  
 Best Local Similarity: 22.59%  
 Query Match: 6.74%  
 RESULT 1143  
 ID ABX34289 standard; DNA; 135638 BP.  
 DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
 PN WO200277179-A2.  
 PD 03-OCT-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 41.04%  
 Best Local Similarity: 25.47%  
 Query Match: 6.74%  
 RESULT 1145  
 ID AAH64966 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 1.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.29%  
 Best Local Similarity: 25.00%  
 Query Match: 6.74%  
 RESULT 1146  
 ID ACD93801 standard; cDNA; 536 BP.  
 DE Human colon cancer cell expressed cDNA #2213.  
 PN US2002155438-A1.  
 PD 24-OCT-2002.  
 PA (SIMP/) SIMPSON A J G.  
 PA (NETO/) NETO E D.  
 PA (BREN/) BRENTANI R R.  
 Percent Similarity: 34.64%  
 Best Local Similarity: 28.49%  
 Query Match: 6.70%  
 RESULT 1147  
 ID ADM94403 standard; cDNA; 1069 BP.  
 DE Wheat MRP4 ABC transporter cDNA #2.  
 PN US6677502-B1.  
 PD 13-JAN-2004.

PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.59%  
 Best Local Similarity: 23.78%  
 Query Match: 6.70%  
 RESULT 1148  
 ID ADT47090 standard; cDNA; 1338 BP.  
 DE Bacterial polynucleotide #21841.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 37.35%  
 Best Local Similarity: 25.29%  
 Query Match: 6.70%  
 RESULT 1149  
 ID ADJ79603 standard; DNA; 1521 BP.  
 DE Glyphosphate resistant corn EPSPS DNA with corn codon usage ID10.  
 PN WO2004009761-A2.  
 PD 29-JAN-2004.  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 Percent Similarity: 36.79%  
 Best Local Similarity: 25.42%  
 Query Match: 6.70%  
 RESULT 1150  
 ID ADH76897 standard; cDNA; 1670 BP.  
 DE Human SOX18 cDNA.  
 PN US2002142415-A1.  
 PD 03-OCT-2002.  
 PA (KOOP/) KOOPMAN P A.  
 PA (MUSC/) MUSCAT G E O.  
 Percent Similarity: 34.28%  
 Best Local Similarity: 23.67%  
 Query Match: 6.70%  
 RESULT 1151  
 ID ABD08413 standard; DNA; 1929 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7017.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.75%  
 Best Local Similarity: 28.21%  
 Query Match: 6.70%  
 RESULT 1152  
 ID ABD08507 standard; DNA; 1947 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7111.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.75%  
 Best Local Similarity: 28.21%  
 Query Match: 6.70%  
 RESULT 1153  
 ID ADA69772 standard; DNA; 2016 BP.  
 DE Rice gene, SEQ ID 3095.  
 PN WO200300898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 32.14%  
 Best Local Similarity: 23.93%  
 Query Match: 6.70%  
 RESULT 1154  
 ID ADB94163 standard; DNA; 2160 BP.  
 DE Gene expression estimation method-related DNA sequence #23.  
 PN WO200304227-A1.  
 PD 30-MAY-2003.  
 PA (NAG-) NAT INST AGROBIOLOGICAL SCI.  
 Percent Similarity: 32.14%  
 Best Local Similarity: 23.93%  
 Query Match: 6.70%

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RESULT 1155
ID AAV62155 standard; DNA; 2341 BP.
DE HSV-2 strain SBS Contig ID 11 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1156
ID ABK14883 standard; DNA; 2499 BP.
DE DNA encoding Tag DNA polymerase cold-sensitive mutant Cs#3.
PN US6333159-B1.
PD 23-DEC-2001.
PA (UNIW ) UNIV WASHINGTON.
Percent Similarity: 41.79%
Best Local Similarity: 26.07%
Query Match: 6.70%
Conservative: 44
Mismatch: 107
Indels: 57
RESULT 1157
ID ABA97303 standard; DNA; 2499 BP.
DE Cold sensitive mutant DNA polymerase DNA #3.
PN US6316202-B1.
PD 13-NOV-2001.
PA (UNIW ) UNIV WASHINGTON.
Percent Similarity: 41.79%
Best Local Similarity: 26.07%
Query Match: 6.70%
Conservative: 44
Mismatch: 107
Indels: 57
RESULT 1158
ID AAV62145 standard; DNA; 2694 BP.
DE HSV-2 strain SBS Contig ID 90 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1159
ID ACC78004 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVT-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.70%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 1160
ID AAK90702 standard; DNA; 3281 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4278.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.23%
Best Local Similarity: 28.08%
Query Match: 6.70%
Conservative: 16
Mismatch: 101
Indels: 70
RESULT 1161
ID AAK90701 standard; DNA; 3704 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4277.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.23%
Best Local Similarity: 28.08%
Query Match: 6.70%
Conservative: 16
Mismatch: 101
Indels: 70
RESULT 1162
ID AAL44297 standard; DNA; 8651 BP.
DE Agropyron medolanus Y1 operon (C50 carotenoid producing operon).
PN WO200241833-A2.
PD 30-MAY-2002.
PA (CRGI ) CARGILL INC.
Percent Similarity: 34.55%
Best Local Similarity: 26.02%
Query Match: 6.70%
Conservative: 21
Mismatch: 87
Indels: 74
RESULT 1163
ID AAV62155 standard; DNA; 2341 BP.
DE HSV-2 strain SBS Contig ID 11 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1164
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1165
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1166
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1167
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1168
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1169
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1170
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1171
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1172
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1173
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1174
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1175
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58

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ID ABD14888 standard; DNA; 1359 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13492.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.39%  
 Best Local Similarity: 22.33%  
 Query Match: 6.66%  
 RESULT 1176  
 ID ABD05006 standard; DNA; 1605 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3610.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 25.97%  
 Query Match: 6.66%  
 RESULT 1177  
 ID ADT42143 standard; cDNA; 2418 BP.  
 DE Bacterial polynucleotide #16894.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 34.40%  
 Best Local Similarity: 23.40%  
 Query Match: 6.66%  
 RESULT 1178  
 ID ACC77989 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 6.66%  
 RESULT 1179  
 ID ABD05159 standard; DNA; 3270 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3763.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 25.97%  
 Query Match: 6.66%  
 RESULT 1180  
 ID AAF90037 standard; DNA; 6462 BP.  
 DE Nucleotide sequence of a type I polyketide synthase.  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1181  
 ID AAS32623 standard; DNA; 10646 BP.  
 DE Human genomic DNA for novel endocrine antigen, SEQ ID No 577.  
 PN WO200155319-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.23%  
 Best Local Similarity: 30.14%  
 Query Match: 6.66%  
 RESULT 1182  
 ID AAA81519 standard; DNA; 16677 BP.  
 DE N. meningitidis partial DNA sequence gnm\_66 SEQ ID NO:66.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR ) CHIRON CORP.  
 Percent Similarity: 37.80%  
 Conservative: 19  
 Mismatches: 69  
 Indels: 59

Best Local Similarity: 24.39%  
 Query Match: 6.66%  
 RESULT 1183  
 ID AAF90033 standard; DNA; 34071 BP.  
 DE Nucleotide sequence of cosmid a26g1 (coding strand).  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1184  
 ID AAF90032 standard; DNA; 42717 BP.  
 DE Nucleotide sequence of cosmid a26g1 (non-coding strand).  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1185  
 ID AAF21612 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:113.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 37.80%  
 Best Local Similarity: 24.39%  
 Query Match: 6.66%  
 RESULT 1187  
 ID AAC55087 standard; DNA; 540 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 80072.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Percent Similarity: 54.24%  
 Best Local Similarity: 33.90%  
 Query Match: 6.63%  
 RESULT 1188  
 ID ACF06134 standard; DNA; 1254 BP.  
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:51.  
 PN WO2003052050-A2.  
 PD 26-JUN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Percent Similarity: 33.44%  
 Best Local Similarity: 25.08%  
 Query Match: 6.63%  
 RESULT 1189  
 ID ACA38073 standard; DNA; 1374 BP.  
 DE Prokaryotic essential gene #19730.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 32.31%  
 Query Match: 6.63%  
 RESULT 1190  
 ID ABX34196 standard; cDNA; 1568 BP.  
 DE Human FBX031-3 (F-Box only protein 3) cDNA #2.  
 PN WO200281514-A2.  
 PD 17-OCT-2002.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 Percent Similarity: 32.26%  
 Best Local Similarity: 25.81%  
 Query Match: 6.63%  
 RESULT 1191  
 ID ABX34198 standard; cDNA; 1602 BP.  
 DE Human FBX031-4 (F-Box only protein 3) alternate form 4) cDNA #2.  
 PN WO200281514-A2.

PD 17-OCT-2002.  
PA (ISIS-) ISIS INNOVATION LTD.  
Percent Similarity: 32.26% Conservative: 20  
Best Local Similarity: 25.81% Mismatches: 96  
Query Match: 6.63% Indels: 114  
RESULT 1192  
ID AAN90395 standard; DNA; 1905 BP.  
DE Genomic/cDNA composite DNA of bovine Mullerian inhibiting substance.  
PN WO8906695-A.  
PD 27-JUL-1989.  
PA (BIOJ ) BIOGEN INC.  
Percent Similarity: 35.28% Conservative: 30  
Best Local Similarity: 25.57% Mismatches: 123  
Query Match: 6.63% Indels: 77  
RESULT 1193  
ID ACC77602 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 39.31% Conservative: 42  
Best Local Similarity: 24.83% Mismatches: 99  
Query Match: 6.63% Indels: 79  
RESULT 1194  
ID ACC77583 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 42.03% Conservative: 43  
Best Local Similarity: 26.62% Mismatches: 109  
Query Match: 6.63% Indels: 53  
RESULT 1195  
ID ACN37398 standard; cDNA; 3705 BP.  
DE Tumor-associated antigenic target (TAT) cDNA DNA323852, SEQ ID NO:254.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.19% Conservative: 25  
Best Local Similarity: 25.93% Mismatches: 76  
Query Match: 6.63% Indels: 99  
RESULT 1196  
ID ABL27024 standard; DNA; 4706 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32545.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.80% Conservative: 18  
Best Local Similarity: 28.40% Mismatches: 102  
Query Match: 6.63% Indels: 55  
RESULT 1197  
ID ADP21336 standard; DNA; 8374 BP.  
DE Gene CACNAIC for screening for cardiac therapeutic preparation.  
PN WO2004050894-A2.  
PD 17-JUN-2004.  
PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
Percent Similarity: 32.52% Conservative: 30  
Best Local Similarity: 23.40% Mismatches: 96  
Query Match: 6.63% Indels: 127  
RESULT 1198  
ID ADG75175 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 34.46% Conservative: 22  
Best Local Similarity: 27.03% Mismatches: 109  
Query Match: 6.63% Indels: 86  
RESULT 1199  
ID ADG75118 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
PN WO2003086308-A2.  
PD 23-OCT-2003.

PA (CORI-) CORIXA CORP.  
Percent Similarity: 34.46% Conservative: 22  
Best Local Similarity: 27.03% Mismatches: 109  
Query Match: 6.63% Indels: 86  
RESULT 1200  
ID ABD10349 standard; DNA; 1008 BP.  
DE Pseudomonas aeruginosa polynucleotide #8953.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.52% Conservative: 15  
Best Local Similarity: 26.90% Mismatches: 83  
Query Match: 6.59% Indels: 46  
RESULT 1201  
ID ABD10349 standard; DNA; 1008 BP.  
DE Pseudomonas aeruginosa polynucleotide #8953.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.52% Conservative: 15  
Best Local Similarity: 26.90% Mismatches: 83  
Query Match: 6.59% Indels: 46  
RESULT 1202  
ID ABD10349 standard; DNA; 1008 BP.  
DE Pseudomonas aeruginosa polynucleotide #8953.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.52% Conservative: 15  
Best Local Similarity: 26.90% Mismatches: 83  
Query Match: 6.59% Indels: 46  
RESULT 1203  
ID AAS54191 standard; DNA; 1014 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #322.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 34.63% Conservative: 22  
Best Local Similarity: 25.11% Mismatches: 85  
Query Match: 6.59% Indels: 66  
RESULT 1204  
ID ACA2441 standard; DNA; 1014 BP.  
DE Prokaryotic essential gene #24098.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 34.63% Conservative: 22  
Best Local Similarity: 25.11% Mismatches: 85  
Query Match: 6.59% Indels: 66  
RESULT 1205  
ID ABD01581 standard; DNA; 1035 BP.  
DE Pseudomonas aeruginosa polynucleotide #185.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.63% Conservative: 22  
Best Local Similarity: 25.11% Mismatches: 85  
Query Match: 6.59% Indels: 66  
RESULT 1206  
ID ABD01558 standard; DNA; 1074 BP.  
DE Pseudomonas aeruginosa polynucleotide #162.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.63% Conservative: 22  
Best Local Similarity: 25.11% Mismatches: 85  
Query Match: 6.59% Indels: 66  
RESULT 1207  
ID ACA23686 standard; DNA; 1263 BP.  
DE Prokaryotic essential gene #5343.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 39.19% Conservative: 37

Best Local Similarity: 22.52% Mismatches: 82  
Query Match: 6.59% Indels: 54  
RESULT 1209  
ID ABD13880 standard; DNA; 1293 BP.  
DE Pseudomonas aeruginosa polynucleotide #12484.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.03% Conservative: 23  
Best Local Similarity: 23.82% Mismatches: 88  
Query Match: 6.59% Indels: 132  
RESULT 1210  
ID ABD14385 standard; DNA; 1422 BP.  
DE Pseudomonas aeruginosa polynucleotide #12989.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.03% Conservative: 23  
Best Local Similarity: 23.82% Mismatches: 88  
Query Match: 6.59% Indels: 132  
RESULT 1211  
ID ADS56274 standard; cDNA; 1437 BP.  
DE Bacterial polynucleotide #8261.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 38.28% Conservative: 29  
Best Local Similarity: 24.40% Mismatches: 92  
Query Match: 6.59% Indels: 37  
RESULT 1212  
ID ABD01554 standard; DNA; 1455 BP.  
DE Pseudomonas aeruginosa polynucleotide #158.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.63% Conservative: 22  
Best Local Similarity: 25.11% Mismatches: 85  
Query Match: 6.59% Indels: 66  
RESULT 1213  
ID ABX70924 standard; cDNA; 1696 BP.  
DE Novel human cDNA sequence #149.  
PN WO200281731-A2.  
PD 17-OCT-2002.  
PA (HYSE/) HYSEQ INC.  
PA (GOOD/) GOODRICH R W.  
Percent Similarity: 34.53% Conservative: 23  
Best Local Similarity: 26.18% Mismatches: 81  
Query Match: 6.59% Indels: 100  
RESULT 1214  
ID AAN70309 standard; cDNA; 1814 BP.  
DE Sequence of bovine mullerian inhibiting substance (MIS) cDNA.  
PN EP221761-A.  
PD 13-MAY-1987.  
PA (BIOJ/) BIOGEN NV.  
PA (GEOH/) GEN HOSPITAL CORP.  
Percent Similarity: 32.03% Conservative: 22  
Best Local Similarity: 24.84% Mismatches: 99  
Query Match: 6.59% Indels: 109  
RESULT 1215  
ID AAS87226 standard; cDNA; 2327 BP.  
DE DNA encoding novel human diagnostic protein #23030.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1216  
ID ACN40432 standard; cDNA; 2327 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA326544, SEQ ID NO:5208.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1217  
ID AAX87254 standard; cDNA; 2413 BP.  
DE cDNA clone encoding human PRO201, amplified in tumour cells.  
PN WO9935170-A2.  
PD 15-JUL-1999.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1218  
ID AAZ32137 standard; cDNA; 2413 BP.  
DE Human PRO201 (Nsp1) protein encoding cDNA clone DNA30676.  
PN WO954467-A1.  
PD 28-OCT-1999.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1219  
ID AAZ89573 standard; cDNA; 2413 BP.  
DE Human PRO201 cDNA.  
PN US6051403-A.  
PD 18-APR-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1220  
ID AAZ89585 standard; cDNA; 2413 BP.  
DE Human PRO201 cDNA.  
PN US6051690-A.  
PD 18-APR-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1221  
ID AAA46900 standard; cDNA; 2413 BP.  
DE cDNA encoding novel polypeptide PRO201.  
PN WO200037640-A2.  
PD 29-JUN-2000.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1222  
ID ADJ58630 standard; cDNA; 2413 BP.  
DE Human DNA30676 cDNA encoding PRO201 (Nsp1) protein.  
PN US2003191283-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1223  
ID ACN92210 standard; DNA; 2454 BP.  
DE Breast cancer related marker, seq id 13360.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 32.92% Conservative: 18  
Best Local Similarity: 25.51% Mismatches: 101  
Query Match: 6.59% Indels: 63  
RESULT 1224  
ID AAV63400 standard; DNA; 2507 BP.  
DE DNA sequence encoding a DNA polymerase enzyme.

Best Local Similarity:	24.78%	Mismatches:	69
Query Match:	6.59%	Indels:	74
RESULT 1232			
ID	AQ083912 standard; cDNA; 3152 BP.		
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #726.		
PN	W02004060270-A2.		
PD	22-JUL-2004.		
PA	(GETH ) GENENTECH INC.		
PA	(WUTD/) WU T D.		
PA	(ZHOU/) ZHOU Y.		
Percent Similarity:	37.83%	Conservative:	30
Best Local Similarity:	24.78%	Mismatches:	69
Query Match:	6.59%	Indels:	74
RESULT 1233			
ID	AQ083232 standard; cDNA; 3152 BP.		
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #46.		
PN	W02004060270-A2.		
PD	22-JUL-2004.		
PA	(GETH ) GENENTECH INC.		
PA	(WUTD/) WU T D.		
PA	(ZHOU/) ZHOU Y.		
Percent Similarity:	37.83%	Conservative:	30
Best Local Similarity:	24.78%	Mismatches:	69
Query Match:	6.59%	Indels:	74
RESULT 1234			
ID	ACN37500 standard; cDNA; 3152 BP.		
DE	Tumour-associated antigenic target (TAT) cDNA DNAl94600, SEQ ID NO:428.		
PN	W02004030615-A2.		
PD	15-APR-2004.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	37.83%	Conservative:	30
Best Local Similarity:	24.78%	Mismatches:	69
Query Match:	6.59%	Indels:	74
RESULT 1235			
ID	ACCT7986 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.59%	Indels:	74
RESULT 1236			
ID	ACCT7953 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	34
Best Local Similarity:	25.00%	Mismatches:	113
Query Match:	6.59%	Indels:	74
RESULT 1237			
ID	ACCT7950 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	34
Best Local Similarity:	25.00%	Mismatches:	113
Query Match:	6.59%	Indels:	74
RESULT 1238			
ID	ACCT7982 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	34
Best Local Similarity:	25.00%	Mismatches:	113
Query Match:	6.59%	Indels:	74
RESULT 1239			
ID	AQ023554 standard; DNA; 3289 BP.		
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 6374.		
PN	W02004048938-A2.		
PD			
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.59%	Indels:	74

PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 32.78% Conservative: 25  
Best Local Similarity: 24.50% Mismatches: 85  
Query Match: 6.59% Indels: 118  
RESULT 1240  
ID ABK94417 standard; cDNA; 3633 BP.  
DE Human cDNA differentially expressed in granulocytic cells #988.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 38.80% Conservative: 39  
Best Local Similarity: 23.20% Mismatches: 97  
Query Match: 6.59% Indels: 57  
RESULT 1241  
ID ABL30051 standard; DNA; 4567 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.64% Conservative: 27  
Best Local Similarity: 27.48% Mismatches: 77  
Query Match: 6.59% Indels: 57  
RESULT 1242  
ID ADNA1761 standard; DNA; 22459 BP.  
DE Novel human secreted protein polynucleotide seqid 883.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYI/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFI/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Percent Similarity: 39.73% Conservative: 15  
Best Local Similarity: 29.45% Mismatches: 60  
Query Match: 6.59% Indels: 28  
RESULT 1243  
ID ABV99730 standard; cDNA; 30350 BP.  
DE Human Ras-like protein encoding cDNA.  
Percent Similarity: 36.03% Conservative: 21  
Best Local Similarity: 28.31% Mismatches: 93  
Query Match: 6.59% Indels: 82  
RESULT 1244  
ID ABZ66810 standard; DNA; 37116 BP.  
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 33.58% Conservative: 14  
Best Local Similarity: 28.30% Mismatches: 96  
Query Match: 6.59% Indels: 81  
RESULT 1245  
ID AAA11992 standard; DNA; 37856 BP.  
DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
PN DE19846493-A1.  
PD 13-APR-2000.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Percent Similarity: 37.27% Conservative: 31  
Best Local Similarity: 25.83% Mismatches: 87  
Query Match: 6.59% Indels: 83  
RESULT 1246  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midecamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.

PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Percent Similarity: 33.33% Conservative: 24  
Best Local Similarity: 25.17% Mismatches: 100  
Query Match: 6.59% Indels: 96  
RESULT 1247  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 38.80% Conservative: 39  
Best Local Similarity: 23.20% Mismatches: 97  
Query Match: 6.59% Indels: 57  
RESULT 1241  
ID ABL30051 standard; DNA; 4567 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.64% Conservative: 27  
Best Local Similarity: 27.48% Mismatches: 77  
Query Match: 6.59% Indels: 57  
RESULT 1242  
ID ADNA1761 standard; DNA; 22459 BP.  
DE Novel human secreted protein polynucleotide seqid 883.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYI/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFI/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Percent Similarity: 39.73% Conservative: 15  
Best Local Similarity: 29.45% Mismatches: 60  
Query Match: 6.59% Indels: 28  
RESULT 1243  
ID ABV99730 standard; cDNA; 30350 BP.  
DE Human Ras-like protein encoding cDNA.  
Percent Similarity: 36.03% Conservative: 21  
Best Local Similarity: 28.31% Mismatches: 93  
Query Match: 6.59% Indels: 82  
RESULT 1244  
ID ABZ66810 standard; DNA; 37116 BP.  
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 33.58% Conservative: 14  
Best Local Similarity: 28.30% Mismatches: 96  
Query Match: 6.59% Indels: 81  
RESULT 1245  
ID AAA11992 standard; DNA; 37856 BP.  
DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
PN DE19846493-A1.  
PD 13-APR-2000.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Percent Similarity: 37.27% Conservative: 31  
Best Local Similarity: 25.83% Mismatches: 87  
Query Match: 6.59% Indels: 83  
RESULT 1246  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midecamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.



RESULT 1259  
 ID ADT46061 standard; cDNA; 1261 BP.  
 DE Bacterial polynucleotide #20812.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 35.79%  
 Best Local Similarity: 24.35%  
 Query Match: 6.55%  
 RESULT 1260  
 ID ADS56330 standard; cDNA; 2402 BP.  
 DE Bacterial polynucleotide #8317.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 32.73%  
 Best Local Similarity: 24.02%  
 Query Match: 6.55%  
 RESULT 1261  
 ID ACA45126 standard; DNA; 2487 BP.  
 DE Prokaryotic essential gene #26783.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.86%  
 Best Local Similarity: 23.03%  
 Query Match: 6.55%  
 RESULT 1262  
 ID ADI92574 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 127.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 42.09%  
 Best Local Similarity: 26.62%  
 Query Match: 6.55%  
 RESULT 1263  
 ID ABK62569 standard; cDNA; 3730 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #476.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1264  
 ID ADB58760 standard; DNA; 3730 BP.  
 DE Toxicity-related gene, SEQ ID 3786.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1265  
 ID ADP71852 standard; DNA; 3730 BP.  
 DE Renal toxin progression gene marker #441.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1266  
 ID ADD40759 standard; cDNA; 3885 BP.

DE Human tenascin-W coding sequence.  
 PN WO2003080663-A2.  
 PD 02-OCT-2003.  
 PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1267  
 ID ACN45195 standard; cDNA; 3885 BP.  
 DE Human mRNA sequence hCT15314.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1268  
 ID ADQ19282 standard; DNA; 4750 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2101.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1269  
 ID ADR89531 standard; DNA; 4750 BP.  
 DE Apoptosis-inducing protein coding sequence, SEQ ID 55.  
 PN WO2004078112-A2.  
 PD 16-SEP-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1270  
 ID ABK84242 standard; cDNA; 43599 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #813.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 35.61%  
 Best Local Similarity: 24.62%  
 Query Match: 6.55%  
 RESULT 1271  
 ID ADE86070 standard; DNA; 47988 BP.  
 DE Streptomyces hygrosopicus non-ribosomal peptide synthetase complex DNA.  
 PN WO2003082909-A1.  
 PD 09-OCT-2003.  
 PA (AMHP) WYETH.  
 Percent Similarity: 38.10%  
 Best Local Similarity: 28.57%  
 Query Match: 6.55%  
 RESULT 1272  
 ID ABD20213 standard; DNA; 849 BP.  
 DE Pseudomonas aeruginosa polynucleotide #617.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.29%  
 Best Local Similarity: 26.80%  
 Query Match: 6.52%  
 RESULT 1273  
 ID ADS14773 standard; DNA; 933 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2339, SEQ ID 328.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 Percent Similarity: 34.52%  
 Best Local Similarity: 26.90%  
 Query Match: 6.52%  
 RESULT 1274  
 ID AAD11173 standard; DNA; 1053 BP.  
 DE Pseudomonas stutzeri open reading frame-P (ORF-P) DNA.

PN WO200153309-A1.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.80% Conservative: 17  
Best Local Similarity: 29.67% Mismatches: 73  
Query Match: 6.52% Indels: 57  
RESULT 1282  
ID ABD02082 standard; DNA; 2379 BP.  
DE Pseudomonas aeruginosa polynucleotide #686.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.24% Conservative: 32  
Best Local Similarity: 23.39% Mismatches: 87  
Query Match: 6.52% Indels: 107  
RESULT 1283  
ID ABD02092 standard; DNA; 2499 BP.  
DE Pseudomonas aeruginosa polynucleotide #696.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.24% Conservative: 32  
Best Local Similarity: 23.39% Mismatches: 87  
Query Match: 6.52% Indels: 107  
RESULT 1284  
ID ADI92882 standard; DNA; 2508 BP.  
DE Construct TthAKK H641A DNA SEQ ID 435.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.33% Conservative: 33  
Best Local Similarity: 24.91% Mismatches: 112  
Query Match: 6.52% Indels: 74  
RESULT 1285  
ID ADI92548 standard; DNA; 2526 BP.  
DE Synthetic 5' nuclease DNA SEQ ID 101.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.30% Conservative: 32  
Best Local Similarity: 25.34% Mismatches: 114  
Query Match: 6.52% Indels: 74  
RESULT 1286  
ID ADI21750 standard; cDNA; 3212 BP.  
DE Novel human protein cDNA #9.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.92% Conservative: 21  
Best Local Similarity: 26.59% Mismatches: 83  
Query Match: 6.52% Indels: 82  
RESULT 1287  
ID AA157998 standard; cDNA; 4071 BP.  
DE Human polynucleotide SEQ ID NO 201.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.63% Conservative: 26  
Best Local Similarity: 27.47% Mismatches: 70  
Query Match: 6.52% Indels: 74  
RESULT 1288  
ID ADE07615 standard; DNA; 4989 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #681.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 49.30% Conservative: 8  
Best Local Similarity: 38.03% Mismatches: 24  
Query Match: 6.52% Indels: 12  
RESULT 1289  
ID AB11939 standard; cDNA; 7335 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30299.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.

PN WO200153309-A1.  
PA (IDAH-) IDAHO RES FOUND INC.  
PA (PASZ/) PASZCZYNSKI A.  
PA (SEBA/) SEBAT J L.  
Percent Similarity: 38.24% Conservative: 21  
Best Local Similarity: 29.41% Mismatches: 88  
Query Match: 6.52% Indels: 60  
RESULT 1275  
ID ADS14581 standard; DNA; 1377 BP.  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2180, SEQ ID 136.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Percent Similarity: 35.91% Conservative: 30  
Best Local Similarity: 25.84% Mismatches: 87  
Query Match: 6.52% Indels: 104  
RESULT 1276  
ID ADH76980 standard; DNA; 1402 BP.  
DE Human SOX18 related DNA.  
PN US2002142415-A1.  
PD 03-OCT-2002.  
PA (KOOP/) KOOPMAN P A.  
PA (MUSC/) MUSCAT G E O.  
Percent Similarity: 35.76% Conservative: 37  
Best Local Similarity: 22.92% Mismatches: 109  
Query Match: 6.52% Indels: 78  
RESULT 1277  
ID ABD04496 standard; DNA; 1575 BP.  
DE Pseudomonas aeruginosa polynucleotide #3100.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 40.00% Conservative: 23  
Best Local Similarity: 29.55% Mismatches: 90  
Query Match: 6.52% Indels: 42  
RESULT 1278  
ID ADS48122 standard; cDNA; 1803 BP.  
DE Bacterial polynucleotide #2865.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 35.18% Conservative: 32  
Best Local Similarity: 22.53% Mismatches: 81  
Query Match: 6.52% Indels: 83  
RESULT 1279  
ID ABD17609 standard; DNA; 1866 BP.  
DE Pseudomonas aeruginosa polynucleotide #16213.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 37.37% Conservative: 35  
Best Local Similarity: 25.28% Mismatches: 80  
Query Match: 6.52% Indels: 102  
RESULT 1280  
ID ABD04585 standard; DNA; 1956 BP.  
DE Pseudomonas aeruginosa polynucleotide #3189.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 40.00% Conservative: 23  
Best Local Similarity: 29.55% Mismatches: 90  
Query Match: 6.52% Indels: 42  
RESULT 1281  
ID ADB63152 standard; cDNA; 2082 BP.  
DE Human cDNA encoding clone SPLEN20043460.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.

Percent Similarity: 34.27% Conservative: 34  
 Best Local Similarity: 22.38% Mismatches: 83  
 Query Match: 6.52% Indels: 106  
 RESULT 1290  
 ID AAH98395 standard; cDNA; 8836 BP.  
 DE Human EST-derived coding sequence SEQ ID NO: 252.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.74% Conservative: 27  
 Best Local Similarity: 24.78% Mismatches: 90  
 Query Match: 6.52% Indels: 138  
 RESULT 1291  
 ID AAS36759 standard; DNA; 9745 BP.  
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2259.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1292  
 ID ADE47453 standard; DNA; 9745 BP.  
 DE Human cardiovascular system related genomic DNA #1019.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1293  
 ID ADJ08871 standard; DNA; 9745 BP.  
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2259.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1294  
 ID ABL11938 standard; cDNA; 10026 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30296.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.27% Conservative: 34  
 Best Local Similarity: 22.38% Mismatches: 83  
 Query Match: 6.52% Indels: 106  
 RESULT 1295  
 ID AAS36758 standard; DNA; 12149 BP.  
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2258.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1296  
 ID ADE47452 standard; DNA; 12149 BP.  
 DE Human cardiovascular system related genomic DNA #1018.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1297  
 ID ADJ08870 standard; DNA; 12149 BP.  
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2258.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20

Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1298  
 ID ABZ74518 standard; DNA; 13361 BP.  
 DE Secreted protein gene 330 genomic fragment HTLCX82, SEQ ID NO:1665.  
 PN WO200277013-A2.  
 PD 03-OCT-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1299  
 ID ADC20950 standard; DNA; 13361 BP.  
 DE Human secreted protein-related DNA sequence #368.  
 PN WO200292787-A2.  
 PD 21-NOV-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1300  
 ID ADC26981 standard; DNA; 20922 BP.  
 DE Sorangium cellulosum tmbA gene cluster tmbB DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Percent Similarity: 34.55% Conservative: 25  
 Best Local Similarity: 25.45% Mismatches: 116  
 Query Match: 6.52% Indels: 65  
 RESULT 1301  
 ID ADQ97295 standard; DNA; 21293 BP.  
 DE Human cancer associated sequence HD08-027, SEQ ID 272.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1302  
 ID AAD11177 standard; DNA; 25801 BP.  
 DE Pseudomonas stutzeri cosmid pT31 DNA.  
 PN WO200153309-A1.  
 PD 26-JUL-2001.  
 PA (IDAH-) IDAHO RES FOUND INC.  
 PA (PASZ/) PASZCZYNSKI A.  
 PA (SEBA/) SEBAT J L.  
 Percent Similarity: 38.24% Conservative: 21  
 Best Local Similarity: 29.41% Mismatches: 88  
 Query Match: 6.52% Indels: 60  
 RESULT 1303  
 ID ACN44790 standard; DNA; 98546 BP.  
 DE Human genomic sequence hCG23145.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 33.45% Conservative: 24  
 Best Local Similarity: 24.91% Mismatches: 104  
 Query Match: 6.52% Indels: 83  
 RESULT 1304  
 ID ADE47452 standard; DNA; 12149 BP.  
 DE Human cardiovascular system related genomic DNA #1018.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1296  
 ID ADE47452 standard; DNA; 12149 BP.  
 DE Human cardiovascular system related genomic DNA #1018.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1297  
 ID ADJ08870 standard; DNA; 12149 BP.  
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2258.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20

Query Match: 6.52% Indels: 55  
 RESULT 1308  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1309  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1310  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1311  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1312  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1313  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1314  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1315  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1316  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1317  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1318  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1319  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1320  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1321  
 ID ADL13684 standard; DNA; 247509 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #216.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (JUL-) INCYTE GENOMICS INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1322  
 ID ADS61562 standard; cDNA; 660 BP.  
 DE Bacterial polynucleotide #13549.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 42.68% Conservative: 28

Best Local Similarity: 25.61% Mismatches: 54  
 Query Match: 6.48% Indels: 40  
 RESULT 1323  
 ID ABD08014 standard; DNA; 930 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6618.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53% Conservative: 19  
 Best Local Similarity: 27.19% Mismatches: 106  
 Query Match: 6.48% Indels: 41  
 RESULT 1324  
 ID ACA36198 standard; DNA; 1027 BP.  
 DE Prokaryotic essential gene #17855.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.32% Conservative: 34  
 Best Local Similarity: 25.35% Mismatches: 105  
 Query Match: 6.48% Indels: 73  
 RESULT 1325  
 ID AAZ91271 standard; DNA; 1074 BP.  
 DE Nucleotide sequence fccr SEQ ID NO:36.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1326  
 ID ABD15610 standard; DNA; 1158 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14214.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.65% Conservative: 22  
 Best Local Similarity: 26.09% Mismatches: 91  
 Query Match: 6.48% Indels: 58  
 RESULT 1327  
 ID ABD08045 standard; DNA; 1308 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6649.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53% Conservative: 19  
 Best Local Similarity: 27.19% Mismatches: 106  
 Query Match: 6.48% Indels: 41  
 RESULT 1328  
 ID AAZ91259 standard; DNA; 1377 BP.  
 DE CoA ligase fccf nucleotide sequence SEQ ID NO:12.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1329  
 ID AAT74890 standard; DNA; 1535 BP.  
 DE Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.  
 PN WO9716548-A1.  
 PD 09-MAY-1997.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 PA (WEIN/) WEINTRAUB N.  
 Percent Similarity: 38.71% Conservative: 11  
 Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1330  
 ID AAV42931 standard; DNA; 1535 BP.  
 DE DNA encoding human neuroD2 protein, which is a bHLH protein.  
 PN US5795723-A.  
 PD 18-AUG-1998.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71% Conservative: 11

Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1331  
 ID ABS56389 standard; DNA; 1535 BP.  
 DE Human BHLH family neuroD2 genomic DNA, clone 14B1.  
 PN US6444463-B1.  
 PD 03-SEP-2002.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71% Conservative: 11  
 Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1332  
 ID ADP72550 standard; DNA; 1580 BP.  
 DE Renal toxin progression gene marker #1139.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 34.11% Conservative: 31  
 Best Local Similarity: 22.09% Mismatches: 79  
 Query Match: 6.48% Indels: 91  
 RESULT 1333  
 ID ABZ11712 standard; cDNA; 1625 BP.  
 DE Human polynucleotide SEQ ID NO 594.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 41.10% Conservative: 39  
 Best Local Similarity: 24.58% Mismatches: 84  
 Query Match: 6.48% Indels: 55  
 RESULT 1334  
 ID ADM44230 standard; cDNA; 1625 BP.  
 DE Novel human arginine-rich protein cDNA #594.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUE/) XUE A.  
 PA (DRNA/) DRMANAC R T.  
 Percent Similarity: 41.10% Conservative: 39  
 Best Local Similarity: 24.58% Mismatches: 84  
 Query Match: 6.48% Indels: 55  
 RESULT 1335  
 ID ABD11546 standard; DNA; 1650 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10150.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91% Conservative: 29  
 Best Local Similarity: 23.88% Mismatches: 83  
 Query Match: 6.48% Indels: 108  
 RESULT 1336  
 ID ABD11322 standard; DNA; 1725 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9926.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91% Conservative: 29  
 Best Local Similarity: 23.88% Mismatches: 83  
 Query Match: 6.48% Indels: 108  
 RESULT 1337  
 ID ABD14631 standard; DNA; 2145 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13235.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.99% Conservative: 24  
 Best Local Similarity: 24.83% Mismatches: 112  
 Query Match: 6.48% Indels: 85  
 RESULT 1338  
 ID ADA52692 standard; cDNA; 2198 BP.  
 DE Human coding sequence, SEQ ID 260.  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 37.44% Conservative: 20  
 Best Local Similarity: 27.59% Mismatches: 49  
 Query Match: 6.48% Indels: 78  
 RESULT 1339  
 ID ABL24533 standard; DNA; 2244 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25072.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Percent Similarity: 41.61% Conservative: 22  
 Best Local Similarity: 26.85% Mismatches: 58  
 Query Match: 6.48% Indels: 29  
 RESULT 1340  
 ID ABA97188 standard; DNA; 2326 BP.  
 DE Goat lactoferrin-associated DNA #2.  
 PN KR98043944-A.  
 PD 05-SEP-1998.  
 PA (KOAD-) KOREA ADV INST SCI & TECHNOLOGY.  
 Percent Similarity: 34.95% Conservative: 27  
 Best Local Similarity: 25.61% Mismatches: 97  
 Query Match: 6.48% Indels: 91  
 RESULT 1341  
 ID ACC77593 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.38% Conservative: 37  
 Best Local Similarity: 26.71% Mismatches: 97  
 Query Match: 6.48% Indels: 81  
 RESULT 1342  
 ID ACC77767 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.14% Conservative: 38  
 Best Local Similarity: 25.09% Mismatches: 102  
 Query Match: 6.48% Indels: 79  
 RESULT 1343  
 ID AAH02112 standard; DNA; 3297 BP.  
 DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2105.  
 PN WO200123604-A2.  
 PD 05-APR-2001.  
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1344  
 ID AAH52090 standard; DNA; 3297 BP.  
 DE Mycobacterium tuberculosis potential drug target gene SEQ ID 144.  
 PN WO200135317-A1.  
 PD 17-MAY-2001.  
 PA (REGC-) UNIV CALIFORNIA.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1345  
 ID ACH97234 standard; DNA; 3390 BP.  
 DE Klebsiella pneumoniae polynucleotide segid 3029.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 26.88% Conservative: 26  
 Best Local Similarity: 20.58% Mismatches: 101  
 Query Match: 6.48% Indels: 201  
 RESULT 1346  
 ID ABD07965 standard; DNA; 3741 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6569.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Percent Similarity:	35.53%	Conservative:	19
Best Local Similarity:	27.19%	Mismatches:	106
Query Match:	6.48%	Indels:	41
RESULT 1347			
ID	AA159784 standard; cDNA; 3913 BP.		
DE	Human polynucleotide SEQ ID NO 3773.		
PN	WO20015312-A1.		
PD	26-JUL-2001.		
PA	(HYSE-) HYSEQ INC.		
Percent Similarity:	38.57%	Conservative:	25
Best Local Similarity:	27.35%	Mismatches:	64
Query Match:	6.48%	Indels:	74
RESULT 1348			
ID	ABD14252 standard; DNA; 4431 BP.		
DE	Pseudomonas aeruginosa polynucleotide #12856.		
PN	US6551795-B1.		
PD	22-APR-2003.		
PA	(GENO-) GENOME THERAPEUTICS CORP.		
Percent Similarity:	30.34%	Conservative:	16
Best Local Similarity:	24.34%	Mismatches:	79
Query Match:	6.48%	Indels:	109
RESULT 1349			
ID	ABL24532 standard; DNA; 4649 BP.		
DE	Drosophila melanogaster genomic polynucleotide SEQ ID NO 25069.		
PN	WO200171042-A2.		
PD	27-SEP-2001.		
PA	(PERE-) PE CORP NY.		
Percent Similarity:	41.61%	Conservative:	22
Best Local Similarity:	26.85%	Mismatches:	58
Query Match:	6.48%	Indels:	29
RESULT 1350			
ID	AAS59642 standard; DNA; 5870 BP.		
DE	Propionibacterium acnes immunogenic protein encoding DNA #137.		
PN	WO200181581-A2.		
PD	01-NOV-2001.		
PA	(CORI-) CORIXA CORP.		
Percent Similarity:	36.22%	Conservative:	25
Best Local Similarity:	26.38%	Mismatches:	87
Query Match:	6.48%	Indels:	75
RESULT 1351			
ID	ACF64571 standard; DNA; 5870 BP.		
DE	Propionibacterium acnes DNA contig sequence #137.		
PN	WO2003033515-A1.		
PD	24-APR-2003.		
PA	(CORI-) CORIXA CORP.		
Percent Similarity:	36.22%	Conservative:	25
Best Local Similarity:	26.38%	Mismatches:	87
Query Match:	6.48%	Indels:	75
RESULT 1352			
ID	ADP55748 standard; cDNA; 5908 BP.		
DE	Human PRO cDNA sequence SEQ ID NO:1724.		
PN	WO2004039956-A2.		
PD	13-MAY-2004.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	34.44%	Conservative:	22
Best Local Similarity:	25.31%	Mismatches:	95
Query Match:	6.48%	Indels:	64
RESULT 1353			
ID	ADH13157 standard; DNA; 6131 BP.		
DE	Human malignant neoplasia-related gene SeqID6.		
PN	EP1365034-A2.		
PD	26-NOV-2003.		
PA	(FARB) BAYER AG.		
Percent Similarity:	38.71%	Conservative:	11
Best Local Similarity:	31.61%	Mismatches:	59
Query Match:	6.48%	Indels:	36
RESULT 1354			
ID	ACA26658 standard; DNA; 7802 BP.		
DE	Prokaryotic essential gene #8315.		
PN	WO20027183-A2.		
PD	03-OCT-2002.		
PA	(ELIT-) ELITRA PHARM INC.		
Percent Similarity:	33.33%	Conservative:	23

  

Best Local Similarity:	24.21%	Mismatches:	90
Query Match:	6.48%	Indels:	78
RESULT 1355			
ID	AAV58938 standard; DNA; 10095 BP.		
DE	Mycobacterium tuberculosis embCAB operon.		
PN	WO9841533-A1.		
PD	24-SEP-1998.		
PA	(YESH) UNIV YESHIVA EINSTEIN COLLEGE.		
Percent Similarity:	36.73%	Conservative:	24
Best Local Similarity:	26.94%	Mismatches:	100
Query Match:	6.48%	Indels:	56
RESULT 1356			
ID	ADN36912 standard; DNA; 20640 BP.		
DE	X. albilineans XALBI gene cluster DNA encoding protein AlBI.		
PN	WO2004035760-A2.		
PD	29-APR-2004.		
PA	(UYFL) UNIV FLORIDA.		
Percent Similarity:	38.13%	Conservative:	32
Best Local Similarity:	25.68%	Mismatches:	116
Query Match:	6.48%	Indels:	44
RESULT 1357			
ID	AAZ91253 standard; DNA; 24494 BP.		
DE	Bacterium 2412.1 fumonisin-catabolising gene cluster.		
PN	WO200004158-A2.		
PD	27-JAN-2000.		
PA	(PION-) PIONEER HI-BRED INT INC.		
Percent Similarity:	37.76%	Conservative:	39
Best Local Similarity:	24.13%	Mismatches:	101
Query Match:	6.48%	Indels:	79
RESULT 1358			
ID	ADN36893 standard; DNA; 55839 BP.		
DE	X. albilineans XALBI gene cluster DNA.		
PN	WO2004035760-A2.		
PD	29-APR-2004.		
PA	(UYFL) UNIV FLORIDA.		
Percent Similarity:	38.13%	Conservative:	32
Best Local Similarity:	25.68%	Mismatches:	116
Query Match:	6.48%	Indels:	44
RESULT 1359			
ID	ADC26995 standard; DNA; 67251 BP.		
DE	Sorangium cellulosum tmbA gene cluster.		
PN	US2003054547-A1.		
PD	20-MAR-2003.		
PA	(JULI/) JULIEN B.		
Percent Similarity:	40.59%	Conservative:	28
Best Local Similarity:	26.73%	Mismatches:	71
Query Match:	6.48%	Indels:	50
RESULT 1360			
Percent Similarity:	37.03%	Conservative:	43
Best Local Similarity:	23.42%	Mismatches:	107
Query Match:	6.48%	Indels:	93
RESULT 1361			
Percent Similarity:	36.73%	Conservative:	24
Best Local Similarity:	26.94%	Mismatches:	100
Query Match:	6.48%	Indels:	56
RESULT 1362			
Percent Similarity:	37.03%	Conservative:	43
Best Local Similarity:	23.42%	Mismatches:	107
Query Match:	6.48%	Indels:	93
RESULT 1363			
Percent Similarity:	36.73%	Conservative:	24
Best Local Similarity:	26.94%	Mismatches:	100
Query Match:	6.48%	Indels:	56
RESULT 1364			
Percent Similarity:	49.53%	Conservative:	23
Best Local Similarity:	28.04%	Mismatches:	36
Query Match:	6.48%	Indels:	18
RESULT 1365			
ID	ABZ38468 standard; DNA; 507 BP.		
DE	N. gonorrhoeae nucleotide sequence SEQ ID 1525.		
PN	WO200279243-A2.		

ID	AAF59130 standard; DNA; 1546 BP.				
DE	Streptomyces sp. SK glucose isomerase nucleotide sequence SEQ ID NO:1				
FN	JF2000333684-A.				
PD	05-DEC-2000.				
PA	(NOVO ) NOVO NORDISK AS.				
Percent Similarity:	36.73%	Conservative:	28		
Best Local Similarity:	26.55%	Mismatches:	77		
Query Match:	6.44%	Indels:	98		
RESULT 1374					
ID	AAS71366 standard; cDNA; 1588 BP.				
DE	DNA encoding novel human diagnostic protein #7170.				
FN	W0200175067-A2.				
PD	11-OCT-2001.				
PA	(HYSE-) HYSEQ INC.				
Percent Similarity:	43.40%	Conservative:	8		
Best Local Similarity:	35.85%	Mismatches:	29		
Query Match:	6.44%	Indels:	31		
RESULT 1375					
ID	ABT19484 standard; DNA; 1666 BP.				
DE	Aspergillus fumigatus essential gene #842.				
FN	W0200286090-A2.				
PD	31-OCT-2002.				
PA	(ELIT-) ELITRA PHARM INC.				
Percent Similarity:	33.72%	Conservative:	29		
Best Local Similarity:	22.48%	Mismatches:	90		
Query Match:	6.44%	Indels:	81		
RESULT 1376					
ID	ACH96895 standard; DNA; 1707 BP.				
DE	Klebsiella pneumoniae polynucleotide seqid 2690.				
FN	US6610836-B1.				
PD	26-AUG-2003.				
PA	(GENO-) GENOME THERAPEUTICS CORP.				
Percent Similarity:	37.84%	Conservative:	24		
Best Local Similarity:	28.57%	Mismatches:	95		
Query Match:	6.44%	Indels:	68		
RESULT 1377					
ID	ABD07686 standard; DNA; 1989 BP.				
DE	Pseudomonas aeruginosa polynucleotide #6290.				
FN	US6551795-B1.				
PD	22-APR-2003.				
PA	(GENO-) GENOME THERAPEUTICS CORP.				
Percent Similarity:	35.99%	Conservative:	34		
Best Local Similarity:	24.22%	Mismatches:	97		
Query Match:	6.44%	Indels:	89		
RESULT 1378					
ID	AQ023026 standard; DNA; 1990 BP.				
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 5846.				
FN	W02004048938-A2.				
PD	10-JUN-2004.				
PA	(PROT-) PROTEIN DESIGN LABS INC.				
Percent Similarity:	33.90%	Conservative:	20		
Best Local Similarity:	25.42%	Mismatches:	82		
Query Match:	6.44%	Indels:	75		
RESULT 1379					
ID	ADM47721 standard; DNA; 2005 BP.				
DE	Polynucleotide sequence #139 useful in producing transgenic plants.				
FN	US2003233670-A1.				
PD	18-DEC-2003.				
PA	(EDGE/) EDGERTON M D.				
PA	(CHOW/) CHOMET P S.				
PA	(LACC/) LACCETTI L B.				
Percent Similarity:	35.39%	Conservative:	23		
Best Local Similarity:	25.93%	Mismatches:	81		
Query Match:	6.44%	Indels:	76		
RESULT 1380					
ID	ADB62264 standard; cDNA; 2165 BP.				
DE	Human cDNA encoding clone CTONG20189000.				
FN	EP1308459-A2.				
PD	07-MAY-2003.				
PA	(HELL-) HELIX RES INST.				
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.				
Percent Similarity:	38.89%	Conservative:	21		
Best Local Similarity:	28.64%	Mismatches:	84		

Query Match: 6.44% Indels: 43  
 RESULT 1381  
 ID ABD02122 standard; DNA; 2367 BP.  
 DE Pseudomonas aeruginosa polynucleotide #726.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89% Conservative: 28  
 Best Local Similarity: 25.93% Mismatches: 65  
 Indels: 67  
 Query Match:  
 RESULT 1382  
 ID ABA00886 standard; DNA; 2502 BP.  
 DE Novel TepJ51 DNA polymerase coding sequence.  
 PN WO2003004632-A2.  
 PD 16-JAN-2003.  
 PA (AMSH ) AMERSHAM BIOSCIENCES CORP.  
 Percent Similarity: 34.44% Conservative: 22  
 Best Local Similarity: 26.30% Mismatches: 94  
 Indels: 83  
 Query Match:  
 RESULT 1383  
 ID AAS62249 standard; cDNA; 2740 BP.  
 DE cDNA sequence #36 encoding novel human secreted protein.  
 PN WO200177291-A2.  
 PD 18-OCT-2001.  
 PA (GEMY ) GENETICS INST INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Indels: 40  
 Query Match:  
 RESULT 1384  
 ID ACN37277 standard; cDNA; 2779 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA323744, SEQ ID NO:55.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Indels: 43  
 Query Match:  
 RESULT 1385  
 ID AAT32326 standard; DNA; 3049 BP.  
 DE Thermus flavus DNA polymerase I coding sequence.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.86% Conservative: 32  
 Best Local Similarity: 25.94% Mismatches: 112  
 Indels: 75  
 Query Match:  
 RESULT 1386  
 ID AAD29059 standard; cDNA; 3075 BP.  
 DE Human guanine nucleotide exchange factor (GEF) 32529 cDNA.  
 PN WO200206325-A2.  
 PD 24-JAN-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Indels: 43  
 Query Match:  
 RESULT 1387  
 ID ADQ85401 standard; cDNA; 3148 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2215.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 41.70% Conservative: 24  
 Best Local Similarity: 30.94% Mismatches: 75  
 Indels: 57  
 Query Match:  
 RESULT 1388  
 ID ACN39921 standard; cDNA; 3148 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326094, SEQ ID NO:4368.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 41.70% Conservative: 24

Best Local Similarity: 30.94% Mismatches: 75  
 Query Match: 6.44% Indels: 57  
 RESULT 1389  
 ID ADI81640 standard; DNA; 3213 BP.  
 DE Malaria mosquito DNA encoding protein ebip7471.  
 PN US2004009537-A1.  
 PD 15-JAN-2004.  
 PA (ROOS/) ROOS J.  
 PA (STAU/) STAUDERMAN K.  
 PA (VELI/) VELICELEBI G.  
 Percent Similarity: 41.97% Conservative: 34  
 Best Local Similarity: 29.56% Mismatches: 90  
 Indels: 69  
 Query Match:  
 RESULT 1390  
 ID ACC77949 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Indels: 74  
 Query Match:  
 RESULT 1391  
 ID ACC77952 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Indels: 74  
 Query Match:  
 RESULT 1392  
 ID ACC77959 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Indels: 74  
 Query Match:  
 RESULT 1393  
 ID ABT17890 standard; DNA; 3666 BP.  
 DE Aspergillus fumigatus essential gene #248.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.72% Conservative: 29  
 Best Local Similarity: 22.48% Mismatches: 90  
 Indels: 81  
 Query Match:  
 RESULT 1394  
 ID ADC10041 standard; DNA; 3721 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 61.  
 PN WO200300842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 41.70% Conservative: 24  
 Best Local Similarity: 30.94% Mismatches: 75  
 Indels: 57  
 Query Match:  
 RESULT 1395  
 ID ABD05211 standard; DNA; 3825 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3815.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.77% Conservative: 20  
 Best Local Similarity: 28.07% Mismatches: 68  
 Indels: 35  
 Query Match:  
 RESULT 1396  
 ID ABD05091 standard; DNA; 4506 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3695.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.



Percent Similarity: 39.77% Conservative: 20  
 Best Local Similarity: 28.07% Mismatches: 68  
 Query Match: 6.44% Indels: 35  
 RESULT 1397  
 ID AAC86156 standard; cDNA; 4815 BP.  
 DE FCT84 nucleic acid.  
 PN WO200146231-A2.  
 PD 28-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Query Match: 6.44% Indels: 43  
 RESULT 1398  
 ID ADR24186 standard; DNA; 5285 BP.  
 DE Breast cancer prognosis marker #47.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1399  
 ID AAD27271 standard; cDNA; 5540 BP.  
 DE Human transporter and ion channel-18 (TRICH-18) cDNA.  
 PN WO200192304-A2.  
 PD 06-DEC-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1400  
 ID AAD54236 standard; DNA; 6297 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 39.06% Conservative: 30  
 Best Local Similarity: 26.18% Mismatches: 90  
 Query Match: 6.44% Indels: 55  
 RESULT 1401  
 ID AAT06768 standard; DNA; 7000 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PN WO9533818-A2.  
 PD 14-DEC-1995.  
 PA (CIBA) CIBA GEIGY AG.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1402  
 ID AAT89955 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster genomic DNA.  
 PN US5662898-A.  
 PD 02-SEP-1997.  
 PA (CIBA) CIBA GEIGY CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1403  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PN US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1404  
 ID AAV39840 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PN WO9824919-A1.  
 PD 11-JUN-1998.  
 PA (NOVS) NOVARTIS AG.

Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1405  
 ID AAX9371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PN US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS) NOVARTIS AG.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1406  
 ID AAAV5298 standard; DNA; 7001 BP.  
 DE DNA sequence of Pseudomonas fluorescens pyrrolnitrin gene region.  
 PN US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1407  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PN WO200222684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1408  
 ID ACD28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PN US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA/) MURAD F.  
 PA (SHAR/) SHARINA I G.  
 PA (KRUM/) KRUMENACKER J S.  
 PA (MART/) MARTIN E.  
 Percent Similarity: 41.73% Conservative: 19  
 Best Local Similarity: 28.06% Mismatches: 53  
 Query Match: 6.44% Indels: 28  
 RESULT 1409  
 ID ADL33384 standard; DNA; 7706 BP.  
 DE Human transporter and ion channel (TRICH) gene #29.  
 PN WO2003083085-A2.  
 PD 09-OCT-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1410  
 ID ABX70982 standard; cDNA; 8037 BP.  
 DE Novel human cDNA sequence #207.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.  
 PA (HYSE-) HYSEQ INC.  
 PA (GOOD/) GOODRICH R W.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1411  
 ID AAF57452 standard; cDNA; 8040 BP.  
 DE Human ABCA2 transporter protein encoding cDNA.  
 PN WO200121798-A2.  
 PD 29-MAR-2001.  
 PA (FOXC-) FOX CHASE CANCER CENT.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1412  
 ID ABV74350 standard; DNA; 8056 BP.  
 DE Human ABC transporter ABCA2 encoding polynucleotide SEQ ID NO 3.

PN WO200264781-A2.  
 PD 22-AUG-2002.  
 PA (ACTI-) ACTIVE PASS PHARM INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1413  
 ID AAH75187 standard; cDNA; 8195 BP.  
 DE Nucleotide sequence of a human 17114 transporter polypeptide.  
 PN WO200164875-A2.  
 PD 07-SEP-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1414  
 ID ABL53009 standard; DNA; 8269 BP.  
 DE Human ATP binding cassette transporter protein, ABCA2, coding sequence.  
 PN WO200208424-A1.  
 PD 31-JAN-2002.  
 PA (BANY) BANYU PHARM CO LTD.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1415  
 ID AAK68713 standard; DNA; 11477 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23525.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 RESULT 1416  
 ID AAK71247 standard; DNA; 11477 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26059.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 RESULT 1417  
 ID AAK68712 standard; DNA; 11482 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 RESULT 1418  
 ID AAK71246 standard; DNA; 11482 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 RESULT 1419  
 ID AAS59566 standard; DNA; 34088 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #61.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 25.10%  
 Query Match: 6.44%  
 RESULT 1420  
 ID ACF64495 standard; DNA; 34088 BP.  
 DE Propionibacterium acnes DNA contig sequence #61.

PN WO200303515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 25.10%  
 Query Match: 6.44%  
 RESULT 1421  
 ID ADH48030 standard; DNA; 37507 BP.  
 DE Clone PS3-135 DNA sequence SEQ ID NO:2.  
 PN EP1386966-A1.  
 PD 04-FEB-2004.  
 PA (LIBR-) LIBRAGEN.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 31.25%  
 Query Match: 6.44%  
 RESULT 1422  
 ID AAD54230 standard; DNA; 50543 BP.  
 DE Streptomyces amphibiosporus lactimidomycin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 39.06%  
 Best Local Similarity: 26.18%  
 Query Match: 6.44%  
 RESULT 1423  
 ID AAC55842 standard; DNA; 53500 BP.  
 DE Complete nucleotide sequence of the mitomycin biosynthetic genes.  
 PN WO200053737-A2.  
 PD 14-SEP-2000.  
 PA (MINU) UNIV MINNESOTA.  
 PA (SHER/) SHERMAN D H.  
 PA (MAOY/) MAO Y.  
 PA (VARO/) VAROGLU M.  
 PA (HENM/) HE M.  
 PA (SHEL/) SHELDON P C.  
 Percent Similarity: 34.74%  
 Best Local Similarity: 25.96%  
 Query Match: 6.44%  
 RESULT 1424  
 ID ADE10261 standard; DNA; 53500 BP.  
 DE S. lavendulae mitomycin biosynthetic genes complete sequence.  
 PN US2003134398-A1.  
 PD 17-JUL-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (MAOY/) MAO Y.  
 PA (VARO/) VAROGLU M.  
 PA (HENM/) HE M.  
 PA (SHEL/) SHELDON P.  
 Percent Similarity: 34.74%  
 Best Local Similarity: 25.96%  
 Query Match: 6.44%  
 RESULT 1425  
 ID AAF28545 standard; DNA; 62909 BP.  
 DE Genomic fragment #32.  
 PN WO200078968-A2.  
 PD 28-DEC-2000.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 44.26%  
 Best Local Similarity: 27.87%  
 Query Match: 6.44%  
 RESULT 1426  
 ID ACC45150 standard; DNA; 96649 BP.  
 DE Human NAC nucleotide sequence SEQ ID NO:10.  
 PN WO2003024988-A1.  
 PD 27-MAR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 RESULT 1427  
 Percent Similarity: 32.86%  
 Best Local Similarity: 20.86%  
 Query Match: 6.44%

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RESULT 1428
Percent Similarity: 32.86%
Best Local Similarity: 20.86%
Query Match: 6.44%
Indels: 129
Conservative: 42
Mismatches: 106
Indels: 129

ID ADT48119 standard; cDNA; 771 BP.
DE Bacterial polynucleotide #22870.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 35.09%
Best Local Similarity: 21.51%
Query Match: 6.40%
Indels: 100
Conservative: 36
Mismatches: 72
Indels: 100

RESULT 1430
ID ABD07574 standard; DNA; 822 BP.
DE Pseudomonas aeruginosa polynucleotide #6178.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.59%
Best Local Similarity: 26.48%
Query Match: 6.40%
Indels: 78
Conservative: 29
Mismatches: 105
Indels: 78

RESULT 1431
ID ADT42845 standard; cDNA; 855 BP.
DE Bacterial polynucleotide #17596.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 38.33%
Best Local Similarity: 25.42%
Query Match: 6.40%
Indels: 50
Conservative: 31
Mismatches: 98
Indels: 50

RESULT 1432
ID AAN70355 standard; cDNA to mRNA; 909 BP.
DE Sequence encoding AA sequence (III) of a polypeptide having human
DE haematopoietic cell growth potentiating factor (HCGPF) activity.
PN EP232707-A.
PD 19-AUG-1987.
PA (AJIN ) AJINOMOTO KK.
Percent Similarity: 38.58%
Best Local Similarity: 27.17%
Query Match: 6.40%
Indels: 63
Conservative: 29
Mismatches: 94
Indels: 63

RESULT 1433
ID ADS59940 standard; cDNA; 921 BP.
DE Bacterial polynucleotide #11927.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 36.62%
Best Local Similarity: 23.24%
Query Match: 6.40%
Indels: 78
Conservative: 38
Mismatches: 102
Indels: 78

RESULT 1434
ID ADC26975 standard; DNA; 942 BP.
DE Sorangium cellulosum tmba gene cluster ORF 3 DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Percent Similarity: 40.50%
Best Local Similarity: 27.50%
Query Match: 6.40%
Indels: 48
Conservative: 26
Mismatches: 73
Indels: 48

RESULT 1435
ID ADJ39859 standard; cDNA; 1030 BP.
DE

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DE Plant cDNA #859.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 34.15%
Best Local Similarity: 24.39%
Query Match: 6.40%
Indels: 106
Conservative: 28
Mismatches: 83
Indels: 106

RESULT 1436
ID AAC74893 standard; cDNA; 1119 BP.
DE Human ORFX ORF448 polynucleotide sequence SEQ ID NO:895.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 37.75%
Best Local Similarity: 26.51%
Query Match: 6.40%
Indels: 69
Conservative: 28
Mismatches: 86
Indels: 69

RESULT 1437
ID ABD08503 standard; DNA; 1221 BP.
DE Pseudomonas aeruginosa polynucleotide #7107.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.12%
Best Local Similarity: 24.08%
Query Match: 6.40%
Indels: 90
Conservative: 36
Mismatches: 101
Indels: 90

RESULT 1438
ID ADI21915 standard; cDNA; 1368 BP.
DE Novel human protein cDNA #174.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 35.80%
Best Local Similarity: 26.46%
Query Match: 6.40%
Indels: 61
Conservative: 24
Mismatches: 104
Indels: 61

RESULT 1439
ID ABD10627 standard; DNA; 1488 BP.
DE Pseudomonas aeruginosa polynucleotide #9231.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 34.20%
Best Local Similarity: 26.94%
Query Match: 6.40%
Indels: 67
Conservative: 14
Mismatches: 60
Indels: 67

RESULT 1440
ID ABT19078 standard; DNA; 1581 BP.
DE Aspergillus fumigatus essential gene #1436.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.47%
Best Local Similarity: 21.37%
Query Match: 6.40%
Indels: 82
Conservative: 30
Mismatches: 83
Indels: 82

RESULT 1441
ID AAQ92784 standard; cDNA; 1906 BP.
DE Mullerian inhibiting substance cDNA.
PN US5427780-A.
PD 27-JUN-1995.
PA (BIOJ ) BIOGEN INC.
PA (GEO ) GEN HOSPITAL CORP.
Percent Similarity: 32.41%
Best Local Similarity: 24.69%
Query Match: 6.40%
Indels: 107
Conservative: 25
Mismatches: 112
Indels: 107

RESULT 1442

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DE	Human bone marrow expressed single exon probe	SEQ ID NO: 14327.
FN	W0200157276-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1451		
ID	AAK14023 standard; DNA; 2144 BP.	
DE	Human brain expressed single exon probe	SEQ ID NO: 14014.
FN	W0200157275-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1452		
ID	ABS39357 standard; DNA; 2144 BP.	
DE	Human liver single exon probe, SEQ ID No 14347.	
FN	W0200157273-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1453		
ID	AA106275 standard; DNA; 2144 BP.	
DE	Probe #6266 used to measure gene expression in human breast sample.	
FN	W0200157270-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1454		
ID	AS13864 standard; DNA; 2144 BP.	
DE	Human genome-derived single exon probe ORF from lung SEQ ID No 13855.	
FN	W0200186003-A2.	
PD	15-NOV-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1455		
ID	ACN43048 standard; cDNA; 2155 BP.	
DE	Human diagnostic and therapeutic polynucleotide SEQ ID NO:1923.	
FN	W02004023973-A2.	
PD	23-MAR-2004.	
PA	(INCY-) INCYTE CORP.	
Percent Similarity:	38.35%	Conservative: 27
Best Local Similarity:	28.67%	Mismatches: 95
Query Match:	6.40%	Indels: 78
RESULT 1456		
ID	AA161256 standard; cDNA; 2174 BP.	
DE	Human polynucleotide SEQ ID NO 5245.	
FN	W0200153312-A1.	
PD	26-JUL-2001.	
PA	(HYSE-) HYSEQ INC.	
Percent Similarity:	30.69%	Conservative: 12
Best Local Similarity:	26.35%	Mismatches: 87
Query Match:	6.40%	Indels: 105
RESULT 1457		
ID	ADG91053 standard; DNA; 2280 BP.	
DE	Hepatic specific nucleic acid encoding sequence #242.	
FN	W0200306877-A2.	
PD	14-AUG-2003.	
PA	(DIAD-) DIADEXUS INC.	
Percent Similarity:	42.75%	Conservative: 36
Best Local Similarity:	29.71%	Mismatches: 85
Query Match:	6.40%	Indels: 74
RESULT 1458		
ID	ADG91055 standard; DNA; 2321 BP.	
DE	Hepatic specific nucleic acid encoding sequence #244.	

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PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1459
ID ADT47024 standard; cDNA; 2412 BP.
DE Bacterial polynucleotide #21775.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 41.11%
Best Local Similarity: 27.41%
Mismatches: 87
Indels: 72
Query Match: 6.40%
RESULT 1460
ID ADG91049 standard; DNA; 2457 BP.
DE Hepatic specific nucleic acid encoding sequence #238.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1461
ID ACA2329 standard; DNA; 2463 BP.
DE Prokaryotic essential gene #2396.
PN WO2003066877-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.65%
Best Local Similarity: 26.35%
Mismatches: 117
Indels: 94
Query Match: 6.40%
RESULT 1462
ID ADG91048 standard; DNA; 2489 BP.
DE Hepatic specific nucleic acid encoding sequence #237.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1463
ID ADI2554 standard; DNA; 2517 BP.
DE Synthetic 5' nuclease DNA SEQ ID 107.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 38.28%
Best Local Similarity: 24.48%
Mismatches: 102
Indels: 79
Query Match: 6.40%
RESULT 1464
ID ADG91047 standard; DNA; 2520 BP.
DE Hepatic specific nucleic acid encoding sequence #236.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1465
ID ADG91054 standard; DNA; 2641 BP.
DE Hepatic specific nucleic acid encoding sequence #243.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1466
ID ABD17161 standard; DNA; 2814 BP.
DE Pseudomonas aeruginosa polynucleotide #15765.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 33.65%
Best Local Similarity: 26.35%
Mismatches: 117
Indels: 94
Query Match: 6.40%
RESULT 1467
ID ABD08894 standard; DNA; 3012 BP.
DE Pseudomonas aeruginosa polynucleotide #7498.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.86%
Best Local Similarity: 24.15%
Mismatches: 92
Indels: 57
Query Match: 6.40%
RESULT 1468
ID ACC77568 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1469
ID ACC77580 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1470
ID ACC77561 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 42.09%
Best Local Similarity: 26.62%
Mismatches: 109
Indels: 53
Query Match: 6.40%
RESULT 1471
ID ACC77598 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.62%
Best Local Similarity: 24.83%
Mismatches: 101
Indels: 79
Query Match: 6.40%
RESULT 1472
ID ACC77839 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1473
ID ACC77780 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.62%
Best Local Similarity: 25.17%
Mismatches: 101
Indels: 79
Query Match: 6.40%
RESULT 1474

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ID ACC77777 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 38.62%  
Best Local Similarity: 25.17%  
Query Match: 6.40%  
Conservative: 39  
Mismatches: 101  
Indels: 79  
RESULT 1475  
ID ABD17264 standard; DNA; 3357 BP.  
DE Pseudomonas aeruginosa polynucleotide #15868.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 33.65%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 117  
Indels: 94  
RESULT 1476  
ID ADL45191 standard; DNA; 3574 BP.  
DE Human ovarian cancer DNA marker #19081.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Percent Similarity: 36.09%  
Best Local Similarity: 23.91%  
Query Match: 6.40%  
Conservative: 28  
Mismatches: 73  
Indels: 74  
RESULT 1477  
ID AAX87412 standard; cDNA; 3607 BP.  
DE Hepatocellular carcinoma marker gene L4 cDNA.  
PN WO9939200-A1.  
PD 05-AUG-1999.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1478  
ID AAI59470 standard; cDNA; 3613 BP.  
DE Human polynucleotide SEQ ID NO 1673.  
PN WO200153312-A1.  
PD 26-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1479  
ID ADQ86127 standard; cDNA; 4093 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2999.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1480  
ID ADE83409 standard; DNA; 4134 BP.  
DE Rat gene M73049, SEQ ID NO 11004.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Percent Similarity: 35.62%  
Best Local Similarity: 25.75%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 94  
Indels: 56  
RESULT 1481  
ID ADH76479 standard; DNA; 11364 BP.  
DE Chimeric pPCR-GalV-1 plasmid DNA sequence.  
PN FR2832424-A1.  
PD 23-MAY-2003.  
PA (GENE-) GENETHON III.  
Percent Similarity: 35.31%  
Best Local Similarity: 24.42%  
Query Match: 6.40%  
Conservative: 33  
Mismatches: 91

Query Match: 6.40%  
Indels: 105  
RESULT 1482  
ID ABA20357 standard; DNA; 11585 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12688.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1483  
ID AAH48620 standard; DNA; 16951 BP.  
DE Human fascin DNA fragment SEQ ID 72.  
PN WO200151631-A2.  
PD 19-JUL-2001.  
PA (RESK/) RESKE-KUNZ A.  
PA (ROSS/) ROSS X.  
PA (ROSS/) ROSS R.  
PA (BROS/) BROS M.  
Percent Similarity: 31.43%  
Best Local Similarity: 23.49%  
Query Match: 6.40%  
Conservative: 25  
Mismatches: 98  
Indels: 118  
RESULT 1484  
ID AAH48622 standard; DNA; 16951 BP.  
DE Human fascin DNA fragment #2.  
PN WO200151631-A2.  
PD 19-JUL-2001.  
PA (RESK/) RESKE-KUNZ A.  
PA (ROSS/) ROSS X.  
PA (ROSS/) ROSS R.  
PA (BROS/) BROS M.  
Percent Similarity: 31.43%  
Best Local Similarity: 23.49%  
Query Match: 6.40%  
Conservative: 25  
Mismatches: 98  
Indels: 118  
RESULT 1485  
ID AAF30757 standard; DNA; 47981 BP.  
DE Micromonospora megalomicea megalomicin biosynthetic gene cluster.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 34.93%  
Best Local Similarity: 23.92%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 88  
Indels: 48  
RESULT 1487  
ID AAF14299 standard; cDNA; 637 BP.  
DE Aspergillus oryzae EST SEQ ID NO:6822.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 36.49%  
Best Local Similarity: 25.12%  
Query Match: 6.37%  
Conservative: 24  
Mismatches: 59  
Indels: 75  
RESULT 1488  
ID ABZ37810 standard; DNA; 810 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 209.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 39.04%  
Best Local Similarity: 27.63%  
Query Match: 6.37%  
Conservative: 26  
Mismatches: 84  
Indels: 56  
RESULT 1489  
ID ABZ40942 standard; DNA; 810 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 6473.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 39.04%  
Best Local Similarity: 27.63%  
Query Match: 6.37%  
Conservative: 26  
Mismatches: 84  
Indels: 56  
RESULT 1490

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ID ABD14325 standard; DNA; 909 BP.
DE Pseudomonas aeruginosa polynucleotide #12929.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 32.30%
Best Local Similarity: 25.77%
Query Match: 6.37%
Conservative: 19
Mismatch: 97
Indels: 100
RESULT 1491
ID ABZ80091 standard; cDNA; 930 BP.
DE Synecococcus methyltransferase encoding cDNA SEQ ID NO:44.
PN WO2003016482-A2.
PD 27-FEB-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Percent Similarity: 35.20%
Best Local Similarity: 26.53%
Query Match: 6.37%
Conservative: 17
Mismatch: 61
Indels: 66
RESULT 1492
ID ABZ37722 standard; DNA; 981 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 33.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 39.04%
Best Local Similarity: 27.63%
Query Match: 6.37%
Conservative: 26
Mismatch: 84
Indels: 56
RESULT 1493
ID ABZ41892 standard; DNA; 1023 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 8373.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 39.04%
Best Local Similarity: 27.63%
Query Match: 6.37%
Conservative: 26
Mismatch: 84
Indels: 56
RESULT 1494
ID ACA25487 standard; DNA; 1221 BP.
DE Prokaryotic essential gene #7144.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 35.58%
Best Local Similarity: 24.34%
Query Match: 6.37%
Conservative: 30
Mismatch: 78
Indels: 94
RESULT 1495
ID ABD10094 standard; DNA; 1269 BP.
DE Pseudomonas aeruginosa polynucleotide #8698.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.59%
Best Local Similarity: 23.68%
Query Match: 6.37%
Conservative: 37
Mismatch: 97
Indels: 69
RESULT 1496
ID ABA21155 standard; DNA; 1695 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13486.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.98%
Best Local Similarity: 27.66%
Query Match: 6.37%
Conservative: 10
Mismatch: 92
Indels: 34
RESULT 1497
ID AAS30164 standard; DNA; 1695 BP.
DE Human lung antigen genomic DNA #234.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.98%
Best Local Similarity: 27.66%
Query Match: 6.37%
Conservative: 10
Mismatch: 92
Indels: 34
RESULT 1498
ID ADB33501 standard; DNA; 1695 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 428.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.98%
Best Local Similarity: 27.66%
Query Match: 6.37%
Conservative: 10
Mismatch: 92
Indels: 34
RESULT 1499
ID ABD10477 standard; DNA; 1944 BP.
DE Pseudomonas aeruginosa polynucleotide #9081.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.59%
Best Local Similarity: 23.68%
Query Match: 6.37%
Conservative: 37
Mismatch: 97
Indels: 69
RESULT 1500
ID ADT45918 standard; cDNA; 1944 BP.
DE Bacterial polynucleotide #20669.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 39.85%
Best Local Similarity: 27.82%
Query Match: 6.37%
Conservative: 32
Mismatch: 74
Indels: 87

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 21:20:51 ; Search time 4655 Seconds

(without alignments)  
2727.232 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

Sequence: 1 MTQVPRLSVPRALALGSA.....VRVYISLLPLDGLTLAFKI 262

Scoring table:

	Xgapop 10.0	Xgapext 0.5
Xgapop 10.0	Ygapext 0.5	
Ygapop 6.0	Fgapext 7.0	
Delop 6.0	Delext. 7.0	

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-DB=GenEmbl -QMT=fastax -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blgsum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10017407 @CGN 1.1 4200 @runat.19042005.142533.29467 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1343	100.0	789	6	CQ721501 Sequence
2	1343	100.0	789	6	AX338456 Sequence
3	1343	100.0	913	9	BC023663 Homo sapi
4	1343	100.0	985	6	BD222712 Human sig

5	1343	100.0	989	6	AX201342 Sequence
6	1343	100.0	989	6	AX697237 Sequence
7	1343	100.0	989	9	AY358476 Homo sapi
8	1343	100.0	1037	6	AX338454 Sequence
9	1343	100.0	1041	9	BC047774 Homo sapi
10	1337	99.6	988	9	AK074421 Homo sapi
11	1156	86.1	946	10	BC049670 Mus muscu
12	1028	76.5	38679	9	AL390034 Human DNA
13	1028	76.5	169612	2	AC027393 Homo sapi
14	870.5	64.8	89888	2	AY294423 3
15	870.5	64.8	161371	10	AC132590 Mus muscu
16	850.5	63.3	228354	2	AC137429 Rattus no
17	850.5	63.3	266634	2	AC123487 Rattus no
18	722	53.8	110000	2	AC105718 3
19	676.5	50.4	237829	2	AC120475
20	520	38.7	237221	1	AP003599
21	507.5	37.8	157428	10	AL606832 Mouse DNA
22	507.5	37.8	209643	10	AC080018 Mus muscu
23	484	36.0	300465	1	AE016962 Cxiella
24	477.5	35.6	110000	1	CR628337 25
25	474.5	35.3	2955	1	AF075724 Legionell
26	474.5	35.3	110000	1	AE017354 25
27	469.5	35.0	110000	1	CR628336 25
28	453	33.7	11171	6	CQ801141
29	450.5	33.5	10882	1	AE002493
30	450.5	33.5	349980	6	AX044032 Sequence
31	445.5	33.2	304282	1	AE016910 Chromobac
32	443	33.0	329861	1	MM522491
33	438.5	32.7	14100	1	MXU24657
34	438	32.6	675	6	CQ801150 Sequence
35	436	32.5	1210	8	AK063541 Oryza sat
36	431.5	32.1	10840	1	AE004550 Pseudomon
37	425.5	31.7	2381	1	STWMDMC
38	425.5	31.7	2381	1	EO6690 DNA encodin
39	424	31.6	663	12	AY657514 Synthetic
40	413	30.8	1218	6	AX146637 Sequence
41	409.5	30.5	69644	1	AY179507 Streptomy
42	408	30.4	1167	8	ZMA242981 Zea mays
43	405.5	30.2	980	6	AR236704 Sequence
44	405	30.2	134199	1	SYCSLRF
45	401	29.9	891	6	AR236694 Sequence
46	398.5	29.7	744	6	CQ760958 Sequence
47	398.5	29.7	744	6	AX259371 Sequence
48	398.5	29.7	966	6	MSU20736
49	398.5	29.7	1906	6	CQ760964 Sequence
50	398	29.6	837	8	AY094008 Arabidops
51	398	29.6	1068	8	EG12228 E.gunnii m
52	398	29.6	1107	8	AY070483 Arabidops
53	396	29.5	783	6	AX654276 Sequence
54	396	29.5	976	8	AB110168 Oryza sat
55	396	29.5	996	8	AK104326 Oryza sat
56	396	29.5	1052	8	AK065744 Oryza sat
57	396	29.5	1058	6	AR236699 Sequence
58	396	29.5	1096	8	AK104801 Oryza sat
59	396	29.5	1098	8	AK071482 Oryza sat
60	394	29.3	1078	6	AR236714 Sequence
61	394	29.3	1078	8	BT009389 Triticum
62	394	29.3	188267	2	AC137230 Rattus no
63	393	29.3	1006	8	AF046122 Eucalyptu
64	393	29.3	1338	6	AX654529 Sequence
65	392.5	29.2	962	6	AR236705 Sequence
66	392.5	29.2	1023	6	AR236706 Sequence
67	392.5	29.2	1895	8	AK106735 Oryza sat
68	391.5	29.2	780	6	CQ804646 Sequence
69	391.5	29.2	780	6	CQ805684 Sequence
70	391.5	29.2	780	8	AY143979 Arabidops
71	391.5	29.2	815	8	AY081457 Arabidops
72	391.5	29.2	976	8	VVCCOAMT
73	391.5	29.2	999	8	AY062630 Arabidops
74	391.5	29.2	1026	8	AY057554 Arabidops
75	389	29.0	997	6	AR236700 Sequence
76	388.5	28.9	1025	8	PBTJAJ4894
77	387.5	28.9	939	8	PBTJAJ4896

78	387.5	28.9	963	8	AY620245	Ammi maji	151	353.5	26.3	1152	8	AY279032	Zea mays
79	387.5	28.9	1049	8	PBTAJ4895	AJ224895 Populus b	152	353	26.3	1180	6	AX798857	Sequence
80	387.5	28.9	1258	8	PUMCCOAMT	M69184 Petroselinu	153	351.5	26.2	1466	8	AK065515	Oryza sat
81	387	28.8	953	6	AR236716	Sequence	154	350.5	26.1	1136	8	AY279034	Zea mays
82	387	28.8	953	8	BT009334	Sequence	155	350.5	26.1	1181	6	AX798855	Sequence
83	386.5	28.8	967	6	AR225249	Sequence	156	350.5	26.1	1181	8	AY279005	Zea mays
84	386.5	28.8	1046	8	PTU27116	Sequence	157	350.5	26.1	1181	8	AY279024	Zea mays
85	386	28.7	798	6	AX660925	Sequence	158	350.5	26.1	1181	8	AY279026	Zea mays
86	386	28.7	1012	6	BD224370	Materials	159	349.5	26.0	300299	1	AE017288	Leptospir
87	386	28.7	1012	6	AR216420	Sequence	160	348	25.9	77534	1	AF235504	Streptomy
88	386	28.7	1012	6	AR432822	Sequence	161	348	25.9	77536	6	BD235937	polyretid
89	386	28.7	1026	6	AR066484	Sequence	162	348	25.9	77536	6	AR271638	Sequence
90	386	28.7	1026	6	AR074097	Sequence	163	348	25.9	77536	6	AR564393	Sequence
91	386	28.7	1026	6	AR143609	Sequence	164	347.5	25.9	706	8	PBA130841	Sequence
92	386	28.7	1026	6	BD224282	Sequence	165	346	25.8	1013	8	SLASADEN	L22203 Stellaria l
93	386	28.7	1026	6	AR216332	Sequence	166	345.5	25.7	10029	1	AE011228	Leptospir
94	386	28.7	1026	6	AR432734	Sequence	167	345	25.7	890	8	AY145521	Mesembrya
95	386	28.7	1026	6	BD005645	Materials	168	345	25.7	1145	8	AY279031	Zea mays
96	386	28.7	1026	6	AR236712	Sequence	169	345	25.7	1150	8	AY279012	Zea mays
97	386	28.7	1118	8	BT009186	Sequence	170	345	25.7	1150	8	AY279013	Zea mays
98	386	28.7	1146	6	AR236695	Sequence	171	345	25.7	1150	8	AY279030	Zea mays
99	385.5	28.7	726	8	AF240466	Populus t	172	345	25.7	1150	8	AY279033	Zea mays
100	385.5	28.7	931	6	AR236702	Sequence	173	345	25.7	1150	8	AY279035	Zea mays
101	385	28.7	1136	8	ZMA242380	Sequence	174	343	25.5	1206	8	AY279008	Zea mays
102	384.5	28.6	1033	8	AY088577	Arabidops	175	343	25.5	1209	8	AY279028	Zea mays
103	384	28.6	783	6	AX654528	Sequence	176	343	25.5	1222	8	AY279029	Zea mays
104	384	28.6	1149	8	AK061757	Oryza sat	177	341	25.4	982	6	AR236709	Sequence
105	383.5	28.6	1016	8	NTCCOAMT	Z56282 N.tabacum m	c 178	340	25.3	82746	1	AF453501	Actinosyn
106	383.5	28.6	1023	8	AB061268	Solanum t	179	338	25.2	1227	8	NT282982	Nicotina ta
107	383.5	28.6	1057	8	AR236696	Sequence	180	337.5	25.1	1451	8	AY279004	Zea mays
108	382.5	28.5	929	6	AR236703	Sequence	181	337	25.1	1182	8	AY279009	Zea mays
109	381	28.4	1049	6	AR236715	Sequence	182	336.5	25.1	1434	8	AY279014	Zea mays
110	379.5	28.3	845	6	AR225248	Sequence	183	335	24.9	1463	8	AY279016	Zea mays
111	379.5	28.3	1258	6	A22706	Cafreoyl-Co	184	335	24.9	1464	8	AY279015	Zea mays
112	379	28.2	1112	6	AX660732	Sequence	185	333	24.8	1172	8	AY279006	Zea mays
113	377.5	28.1	959	8	AB108479	Oryza sat	186	333	24.8	1172	8	AY279007	Zea mays
114	377	28.1	875	8	AB158406	Triticum	187	333	24.8	1172	8	AY279025	Zea mays
115	377	28.1	1018	8	BT009093	Triticum	188	333	24.8	1172	8	AY279027	Zea mays
116	376	28.0	909	8	BT013139	Lycopersi	189	333	24.8	1442	8	AY279019	Zea mays
117	376	28.0	923	6	AR236697	Sequence	190	333	24.8	1444	8	AY279017	Zea mays
118	373.5	27.8	816	8	AF022775	Nicotiana	191	333	24.8	1445	8	AY279018	Zea mays
119	373.5	27.8	870	6	AR225246	Sequence	192	333	24.8	1445	8	AY279022	Zea mays
120	373.5	27.8	950	8	NTU38612	Nicotiana t	193	332.5	24.8	591	8	AY607699	Apium Gra
121	373.5	27.8	895	8	NTU62736	Nicotiana t	194	332.5	24.8	1438	8	AY279021	Zea mays
122	373.5	27.8	1003	8	NTU62735	Nicotiana t	195	332.5	24.8	1451	8	AY279020	Zea mays
123	373.5	27.8	1014	8	NTU62734	Nicotiana t	196	331	24.6	908	8	AY500159	Corchorus
124	372.5	27.7	811	6	AR225247	Sequence	197	331	24.6	1298	8	AY323254	Zea mays
125	372.5	27.7	1104	8	AF053553	Mesembrya	198	331	24.6	1298	8	AY323255	Zea mays
126	372.5	27.7	1258	6	AR122016	Sequence	199	331	24.6	1298	8	AY323258	Zea mays
127	372.5	27.7	1258	6	I92681	Sequence 1	200	331	24.6	1298	8	AY323259	Zea mays
128	369	27.5	730	8	AY056313	Arabidops	201	331	24.6	1298	8	AY323260	Zea mays
129	369	27.5	956	8	AF360317	Arabidops	202	331	24.6	1298	8	AY323261	Zea mays
130	369	27.5	1098	8	AY128822	Arabidops	203	331	24.6	1298	8	AY323263	Zea mays
131	369	27.5	1185	8	AY087981	Arabidops	204	331	24.6	1298	8	AY323265	Zea mays
132	369	27.5	1201	8	AY093172	Arabidops	205	331	24.6	1536	8	AY323241	Zea mays
133	369	27.5	1252	6	Q0857676	Sequence	206	331	24.6	1536	8	AY323243	Zea mays
134	368.5	27.4	744	8	AF327458	Populus a	207	331	24.6	1536	8	AY323245	Zea mays
135	368.5	27.4	1013	8	AF168780	Eucalyptu	208	331	24.6	1536	8	AY323247	Zea mays
136	368.5	27.4	1018	6	AR236711	Sequence	209	331	24.6	1536	8	AY323248	Zea mays
137	367.5	27.3	835	6	AX660084	Sequence	210	331	24.6	1536	8	AY323250	Zea mays
138	366	27.3	326	6	AX407985	Sequence	211	331	24.6	1537	8	AY323251	Zea mays
139	365	27.2	1232	8	AF036095	Pinus tae	212	330.5	24.6	772	8	FVAJ1447	Fragaria
140	365	27.2	153751	3	AC116551	Diclyostee	213	329.5	24.5	1153	8	AY279010	Zea mays
141	364.5	27.1	918	8	ZEUI3151	Zinnia eleg	214	327.5	24.4	1314	8	AY323253	Zea mays
142	364.5	27.1	1158	8	AY644637	Oryza sat	215	327.5	24.4	1314	8	AY323268	Zea mays
143	364.5	27.1	137354	8	AP000364	Oryza sat	216	327	24.3	1272	8	AY644636	Oryza sat
144	363.5	27.1	1116	8	AY644638	Oryza sat	217	327	24.3	105815	8	AP002536	Sequence
145	362	27.0	917	8	AY087244	Arabidops	218	327	24.3	156054	8	AB023482	Oryza sat
146	360.5	26.8	730	8	AF060180	Nicotiana	219	326	24.3	1311	8	AY323252	Zea mays
147	360	26.8	729	6	AX507705	Sequence	220	326	24.3	1311	8	AY323257	Zea mays
148	354	26.4	912	6	AR236707	Sequence	221	326	24.3	1311	8	AY323264	Zea mays
149	353.5	26.3	1136	8	AY279011	Zea mays	222	326	24.3	1311	8	AY323267	Zea mays
150	353.5	26.3	1152	8	AY279023	Zea mays	223	326	24.3	1549	8	AY323249	Zea mays

224	324	24.1	833	8	AY088274	AY088274 Arabidops	297	224.5	16.7	760	6	BD272991	Materials
225	323	24.1	60090	1	U30252	U30252 Synchococc	298	224.5	16.7	760	6	AR216351	Sequence
226	320.5	23.9	1320	8	AY323271	AY323271 Zea mays	299	224.5	16.7	760	6	AR432753	Sequence
227	318.5	23.7	1309	8	AY323239	AY323239 Zea mays	300	224.5	16.7	760	6	BD005664	Materials
228	318.5	23.7	1309	8	AY323256	AY323256 Zea mays	301	224.5	16.7	300800	1	SC0939112	Streptomy
229	318.5	23.7	1309	8	AY323266	AY323266 Zea mays	302	224.5	16.7	534	6	AR236717	Sequence
230	318	23.7	1537	8	AY323242	AY323242 Zea mays	303	220.5	16.4	110000	1	CP00000118	Continuation (19 o
231	318	23.7	1546	8	AY323244	AY323244 Zea mays	304	220.5	16.4	110000	1	CP00000119	Continuation (20 o
232	317	23.6	1306	8	AY323238	AY323238 Zea mays	305	219.5	16.3	133649	2	BX927362	Danio rer
233	317	23.6	1306	8	AY323240	AY323240 Zea mays	306	219.5	16.3	261352	2	BX957311	Sequence
234	317	23.6	1306	8	AY323262	AY323262 Zea mays	307	218.5	16.3	101966	8	AE012563	Arabidops
235	317	23.6	1306	8	AY323270	AY323270 Zea mays	308	218	16.2	299986	1	AE017240	Mycobacte
236	317	23.6	1544	8	AY323246	AY323246 Zea mays	309	217.5	16.2	304282	1	AE016910	Chromobac
237	311.5	23.2	486	8	AY651026	AY651026 Boehmeria	310	215.5	16.0	622	8	AB076979	Avena sat
238	311.5	23.2	699	6	AX412281	AX412281 Sequence	311	215	16.0	110000	1	AP006618	26
239	311.5	23.2	699	6	AX412282	AX412282 Sequence	312	215	16.0	300425	1	AP005044	Streptomy
240	311.5	23.2	699	6	AX507044	AX507044 Sequence	313	214.5	16.0	292550	1	AP001513	Capillus
241	311.5	23.2	699	6	AX651360	AX651360 Sequence	314	207	15.4	528	6	AR236710	Sequence
242	309	23.0	256879	3	AC116982	AC116982 Dictyoste	315	204.5	15.2	1231	8	AF168778	Sequence
243	307	22.9	930	8	AB000408	AB000408 Populus k	316	204.5	15.2	288437	1	AE017270	Eucalyptu
244	307	22.9	1810	6	E09625	E09625 Streptomyce	317	204	15.2	110000	1	BX908798	21
245	307	22.9	3267	1	STMACYA	D30759 Streptomyce	318	202.5	15.1	110000	1	AE000516	02
246	307	22.9	50398	3	AC024771	AC024771 Caenorhab	319	202.5	15.1	341957	1	BX842572	02
247	307	22.9	206217	2	AC006754	AC006754 Caenorhab	320	202.5	15.1	343050	1	BX248334	02
248	305.5	22.7	965	8	ATHORF	L40031 Arabidops	321	202	15.0	399	6	BD224470	Materials
249	304.5	22.7	112369	8	AC136449	AC136449 Medicago	322	202	15.0	399	6	AR216520	Sequence
250	304.5	22.7	142064	2	AC148528	AC148528 Medicago	323	201.5	15.0	588	6	AR319743	Sequence
251	303.5	22.6	14105	1	AE000743	AE000743 Aquifex a	324	201.5	15.0	3705	8	ATH242988	Arabidops
252	302.5	22.5	94091	8	ATP28A23	AL021961 Arabidops	325	200.5	14.9	632	6	AR227195	Sequence
253	302.5	22.5	192861	8	ATCHRIV80	AL161584 Arabidops	326	196	14.6	83433	2	AP006501	12
254	299.5	22.3	1010	8	AB035144	AB035144 Citrus na	327	190	14.1	300150	1	AP004594	02
255	298.5	22.2	1075	6	BD224331	BD224331 Materials	328	185.5	13.8	13399	1	AE013088	Sequence
256	298.5	22.2	1075	6	BD224331	BD224331 Materials	329	185	13.8	50398	3	AC024771	Sequence
257	298.5	22.2	1075	6	AR216381	AR216381 Sequence	330	185	13.8	110000	1	BX571966	17
258	298.5	22.2	1075	6	BD432783	BD432783 Sequence	331	185	13.8	206217	2	AC006754	02
259	298.5	22.2	1075	6	BD005694	BD005694 Materials	332	184.5	13.7	265006	1	AE017259	Sequence
260	298	22.2	3072	8	PTR223620	AY232620 Populus t	333	183.5	13.7	287428	1	AE017280	Sequence
261	297.5	22.2	1308	8	AY579076	AY579076 Broussonet	334	183	13.6	594	6	AR216431	Sequence
262	294	21.9	1529	8	AY579076	AY579076 Broussonet	335	183	13.6	594	6	AR216431	Sequence
263	291	21.7	1074	6	BD244145	BD244145 Materials	336	183	13.6	594	6	AR432833	Sequence
264	291	21.7	1074	6	BD244145	BD244145 Materials	337	181.5	13.5	505	6	AR236708	Sequence
265	291	21.7	1074	6	AR216380	AR216380 Sequence	338	180.5	13.4	297850	1	AP006577	Gloeobact
266	291	21.7	1074	6	AR432782	AR432782 Sequence	339	180	13.4	607	6	BD074114	Sequence
267	291	21.7	1074	6	BD005693	BD005693 Materials	340	180	13.4	607	6	BD224299	Materials
268	290.5	21.6	2000	6	AX461218	AX461218 Sequence	341	180	13.4	607	6	BD273001	Materials
269	290.5	21.6	89904	6	ATT25K17	AL049171 Arabidops	342	180	13.4	607	6	AR216349	Sequence
270	290.5	21.6	196286	8	ATCHRIV64	AL161564 Arabidops	343	180	13.4	607	6	AR432751	Sequence
271	287.5	21.4	1703	1	SYOPAPSA	M84476 Synchococc	344	180	13.4	607	6	BD005662	Materials
272	286.5	21.3	109519	6	AX195929	AX195929 Sequence	345	179	13.3	29255	6	CQ363728	Sequence
273	285	21.2	2983	8	AP09505	AP09505 Sequence 2	346	179	13.3	110000	1	AE017283	06
274	284	21.1	145828	8	AP005392	AP005392 Oryza sat	347	179	13.3	110000	1	AE017283	07
275	284	21.1	154188	8	AP005633	AP005633 Oryza sat	348	178.5	13.3	142001	8	ATF21F14	07
276	280	20.8	3162	8	PCCOAMT	Z33878 P. crispum g	349	178	13.3	584	6	AX660579	Sequence
277	280	20.8	6662	8	PCCOAMTR	Z54483 P. crispum g	350	178	13.3	110000	1	AP006618	49
278	279	20.7	651	6	AX196012	AX196012 Sequence	351	176.5	13.1	510	6	AR236698	02
279	277.5	20.7	3800	8	AX89904	AX89904 Sequence 1	352	176.5	13.1	600	6	AR236713	Sequence
280	277.5	20.7	3800	8	PTR223621	AY223621 Populus t	353	176.5	13.1	311000	1	SC0939122	Streptomy
281	276.5	20.6	343	6	AX400599	AX400599 Sequence	354	176	13.1	110000	1	CP000011	09
282	269	20.0	1944	1	AF145250	AF145250 Rhodother	355	176	13.1	110000	1	CP000011	10
283	266.5	19.8	8868	3	CEY32B12A	AL023834 Caenorhab	356	176	13.1	346357	1	BX842647	02
284	261.5	19.5	1673	8	AY6001140	AY6001140 Broussonet	357	175.5	13.1	320150	1	AP005033	Sequence
285	258	19.2	675	6	AR390021	AR390021 Sequence	358	174	13.0	296	6	BD224471	Materials
286	244.5	18.2	110000	1	AP006841	Continuation (52 o	359	174	13.0	296	6	AR216521	Sequence
287	244.5	18.2	347660	1	AP002994	AP002994 Mesorhizo	360	172.5	12.8	110000	1	AE017225	41
288	235.5	17.5	30029	1	AE017178	AE017178 Porphyrom	361	172.5	12.8	110000	1	AE017334	41
289	235.5	17.5	305961	1	AE016937	AE016937 Bacteroid	362	172.5	12.8	110000	1	AE017355	41
290	232.5	17.3	323	8	AF534905	AF534905 Coffea ca	363	172.5	12.8	110000	1	CP000001	42
291	232	17.3	607	8	AY098515	AY098515 Ananas co	364	172.5	12.8	110000	1	CR543861	12
292	229.5	17.1	536	8	AY161276	AY161276 Populus b	365	172.5	12.8	288814	1	AE017278	02
293	229.5	17.1	234545	5	BX470214	BX470214 Zebrafish	366	172.5	12.8	290029	1	AE017038	Sequence
294	228	17.0	105863	8	AC004133	AC004133 Genomic s	367	172	12.8	10445	1	AE014716	Sequence
295	224.5	16.7	760	6	AR074116	AR074116 Sequence	368	172	12.8	349980	6	AX492784	Sequence
296	224.5	16.7	760	6	BD224301	BD224301 Materials	369	172	12.8	349980	6	AX553951	Sequence

370	171.5	12.8	562	6	AR074144	Sequence	443	126	9.4	777	6	AX377804	Sequence
371	171.5	12.8	562	6	BD224329	Materials	444	125.5	9.3	705	6	CQ649678	Sequence
372	171.5	12.8	562	6	BD272987	Materials	445	125.5	9.3	20639	1	AE014228	Streptoco
373	171.5	12.8	562	6	AR216379	Sequence	446	125.5	9.3	349980	6	CQ655069	Sequence
374	171.5	12.8	562	6	AR432781	Sequence	447	125.5	9.3	349980	6	AX954529	Sequence
375	171.5	12.8	562	6	BD005692	Materials	448	124.5	9.3	708	6	AX607661	Sequence
376	171.5	12.8	301332	1	AE017012	Bacillus	c 449	124.5	9.3	6641	6	AX602145	Sequence
377	170	12.7	75216	6	AX704275	Sequence	c 450	124.5	9.3	167050	1	SAG766847	Streptoco
378	170	12.7	110000	1	AE000516	Continuation (14 o	c 451	124.5	9.3	292200	1	SC0939129	Streptomyc
379	170	12.7	299450	1	BD248338	Sequence	452	124	9.2	1605	1	AF016233	Enterococ
380	170	12.7	349306	1	AX842575	Mycobacte	453	124	9.2	110000	1	AE017225	22
381	169	12.6	1289	6	AX414722	Sequence	454	124	9.2	110000	1	AE017334	22
382	169	12.6	240050	1	AL591979	Listeria	455	124	9.2	110000	1	AE017355	23
383	169	12.6	349980	6	AX641668	Sequence	456	124	9.2	293264	1	AE017031	Bacillus
384	169	12.6	349980	6	AX641669	Sequence	457	123	9.2	498	6	AR347999	Sequence
385	168.5	12.5	302325	1	AE017236	Mycobacte	c 458	123	9.2	3673	1	AF269748	Staphyloc
386	168	12.5	2233	6	AX416554	Sequence	c 459	123	9.2	3673	6	AR485702	Sequence
387	168	12.5	290507	1	AE017327	Listeria	c 460	123	9.2	3673	6	AX145066	Sequence
388	166.5	12.4	403	8	AY725190	Arachis h	c 461	123	9.2	300029	1	AE016748	Staphyloc
389	166.5	12.4	403	8	AY725191	Arachis h	462	122	9.1	201	11	BV202015	20798
390	166.5	12.4	403	8	AY725192	Arachis h	463	122	9.1	110000	1	CP000001	23
391	166.5	12.4	403	8	AY725193	Arachis h	464	121.5	9.0	711	6	AX568724	Sequence
392	166.5	12.4	403	8	AY725194	Arachis h	465	121.5	9.0	714	6	AR481634	Sequence
393	166	12.4	4560	1	LLVSPFEP	X99710 L.lactis OR	466	121.5	9.0	11309	6	CQ789017	Sequence
394	164.5	12.2	296750	1	AP003191	AP003191 Clostridi	467	121.5	9.0	11309	6	AR218876	Sequence
395	164	12.2	399	6	BD224469	Materials	468	121.5	9.0	11309	6	BD003788	Polynucle
396	164	12.2	399	6	AL216519	Sequence	469	121.5	9.0	11552	1	AE008462	Streptoco
397	164	12.2	33050	1	AL596168	Listeria	470	121.5	9.0	13378	1	AE007401	Streptoco
398	164	12.2	349980	6	AX413017	Sequence	471	121.5	9.0	111135	2	SPNEU1906	2
399	164	12.2	349980	6	AX417044	Sequence	472	121.5	9.0	349980	6	AX571762	Sequence
400	164	12.2	349980	6	AX417045	Sequence	473	121	9.0	518	6	CQ720861	Sequence
401	162.5	12.1	702	6	AR320113	Sequence	c 474	120	8.9	301550	1	AP003134	Staphyloc
402	162.5	12.1	12898	1	AE006403	Lactococ	c 475	120	8.9	303450	1	SC0939130	Streptomyc
403	162	12.1	13325	1	AE005016	Halobacte	c 476	120	8.9	346300	1	AP003362	Staphyloc
404	161.5	12.0	348450	1	MLEPRTN4	AL583920 Mycobacte	c 477	119.5	8.9	298050	1	BP321861	Nitrosomo
405	159.5	11.9	299550	1	AP001511	Bacillus	c 478	119	8.9	12014	1	AE010732	Methanosa
406	158	11.8	38675	1	MLU15180	U01580 Mycobacteri	479	118.5	8.8	1262	10	BC010402	Mus muscu
407	158	11.8	38675	6	AR345367	Sequence	480	118	8.8	507	6	AX207630	Sequence
408	158	11.7	110000	1	AE016822	Continuation (10 o	c 481	118	8.8	37768	3	U40414	Caenorhabdi
409	157	11.7	801	6	AR394036	Sequence	482	118	8.8	288404	1	AE017272	Bacillus
410	157	11.7	301278	1	AE015939	AE015939 Clostridi	483	116.5	8.7	10763	1	AE010544	Fusobacte
411	157	11.7	302132	1	AE016955	Enterococ	484	116	8.6	110000	1	AX571965	33
412	156	11.6	19024	6	BD193585	BD193585 Enterococ	485	115	8.6	639	6	BD163441	Novel pol
413	154	11.5	8367	1	AP400582	AP400582 Acinetoba	486	115	8.6	639	6	AX121324	Sequence
414	154	11.5	110000	1	CR543861	Continuation (15 o	487	115	8.6	769	6	AX771879	Sequence
415	150.5	11.2	81866	8	NC64C2	Continuation (6 of	c 488	115	8.6	333150	1	AP005277	Sequence
416	149.5	11.1	508	6	AR236701	BX294009 Neurospor	c 489	115	8.6	349459	1	AX927151	Corynebac
417	149.5	11.1	110000	1	AE017333	Continuation (28 o	c 490	115	8.6	349980	6	AX127146	Sequence
418	149.5	11.1	110000	1	CP000002	Continuation (28 o	c 491	114.5	8.5	2868	1	AB049411	Acinetoba
419	147	10.9	1433	8	AF168779	AF168779 Eucalyptu	c 492	114.5	8.5	143109	8	OSJN00224	Oryza sat
420	147	10.9	199173	1	BSUB0014	Z99117 Bacillus su	c 493	114.5	8.5	300750	1	AP005217	Corynebac
421	146.5	10.9	110000	1	AE017180	Continuation (6 of	494	114	8.5	636	6	AX617408	Sequence
422	145	10.8	1504	8	AY267760	AY267760 Fusarium	495	114	8.5	1255	10	AF076156	Mus muscu
423	144	10.7	300050	1	AP004599	AP004599 Oceanobac	496	114	8.5	1605	8	PAN245505	Podospora
424	141	10.5	957	5	BX930132	BX930132 Gallus ga	c 497	114	8.5	110000	1	AE000516	19
425	139	10.3	51454	1	AE004157	AE004157 Streptoco	c 498	114	8.5	110000	1	AX571857	16
426	139	10.3	310950	1	AP005143	AP005143 Streptoco	c 499	114	8.5	291050	1	AX248340	Mycobacte
427	137	10.2	115339	8	AP003940	AP003940 Oryza sat	c 500	114	8.5	333750	1	AP004827	Staphyloc
428	137	10.2	174478	8	AP005467	AP005467 Oryza sat	c 501	114	8.5	347496	1	AX842577	Mycobacte
429	136	10.1	705	6	CQ649680	CQ649680 Sequence	c 502	113.5	8.5	5514	6	CQ587772	Sequence
430	136	10.1	10844	1	AE010060	AE010060 Streptoco	c 503	112	8.3	2086	6	AX394673	Sequence
431	136	10.1	11615	1	AE006576	AE006576 Streptoco	504	112	8.3	7912	10	RNCATOMET	Z12651 R.norvegicu
432	136	10.1	110000	1	CP000003	Continuation (11 o	c 505	112	8.3	110000	1	AX571856	17
433	136	10.1	110000	1	CP000003	Continuation (12 o	c 506	112	8.3	300052	1	AE017232	Mycobacte
434	134	10.0	324050	1	AX251410	AX251410 Tropherym	507	112	8.3	300115	1	AP005076	Vibrio pa
435	134	10.0	324227	1	AE016852	AE016852 Tropherym	c 508	112	8.3	300750	1	AP005217	Corynebac
436	131	9.8	304262	1	AE017005	AE017005 Bacillus	c 509	111.5	8.3	110000	1	AE017282	28
437	130.5	9.7	12012	1	AE014908	AE014908 Streptoco	510	111	8.3	495	6	AR485101	Sequence
438	130	9.7	10398	1	AE011847	AE011847 Xanthomon	511	111	8.3	495	6	AX144317	Sequence
439	128	9.5	2316	6	AX207632	AX207632 Sequence	c 512	111	8.3	13715	6	AR354077	Sequence
440	127.5	9.5	10069	1	AE007678	AE007678 Clostridi	c 513	111	8.3	13715	6	AR353633	Sequence
441	126.5	9.4	534	6	AX433853	AX433853 Sequence	c 514	111	8.3	38494	6	AR345349	Sequence
442	126	9.4	777	6	AX207628	AX207628 Sequence	c 515	111	8.3	38503	1	MSGB1912CS	L01536 M. leprae g

c 516	110.5	8.2	301443	1	AE017239	AE017239 Mycobacte	589	102	7.6	1405	5	BC082476
c 517	110	8.2	236	6	BD224451	BD224451 Materials	c 590	102	7.6	1746	9	HSU14534
c 518	110	8.2	236	6	AR216501	AR216501 Sequence	c 591	102	7.6	1898	6	I46765
c 519	110	8.2	236	6	AR432903	AR432903 Sequence	c 592	102	7.6	2084	11	BV177077
c 520	110	8.2	509	11	BX784390	BX784390 Pinus pin	c 593	102	7.6	14138	1	AE004766
c 521	110	8.2	247910	1	AE017307	AE017307 Thermus t	c 594	102	7.6	14469	1	AE011498
c 522	109.5	8.2	348411	1	AP003007	AP003007 Mesorhizo	c 595	102	7.6	21540	10	AC115937
c 523	109	8.1	11847	1	AE001918	AE001918 Deinococc	c 596	102	7.6	301250	1	AP005950
c 524	109	8.1	213732	1	AE001862	AE001862 Deinococc	c 597	102	7.6	303550	1	SC0939118
c 525	108.5	8.1	1107	6	CQ812330	CQ812330 Sequence	c 598	102	7.6	305541	1	AE017290
c 526	108.5	8.1	1107	9	HUMCOMTA	M65212 Homo sapien	c 599	102	7.6	348068	1	BX572604
c 527	108.5	8.1	1213	9	BC011935	BC011935 Homo sapi	c 600	101.5	7.6	601	11	BV167609
c 528	108	8.0	320	4	AY340812	AY340812 Canis fam	c 601	101.5	7.6	2039	9	AK130031
c 529	108	8.0	10288	1	AE012905	AE012905 Chlorobab	c 602	101.5	7.6	2084	11	BV177509
c 530	108	8.0	120528	9	AP000812	AP000812 Homo sapi	c 603	101.5	7.6	2084	11	BV179316
c 531	108	8.0	132544	1	AF521085	AF521085 Streptomy	c 604	101.5	7.6	5600	8	AY673000
c 532	108	8.0	155922	2	AP002513	AP002513 Homo sapi	c 605	101.5	7.6	6658	8	AY673001S2
c 533	107.5	8.0	1206	6	AX774876	AX774876 Sequence	c 606	101.5	7.6	153875	9	AC003682
c 534	107.5	8.0	1206	9	HUMCOMTC	M58525 Homo sapien	c 607	101.5	7.6	188324	2	BX530094
c 535	107.5	8.0	1291	6	CQ716680	CQ716680 Sequence	c 608	101.5	7.6	189326	9	AC018462
c 536	107.5	8.0	139628	2	AC150112	AC150112 Gallus ga	c 609	101	7.5	1543	8	AK120652
c 537	107.5	8.0	166863	2	AC150140	AC150140 Gallus ga	c 610	101	7.5	1820	9	BC035516
c 538	107.5	8.0	250950	1	AP005335	AP005335 Vibrio vu	c 611	101	7.5	129778	8	AC091123
c 539	107.5	8.0	302174	1	AE017241	AE017241 Mycobacte	c 612	101	7.5	154625	2	BX323047
c 540	107.5	8.0	304490	1	AE016806	AE016806 Vibrio vu	c 613	101	7.5	163962	9	BS000233
c 541	107	7.9	10113	1	AE0110715	AE0110715 Methanosa	c 614	101	7.5	178158	8	AC084320
c 542	106.5	7.9	816	9	CR456997	CR456997 Homo sapi	c 615	101	7.5	348971	1	BX572594
c 543	105.5	7.9	873	9	CR456422	CR456422 Homo sapi	c 616	100.5	7.5	1447	5	BC049292
c 544	105.5	7.9	9463	1	SGRCTLUS	X95596 S.griseus c	c 617	100.5	7.5	1688	6	AC035537
c 545	105.5	7.9	11464	1	AE005915	AE005915 Caulobact	c 618	100.5	7.5	1888	6	E11457
c 546	105.5	7.9	110000	1	AE017282_18	Continuation (19 o	c 619	100.5	7.5	1815	6	AR477499
c 547	105.5	7.9	110000	1	BX571966_09	Continuation (10 o	c 620	100.5	7.5	1934	9	BC007790
c 548	105.5	7.9	347625	1	BX248356	BX248356 Corynebac	c 621	100.5	7.5	1979	6	AR035536
c 549	105.5	7.9	349354	1	BX640416	BX640416 Bordetell	c 622	100.5	7.5	1979	6	E11456
c 550	105.5	7.9	349354	1	AX394671	AX394671 Sequence	c 623	100.5	7.5	1987	6	AR448000
c 551	105	7.8	1457	6	AX394671	Continuation (15 o	c 624	100.5	7.5	2014	9	BC047750
c 552	105	7.8	110000	2	AP006502_14	Continuation (15 o	c 625	100.5	7.5	2070	9	BC074500
c 553	105	7.8	308050	1	SC0939124	AL939124 Streptomy	c 626	100.5	7.5	247151	2	AC126662
c 554	104.5	7.8	1895	8	AK108846	AK108846 Oryza sat	c 627	100	7.4	2734	8	AK067366
c 555	104.5	7.8	10878	1	AF272737	AF272737 Streptomy	c 628	100	7.4	6806	1	STMTN4556
c 556	104.5	7.8	148762	8	AP002843	AP002843 Oryza sat	c 629	100	7.4	7530	6	CQ848068
c 557	104.5	7.8	276289	1	AE017306	AE017306 Thermus t	c 630	100	7.4	8460	6	CQ847904
c 558	104	7.7	1628	10	AB010089S1	AB010089 Mus muscu	c 631	100	7.4	8460	6	I64893
c 559	104	7.7	158344	10	AL133401	AL133401 Mouse DNA	c 632	100	7.4	8460	9	HSU29344
c 560	104	7.7	180000	1	AF322012S1	AF322012 Bradyrhiz	c 633	100	7.4	10677	1	AE005967
c 561	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 634	100	7.4	10777	1	AV316747_1
c 562	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 635	100	7.4	126845	8	AP005244
c 563	104	7.7	299850	1	AP005949	AP005949 Bradyrhiz	c 636	100	7.4	145911	1	AP003014
c 564	103.5	7.7	1491	10	RATCATAA	M60753 R.norvegicu	c 637	100	7.4	164628	2	AC073646
c 565	103.5	7.7	1527	10	BC081850	BC081850 Rattus no	c 638	100	7.4	179937	2	AF546190
c 566	103.5	7.7	1540	10	RATCATAB	M60754 R.norvegicu	c 639	100	7.4	230146	2	AC134057
c 567	103.5	7.7	2138	1	STWSIGNA	L11648 Streptomyce	c 640	100	7.4	299991	1	AE016776
c 568	103.5	7.7	66669	1	AME16952	Y16952 Amycolatops	c 641	100	7.4	300450	1	AP005960
c 569	103.5	7.7	110000	2	LMFLCHR32_17	Continuation (18 o	c 642	99.5	7.4	3079	1	PDEMXXYZ
c 570	103.5	7.7	233050	1	AL627271	AL627271 Salmonell	c 643	99.5	7.4	3949	5	AF327372
c 571	103.5	7.7	300247	1	AE016837	AE016837 Salmonell	c 644	99.5	7.4	9088	5	AF327372
c 572	103	7.7	3307	8	AK110307	AK110307 Oryza sat	c 645	99.5	7.4	295500	1	AP005954
c 573	103	7.7	10732	1	AE0113407	AE0113407 Methanosa	c 646	99.5	7.4	300350	1	AP006574
c 574	103	7.7	11877	1	AE011683	AE011683 Xanthomon	c 647	99.5	7.4	339681	1	AP003009
c 575	103	7.7	44421	1	AY442951	AY442951 Agrobacte	c 648	99.5	7.4	348171	1	BX640412
c 576	103	7.7	64492	1	AB086653	AB086653 Streptomy	c 649	99	7.4	2010	6	CQ785960
c 577	103	7.7	109192	8	CNS08CCR	AL954153 Oryza sat	c 650	99	7.4	2010	9	HSU07132
c 578	102.5	7.6	1525	8	AF069951	AF069951 Enteromor	c 651	99	7.4	2030	6	I36667
c 579	102.5	7.6	2760	1	TAU62584	U62584 Thermus aqu	c 652	99	7.4	2503	6	I70211
c 580	102.5	7.6	3003	6	CQ845922	CQ845922 Sequence	c 653	99	7.4	2505	6	AR023937
c 581	102.5	7.6	3003	9	AK131436	AK131436 Homo sapi	c 654	99	7.4	2685	6	I15438
c 582	102.5	7.6	3978	6	CQ735548	BX648302 Homo sapi	c 655	99	7.4	2685	6	AX924362
c 583	102.5	7.6	5502	9	HSMB08450	AP004569 Pseudomon	c 656	99	7.4	7528	6	CQ729217
c 584	102.5	7.6	10245	8	AE0043568	AP0031568 Oryza sat	c 657	99	7.4	7536	9	AY451392
c 585	102.5	7.6	157424	8	AP003568	AP005961 Bradyrhiz	c 658	99	7.4	8461	6	CQ785963
c 586	102.5	7.6	298550	1	AP005961	AE017309 Desulfovi	c 659	99	7.4	8461	6	CQ785963
c 587	102.5	7.6	300129	1	AE017309	AE016932 Bacteroid	c 660	99	7.4	8461	6	CQ875346
c 588	102.5	7.6	300531	1	AE016932		c 661	99	7.4	8472	9	BC063242

BC082476 Xenopus 1  
 UI4534 Human orpha  
 I46765 Sequence 1  
 BV177077 sqnm92606  
 AE004766 Pseudomon  
 AE011498 Leptospir  
 AC115937 Mus muscu  
 AP005950 Bradyrhiz  
 AL939118 Streptomy  
 AE017290 Leptospir  
 BX572604 Rhodopseu  
 BV167609 sqnm6022  
 AK130031 Homo sapi  
 BV177509 sqnm95100  
 BV179316 sqnm10484  
 AY673000 Triticum  
 AY673002 Triticum  
 AC003682 Homo sapi  
 BX530094 Homo sapi  
 AC018462 Homo sapi  
 AK120652 Oryza sat  
 BC035516 Homo sapi  
 AC091123 Oryza sat  
 BX323047 Danio rer  
 BS000233 Pan trogl  
 AC084320 Oryza sat  
 BX572594 Rhodopseu  
 BC049292 Xenopus 1  
 AR035537 Sequence  
 E11457 cDNA encodi  
 AR477499 Sequence  
 BC007790 Homo sapi  
 AR035536 Sequence  
 E11456 cDNA encodi  
 AR448000 Sequence  
 BC047750 Homo sapi  
 BC074500 Homo sapi  
 AK126662 Rattus no  
 AK067366 Oryza sat  
 M29297 S.fradiae c  
 CQ848068 Sequence  
 CQ847904 Sequence  
 I64893 Sequence 9  
 U29344 Human brea  
 AE005967 Caulobact  
 Continuation (2 of  
 AP005244 Oryza sat  
 AP003014 Mesorhizo  
 AC073646 Homo sapi  
 AF546190 Zea mays  
 AC134057 Rattus no  
 AE016776 Pseudomon  
 AP005960 Bradyrhiz  
 M92421 Paracoccus  
 AB015725 Aeromonas  
 AF327372 Gallus ga  
 AP005954 Bradyrhiz  
 AP006574 Gloeobact  
 AP003009 Mesorhizo  
 BX640412 Bordetell  
 CQ785960 Sequence  
 U07132 Human stero  
 I36667 Sequence 1  
 I70211 Sequence 1  
 AR023937 Sequence 7  
 I15438 Sequence 7  
 AX924362 Sequence  
 CX924386 Sequence  
 CQ729217 Sequence  
 AY451392 Homo sapi  
 CQ785963 Sequence  
 CQ875346 Sequence  
 BC063242 Homo sapi

662	99	7.4	10029	1	AE010416	AE010416 Methanopy	c 735	97	7.2	310029	1	AE016868	AE016868 Pseudomon
663	99	7.4	10202	1	AE004483	AE004483 Pseudomon	736	97	7.2	348074	1	AE016868	AE016868 Pseudomon
664	99	7.4	10843	9	AY148100	AY148100 Homo sapi	c 737	97	7.2	349980	6	AX044033	AX044033 Sequence
665	99	7.4	110000	2	AP006484	AP006484 Cyanidios	738	96.5	7.2	1562	5	CR760877	CR760877 Xenopus t
666	99	7.4	138939	9	AC119675	AC119675 Homo sapi	739	96.5	7.2	11426	1	AE0044590	AE0044590 Pseudomon
667	99	7.4	163978	10	AC140411	AC140411 Mus muscu	740	96.5	7.2	22233	1	SPDBFB	X72850 Spingomona
668	99	7.4	193057	10	AL663067	AL663067 Mouse DNA	741	96.5	7.2	106707	2	AC019314	AC019314 Homo sapi
669	99	7.4	299450	1	AP005938	AP005938 Bradyrhiz	742	96.5	7.2	110000	1	AE016822_04	Continuation (5 of
670	99	7.4	300181	1	AP007318	AP007318 Desulfovi	c 743	96.5	7.2	128342	9	AL627313	AL627313 Human DNA
671	99	7.4	346294	1	AP002299	AP002299 Mesorhizo	744	96.5	7.2	152462	10	AC131998	AC131998 Mus muscu
672	98.5	7.3	1217	9	BC000419	BC000419 Homo sapi	745	96.5	7.2	171525	2	AC145473	AC145473 Rattus no
673	98.5	7.3	1217	9	BC000587	BC000587 Homo sapi	746	96.5	7.2	182061	6	AF281817	AF281817 Tupaia he
674	98.5	7.3	1695	8	AK072232	AK072232 Oryza sat	747	96.5	7.2	195859	14	AF281817	AF281817 Tupaia he
675	98.5	7.3	2384	6	AX747042	AX747042 Sequence	748	96.5	7.2	219252	2	AC026760	AC026760 Mus muscu
676	98.5	7.3	2384	6	AX747042	AX747042 Sequence	749	96.5	7.2	242203	2	AC097860	AC097860 Rattus no
677	98.5	7.3	3147	6	BD132295	BD132295 Anti-bact	c 750	96.5	7.2	258888	2	AC109677	AC109677 Rattus no
678	98.5	7.3	3147	6	AR232445	AR232445 Sequence	c 751	96.5	7.2	272101	1	AE017302	AE017302 Thermus t
679	98.5	7.3	3147	6	AR256497	AR256497 Sequence	c 752	96.5	7.2	299750	1	AP005964	AP005964 Bradyrhiz
680	98.5	7.3	3147	6	AX189015	AX189015 Sequence	c 753	96	7.1	1657	9	AK098658	AK098658 Homo sapi
681	98.5	7.3	4355	1	EC0ARAJ	M64787 E.coli sbcc	c 754	96	7.1	2004	6	BD180143	BD180143 Highly th
682	98.5	7.3	5125	1	EC5BCC	X15981 E.coli sbcc	c 755	96	7.1	2588	1	CFICEXX	L11080 Cellulomona
683	98.5	7.3	8008	1	PAU93274	U93274 Pseudomonas	c 756	96	7.1	10066	14	BHV1205	Z23068 Bovine herp
684	98.5	7.3	11015	1	AE004736	AE004736 Pseudomon	757	96	7.1	15534	6	CQ776613	CQ776613 Sequence
685	98.5	7.3	16675	1	AE011814	AE011814 Xanthomon	758	96	7.1	15534	9	AB051895	AB051895 Homo sapi
686	98.5	7.3	77534	1	AF235504	AF235504 Streptomy	c 759	96	7.1	110000	2	AC151276_0	AC151276 Mus muscu
687	98.5	7.3	77536	6	BD235937	BD235937 Polyketid	c 760	96	7.1	110000	2	AP006497_2	Continuation (3 of
688	98.5	7.3	77536	6	AR271638	AR271638 Sequence	c 761	96	7.1	110000	8	AE016820_03	Continuation (4 of
689	98.5	7.3	77536	6	AR564393	AR564393 Sequence	c 762	96	7.1	160714	2	AC150149	AC150149 Gallus ga
690	98.5	7.3	110000	1	U00096_04	Continuation (5 of	c 763	96	7.1	202432	2	AC143119	AC143119 Macaca mu
691	98.5	7.3	110000	1	AP006618_23	Continuation (24 o	c 764	96	7.1	210472	9	AC035139	AC035139 Homo sapi
692	98.5	7.3	110000	8	AE016819_06	Continuation (7 of	c 765	96	7.1	233568	1	AE0150275	AE0150275 Mus muscu
693	98.5	7.3	128824	1	ECU73857_06	U73857 Escherichia	c 766	96	7.1	301191	1	AE017152	AE017152 Haemophil
694	98.5	7.3	168797	2	AC104882	AC104882 Mus muscu	c 767	96	7.1	308015	1	AE016783	AE016783 Pseudomon
695	98.5	7.3	202000	1	AP000038	AP000038 Aeropyrum	768	95.5	7.1	666	12	AY657499	AY657499 Pseudonic
696	98.5	7.3	296300	1	AP005035	AP005035 Streptomy	c 769	95.5	7.1	2696	8	AK121206	AK121206 Oryza sat
697	98.5	7.3	302300	1	AP005034	AP005034 Streptomy	770	95.5	7.1	2926	1	AY667481	AY667481 Lysobacte
698	98.5	7.3	302550	1	AP006591	AP006591 Gloeobact	c 771	95.5	7.1	3173	6	E05949	E05949 DNA encodin
699	98	7.3	1782	6	BD158070	BD158070 Primer fo	c 772	95.5	7.1	110000	1	BX571965_24	Continuation (25 o
700	98	7.3	1782	6	AX879871	AX879871 Sequence	c 773	95.5	7.1	110000	1	CP000010_18	Continuation (19 o
701	98	7.3	1782	9	AK022862	AK022862 Homo sapi	c 774	95.5	7.1	110000	1	CP000011_12	Continuation (13 o
702	98	7.3	12772	1	AE004727	AE004727 Pseudomon	c 775	95.5	7.1	110000	8	AE016818_08	Continuation (9 of
703	98	7.3	76196	1	AY354515	AY354515 Streptomy	776	95.5	7.1	121960	2	AC151662	AC151662 basypus n
704	98	7.3	174363	9	AC135506	AC135506 Homo sapi	c 777	95.5	7.1	159119	1	CR792458	CR792458 Gloeobact
705	98	7.3	185146	2	AC104311	AC104311 Homo sapi	778	95.5	7.1	181731	2	CR792458	CR792458 Danio rer
706	98	7.3	215342	2	AC109322	AC109322 Homo sapi	779	95.5	7.1	192302	2	AC134315	AC134315 Lemur cat
707	98	7.3	279312	2	AC126572	AC126572 Rattus no	c 780	95.5	7.1	277000	1	SC0939109	SC0939109 Streptomy
708	98	7.3	310581	1	AE016863	AE016863 Pseudomon	c 781	95.5	7.1	298550	1	AP005029	AP005029 Streptomy
709	98	7.3	348971	1	BX572594	BX572594 Rhodospseu	c 782	95.5	7.1	300350	1	SC0939104	SC0939104 Streptomy
710	97.5	7.3	861	12	AY658649	AY658649 Synthetic	c 783	95.5	7.1	300350	1	AP006574	AP006574 Gloeobact
711	97.5	7.3	1632	6	AR301781	AR301781 Sequence	784	95.5	7.1	300861	1	AE016777	AE016777 Pseudomon
712	97.5	7.3	5525	8	AY672999	AY672999 Triticum	785	95.5	7.1	303550	1	SC0939131	SC0939131 Streptomy
713	97.5	7.3	10130	1	AE002085	AE002085 Deinococc	c 786	95.5	7.1	349672	1	BX640419	BX640419 Bordetell
714	97.5	7.3	20235	6	AR049368	AR049368 Sequence	c 787	95.5	7.1	349726	1	BX640421	BX640421 Bordetell
715	97.5	7.3	20235	6	SEERYAB	SEERYAB	c 788	95	7.1	1416	6	BD155975	BD155975 Primer fo
716	97.5	7.3	20235	6	AR095529	AR095529 Sequence	c 789	95	7.1	1416	6	AX876143	AX876143 Sequence
717	97.5	7.3	20444	1	SEERYABS	X62569 S.erythraea	c 790	95	7.1	1416	9	AK001168	AK001168 Homo sapi
718	97.5	7.3	24494	6	AR301774	AR301774 Sequence	c 791	95	7.1	2597	9	AX055133	AX055133 Homo sapi
719	97.5	7.3	42805	9	AC004221	AC004221 Homo sapi	c 792	95	7.1	2597	9	AX055133	AX055133 Homo sapi
720	97.5	7.3	189091	2	AC118207	AC118207 Mus muscu	c 793	95	7.1	3346	1	PS081032	PS081032 Pseudomonas
721	97.5	7.3	302650	1	AP005958	AP005958 Bradyrhiz	c 794	95	7.1	4941	6	CQ730770	CQ730770 Sequence
722	97.5	7.3	310550	1	SC0939113	SC0939113 Streptomy	c 795	95	7.1	4962	9	AB011162	AB011162 Homo sapi
723	97	7.2	1192	5	BX932533	BX932533 Gallus ga	c 796	95	7.1	4966	9	BC035577	BC035577 Oryza sat
724	97	7.2	2585	1	CFICEX	M15824 Cellulomona	c 797	95	7.1	4976	8	AK110228	AK110228 Oryza sat
725	97	7.2	12541	1	AE001956	AE001956 Deinococc	798	95	7.1	14568	1	AE004453	AE004453 Pseudomon
726	97	7.2	13026	1	AE002510	AE002510 Neisseria	c 799	95	7.1	110000	1	AP006840_28	Continuation (29 o
727	97	7.2	25184	1	AE008779	AE008779 Salmonell	c 800	95	7.1	110000	1	CP000011_11	Continuation (12 o
728	97	7.2	110000	1	AP006618_54	Continuation (55 o	c 801	95	7.1	110000	6	BD430793_02	Continuation (3 of
729	97	7.2	110000	1	CP000011_01	Continuation (2 of	c 802	95	7.1	147706	8	AC083945	AC083945 Oryza sat
730	97	7.2	241178	2	AC130508	AC130508 Rattus no	c 803	95	7.1	189458	10	AC134908	AC134908 Mus muscu
731	97	7.2	280558	1	AE017301	AE017301 thermus t	c 804	95	7.1	209384	2	AC151295	AC151295 Mus muscu
732	97	7.2	296282	2	AC111857	AC111857 Rattus no	c 805	95	7.1	213817	2	AC123649	AC123649 Mus muscu
733	97	7.2	299175	1	AP005023	AP005023 Streptomy	c 806	95	7.1	220577	2	AC068497	AC068497 Mus muscu
734	97	7.2	300704	1	AE017316	AE017316 Desulfovi	c 807	95	7.1	300029	8	AE017083	AE017083 Oryza sat

C 808	95	7.1	300181	1	AE017318	Deaulyovi	C 881	94	7.0	230993	2	AC150072	AC150072 Gallus ga
C 809	95	7.1	300425	1	AP005038	Streptomy	882	94	7.0	231350	2	AC150501	AC150501 Bos tauru
C 810	95	7.1	303400	1	AP006578	Gloeobact	883	94	7.0	231829	2	AC125936	AC125936 Rattus no
C 811	95	7.1	304681	2	AC016483	Mus muscu	884	94	7.0	233345	2	AC150066	AC150066 Gallus ga
C 812	95	7.1	307150	1	CNSPAX01		885	94	7.0	299850	1	AP005949	AP005949 Bradyrhiz
C 813	95	7.1	339650	1	SC039108	Streptomy	C 886	94	7.0	300200	1	AP005962	AP005962 Bradyrhiz
C 814	95	7.1	349980	6	AX041106	Sequence	C 887	94	7.0	300242	1	AE016790	AE016790 Pseudomon
C 815	94.5	7.0	534	6	CQ735395	Sequence	C 888	94	7.0	300450	1	AP005960	AP005960 Bradyrhiz
C 816	94.5	7.0	975	6	BD179645	Highly th	C 889	94	7.0	301332	1	AE017237	AE017237 Mycobacte
C 817	94.5	7.0	2184	3	DMHREC2C		C 890	94	7.0	302614	1	AE016778	AE016778 Pseudomon
C 818	94.5	7.0	2239	3	AF324956		C 891	94	7.0	303450	1	SC039130	SC039130 Streptomy
C 819	94.5	7.0	2304	6	AR166541		C 892	94	7.0	309050	1	SC039117	SC039117 Streptomy
C 820	94.5	7.0	2304	6	I49731	Sequence 1	C 893	94	7.0	32635	1	AP003005	AP003005 Mesorhizo
C 821	94.5	7.0	2304	6	I74629	Sequence 1	C 894	94	7.0	343504	2	AL158031	AL158031 Homo sapi
C 822	94.5	7.0	2311	6	DMXR2C		C 895	94	7.0	349552	1	BX569690	BX569690 Synchoco
C 823	94.5	7.0	2483	6	CQ580821		C 896	94	7.0	349970	1	BX571659	BX571659 Wolinella
C 824	94.5	7.0	2506	3	AY069393		C 897	93.5	7.0	801	5	BX933718	BX933718 Gallus ga
C 825	94.5	7.0	3412	9	HSM806839		C 898	93.5	7.0	1422	6	BD179676	BD179676 Highly th
C 826	94.5	7.0	4493	6	CQ580820	Sequence	C 899	93.5	7.0	1469	8	CRE577849	CRE577849 Chlamydom
C 827	94.5	7.0	5515	8	AY672997	Triticum	C 900	93.5	7.0	2299	8	AK111159	AK111159 Oryza sat
C 828	94.5	7.0	5516	8	AY672996	Triticum	C 901	93.5	7.0	5398	1	AB032524	AB032524 Streptomy
C 829	94.5	7.0	5570	8	AY672994	Triticum	C 902	93.5	7.0	10294	1	AE005909	AE005909 Caulobact
C 830	94.5	7.0	5582	8	AY672995	Triticum	C 903	93.5	7.0	10556	1	AE011660	AE011660 Xanthomon
C 831	94.5	7.0	14343	9	AY149894	Homo sapi	C 904	93.5	7.0	11134	1	AE012473	AE012473 Xanthomon
C 832	94.5	7.0	14790	1	AE001885	Deinococc	C 905	93.5	7.0	11819	1	AE011801	AE011801 Xanthomon
C 833	94.5	7.0	18737	6	CQ580721	Sequence	C 906	93.5	7.0	31800	2	AC015554	AC015554 Leishmani
C 834	94.5	7.0	18737	6	CQ580728	Sequence	C 907	93.5	7.0	41282	2	AC148873	AC148873 Chlamydom
C 835	94.5	7.0	45672	3	DMC22E5		C 908	93.5	7.0	41987	1	AY498874	AY498874 Streptomy
C 836	94.5	7.0	46012	2	AL513225		C 909	93.5	7.0	82232	1	AY458648	AY458648 Unculture
C 837	94.5	7.0	77656	2	AC017522		C 910	93.5	7.0	110000	1	AP006618	AP006618 Continuation 16 of
C 838	94.5	7.0	110000	1	AE017180	Continuation (17 o	C 911	93.5	7.0	110000	1	AP006618	AP006618 Continuation 17 of
C 839	94.5	7.0	110000	1	AP006840	Continuation (22 o	C 912	93.5	7.0	110000	1	AP006618	AP006618 Continuation 13 o
C 840	94.5	7.0	110000	1	AE017180	Continuation (15 o	C 913	93.5	7.0	154746	14	HSV2HGS2	HSV2HGS2 Herpes simp
C 841	94.5	7.0	165725	2	AC024027	Homo sapi	C 914	93.5	7.0	165358	9	AL353782	AL353782 Human DNA
C 842	94.5	7.0	169618	3	AC105055	Drosophill	C 915	93.5	7.0	166050	1	AL4646085	AL4646085 Ralstonia
C 843	94.5	7.0	177724	3	AC073765	Drosophill	C 916	93.5	7.0	230161	2	AK128213	AK128213 Rattus no
C 844	94.5	7.0	237619	2	AC073765	Mus muscu	C 917	93.5	7.0	298900	1	AP005937	AP005937 Bradyrhiz
C 845	94.5	7.0	240264	2	AC107434		C 918	93.5	7.0	299925	1	AP005039	AP005039 Streptomy
C 846	94.5	7.0	245134	2	AC126639	Rattus no	C 919	93.5	7.0	302675	1	AP005024	AP005024 Streptomy
C 847	94.5	7.0	297800	1	AP006579	Gloeobact	C 920	93.5	7.0	306550	1	BX248342	BX248342 Mycobacte
C 848	94.5	7.0	300100	1	SC0039123	Streptomy	C 921	93.5	7.0	308147	1	AE016915	AE016915 Chromobac
C 849	94.5	7.0	300143	1	AE017185	Prochloro	C 922	93.5	7.0	329709	1	AP002997	AP002997 Mesorhizo
C 850	94.5	7.0	300933	3	AE003422	Drosophill	C 923	93.5	7.0	346287	1	BX572595	BX572595 Rhodopsau
C 851	94	7.0	3058	8	AK110497	Oryza sat	C 924	93.5	7.0	349260	1	BX572595	BX572595 Rhodopsau
C 852	94	7.0	3263	8	AK111218	Oryza sat	C 925	93.5	7.0	349981	1	BX572602	BX572602 Rhodopsau
C 853	94	7.0	4382	14	MMSAAX	M96854 Moloney mur	C 926	93	6.9	331	11	BX546298	BX546298 Arabidops
C 854	94	7.0	7207	1	AF533147	Bacillus	C 927	93	6.9	1410	6	E07846	E07846 DNA sequenc
C 855	94	7.0	9576	6	CQ859238	Sequence	C 928	93	6.9	1462	5	SSA416953	SSA416953 Salmo sal
C 856	94	7.0	9576	6	CQ873385	Sequence	C 929	93	6.9	1468	8	AK107128	AK107128 Oryza sat
C 857	94	7.0	13732	1	AE011982	Xanthomon	C 930	93	6.9	1533	6	BD180585	BD180585 Highly th
C 858	94	7.0	15542	1	AE004504	Pseudomon	C 931	93	6.9	1533	8	AK071802	AK071802 Oryza sat
C 859	94	7.0	17400	9	AF503925	Homo sapi	C 932	93	6.9	1898	6	A91676	A91676 Sequence 1
C 860	94	7.0	58996	1	AB034704	Rubriviva	C 933	93	6.9	1898	10	AF050165	AF050165 Mus muscu
C 861	94	7.0	82144	9	AC099660	Homo sapi	C 934	93	6.9	1988	6	A91678	A91678 Sequence 3
C 862	94	7.0	86996	1	AC067718	Rhodobacter	C 935	93	6.9	2183	8	AK119822	AK119822 Oryza sat
C 863	94	7.0	97995	9	AC067718	Homo sapi	C 936	93	6.9	3051	6	CQ725223	CQ725223 Sequence
C 864	94	7.0	110000	1	AP006618	Continuation (13 o	C 937	93	6.9	3470	6	CQ849801	CQ849801 Sequence
C 865	94	7.0	110000	1	AP006618	Continuation (26 o	C 938	93	6.9	3470	9	AK126854	AK126854 Homo sapi
C 866	94	7.0	110000	1	BX571966	Continuation (2 of	C 939	93	6.9	5591	6	AX511491	AX511491 Sequence
C 867	94	7.0	110000	1	CR522870	Continuation (11 o	C 940	93	6.9	5595	9	AB020683	AB020683 Homo sapi
C 868	94	7.0	110000	2	CEY10588	Continuation (3 of	C 941	93	6.9	5828	14	MLMPROCG	MLMPROCG J02266 Moloney mur
C 869	94	7.0	123402	2	AC148071	Continuation (3 of	C 942	93	6.9	5833	14	AF033813	AF033813 Moloney m
C 870	94	7.0	154605	2	AC046161	Continuation (3 of	C 943	93	6.9	5833	14	REMSVK	REMSVK J02266 Moloney mur
C 871	94	7.0	156677	2	AC092550	Homo sapi	C 944	93	6.9	7788	6	AX803724	AX803724 Sequence
C 872	94	7.0	166050	1	AL4646085	Ralstonia	C 945	93	6.9	8213	1	TSE007744	TSE007744 Thauera s
C 873	94	7.0	169247	9	AL669970	Human DNA	C 946	93	6.9	10765	1	AE004555	AE004555 Pseudomon
C 874	94	7.0	180097	9	AC123978	Papio anu	C 947	93	6.9	10829	1	AE004655	AE004655 Pseudomon
C 875	94	7.0	180159	8	AP003633	Oryza sat	C 948	93	6.9	12891	1	AE004192	AE004192 Vibrio ch
C 876	94	7.0	186311	2	AC146295	Mus muscu	C 949	93	6.9	13750	1	AY260903	AY260903 Rhodospir
C 877	94	7.0	193015	2	AC150074	Gallus ga	C 950	93	6.9	37360	6	AX803722	AX803722 Sequence
C 878	94	7.0	199942	2	AC150038	Gallus ga	C 951	93	6.9	62070	8	NC2E4	NC2E4 AL451022 Neurospor
C 879	94	7.0	220851	2	AC097956	Rattus no	C 952	93	6.9	67523	1	SCU24241	SCU24241 Sorangium c
C 880	94	7.0	230278	14	MCU68299	Mouse cytom	C 953	93	6.9	110000	1	AE000516	AE000516 Continuation 15 of

C 954	93	6.9	110000	1	AE000516_05	Continuation (6 of	ci027	92.5	6.9	2517	6	AX317534	Sequence
C 955	93	6.9	110000	2	AP006495_1	Continuation (2 of	ci028	92.5	6.9	2520	6	AR410555	Sequence
C 956	93	6.9	110000	2	BX255276_07	Continuation (8 of	ci029	92.5	6.9	2520	6	AX317219	Sequence
C 957	93	6.9	110000	8	CR382130_23	Continuation (24 of	ci030	92.5	6.9	2520	6	AX317502	Sequence
C 958	93	6.9	139999	8	AP018727	AC018727 Oryza sat	ci031	92.5	6.9	2520	6	AX317538	Sequence
C 959	93	6.9	148179	9	AP001631	AP001631 Homo sapi	ci032	92.5	6.9	2520	6	AX317540	Sequence
C 960	93	6.9	184026	1	AP006619	AP006619 Nocardia	ci033	92.5	6.9	2520	6	AX317570	Sequence
C 961	93	6.9	188585	10	AC114404	AC114404 Mus muscu	ci034	92.5	6.9	2520	6	AX317574	Sequence
C 962	93	6.9	189050	1	AL646077	AL646077 Ralstonia	ci035	92.5	6.9	2520	6	AX317580	Sequence
C 963	93	6.9	206389	2	AC110327	AC110327 Rattus no	ci036	92.5	6.9	2526	6	AR410413	Sequence
C 964	93	6.9	213050	1	AL646067	AL646067 Ralstonia	ci037	92.5	6.9	2526	6	AR410418	Sequence
C 965	93	6.9	222932	2	AC145345	AC145345 Mus muscu	ci038	92.5	6.9	2526	6	AR410473	Sequence
C 966	93	6.9	255838	2	AC109061	AC109061 Rattus no	ci039	92.5	6.9	2526	6	AR410475	Sequence
C 967	93	6.9	290850	1	SC093912_7	AL939127 Streptomy	ci040	92.5	6.9	2526	6	AR410508	Sequence
C 968	93	6.9	298750	1	AP005375	AP005375 Thermosyn	ci041	92.5	6.9	2526	6	AR410509	Sequence
C 969	93	6.9	300029	8	AE017122	AE017122 Oryza sat	ci042	92.5	6.9	2526	6	AR410510	Sequence
C 970	93	6.9	302835	1	AE012555	AE012555 Xylella f	ci043	92.5	6.9	2526	6	AR410540	Sequence
C 971	93	6.9	318136	1	BX572101	BX572101 Prochloro	ci044	92.5	6.9	2526	6	AR562302	Sequence
C 972	93	6.9	340000	9	AP001748	AP001748 Homo sapi	ci045	92.5	6.9	2526	6	AR562307	Sequence
C 973	93	6.9	342416	1	BX842573	BX842573 Mycobacte	ci046	92.5	6.9	2526	6	AR562362	Sequence
C 974	93	6.9	349142	1	BX572559	BX572559 Rhodopseu	ci047	92.5	6.9	2526	6	AR562364	Sequence
C 975	92.5	6.9	2178	8	NCMOM72	XS3735 N. crassa M	ci048	92.5	6.9	2526	6	AR562397	Sequence
C 976	92.5	6.9	2433	6	AX317584	AX317584 Sequence	ci049	92.5	6.9	2526	6	AR562398	Sequence
C 977	92.5	6.9	2445	6	AX317568	AX317568 Sequence	ci050	92.5	6.9	2526	6	AR562399	Sequence
C 978	92.5	6.9	2445	6	AX317572	AX317572 Sequence	ci051	92.5	6.9	2526	6	AR562429	Sequence
C 979	92.5	6.9	2445	6	AX317576	AX317576 Sequence	ci052	92.5	6.9	2526	6	AR567947	Sequence
C 980	92.5	6.9	2445	6	AX317578	AX317578 Sequence	ci053	92.5	6.9	2526	6	AR567951	Sequence
C 981	92.5	6.9	2493	6	AX317586	AX317586 Sequence	ci054	92.5	6.9	2526	6	AR567953	Sequence
C 982	92.5	6.9	2499	6	AX317582	AX317582 Sequence	ci055	92.5	6.9	2526	6	AR567955	Sequence
C 983	92.5	6.9	2508	6	AX317398	AX317398 Sequence	ci056	92.5	6.9	2526	6	AX317100	Sequence
C 984	92.5	6.9	2508	6	AX317402	AX317402 Sequence	ci057	92.5	6.9	2526	6	AX317101	Sequence
C 985	92.5	6.9	2508	6	AX317404	AX317404 Sequence	ci058	92.5	6.9	2526	6	AX317114	Sequence
C 986	92.5	6.9	2508	6	AX317406	AX317406 Sequence	ci059	92.5	6.9	2526	6	AX317115	Sequence
C 987	92.5	6.9	2508	6	AX317408	AX317408 Sequence	ci060	92.5	6.9	2526	6	AX317116	Sequence
C 988	92.5	6.9	2508	6	AX317412	AX317412 Sequence	ci061	92.5	6.9	2526	6	AX317129	Sequence
C 989	92.5	6.9	2508	6	AX317414	AX317414 Sequence	ci062	92.5	6.9	2526	6	AX317264	Sequence
C 990	92.5	6.9	2508	6	AX317416	AX317416 Sequence	ci063	92.5	6.9	2526	6	AX317270	Sequence
C 991	92.5	6.9	2508	6	AX317420	AX317420 Sequence	ci064	92.5	6.9	2526	6	AX317346	Sequence
C 992	92.5	6.9	2508	6	AX317423	AX317423 Sequence	ci065	92.5	6.9	2526	6	AX317370	Sequence
C 993	92.5	6.9	2508	6	AX317428	AX317428 Sequence	ci066	92.5	6.9	2526	6	AX317372	Sequence
C 994	92.5	6.9	2508	6	AX317436	AX317436 Sequence	ci067	92.5	6.9	2526	6	AX317376	Sequence
C 995	92.5	6.9	2511	6	AR309013	AR309013 Sequence	ci068	92.5	6.9	2526	6	AX317380	Sequence
C 996	92.5	6.9	2511	6	AR317144	AR317144 Sequence	ci069	92.5	6.9	2526	6	AX317384	Sequence
C 997	92.5	6.9	2511	6	AR410409	AR410409 Sequence	ci070	92.5	6.9	2526	6	AX317388	Sequence
C 998	92.5	6.9	2511	6	AR474890	AR474890 Sequence	ci071	92.5	6.9	2526	6	AX317392	Sequence
C 999	92.5	6.9	2511	6	AR562298	AR562298 Sequence	ci072	92.5	6.9	2526	6	AX317396	Sequence
C 1000	92.5	6.9	2511	6	AR567945	AR567945 Sequence	ci073	92.5	6.9	2526	6	AX317449	Sequence
C 1001	92.5	6.9	2511	6	AX317259	AX317259 Sequence	ci074	92.5	6.9	2526	6	AX317452	Sequence
C 1002	92.5	6.9	2511	6	AX555663	AX555663 Sequence	ci075	92.5	6.9	2526	6	AX317456	Sequence
C 1003	92.5	6.9	2511	6	AX698681	AX698681 Sequence	ci076	92.5	6.9	2526	6	AX317468	Sequence
C 1004	92.5	6.9	2511	6	BD095937	BD095937 FBN-1 end	ci077	92.5	6.9	2526	6	AX317494	Sequence
C 1005	92.5	6.9	2514	6	AR410541	AR410541 Sequence	ci078	92.5	6.9	2526	6	AX317555	Sequence
C 1006	92.5	6.9	2514	6	AR562430	AR562430 Sequence	ci079	92.5	6.9	2526	6	AX698683	Sequence
C 1007	92.5	6.9	2514	6	AX317130	AX317130 Sequence	ci080	92.5	6.9	2526	6	AX698688	Sequence
C 1008	92.5	6.9	2514	6	AX317451	AX317451 Sequence	ci081	92.5	6.9	2526	6	AX698691	Sequence
C 1009	92.5	6.9	2514	6	AX317472	AX317472 Sequence	ci082	92.5	6.9	2526	6	AX698694	Sequence
C 1010	92.5	6.9	2514	6	AX317496	AX317496 Sequence	ci083	92.5	6.9	2532	6	AX317460	Sequence
C 1011	92.5	6.9	2517	6	AR410420	AR410420 Sequence	ci084	92.5	6.9	2532	6	AX317464	Sequence
C 1012	92.5	6.9	2517	6	AR410524	AR410524 Sequence	ci085	92.5	6.9	2619	6	AX317560	Sequence
C 1013	92.5	6.9	2517	6	AR562309	AR562309 Sequence	ci086	92.5	6.9	2643	6	AX317556	Sequence
C 1014	92.5	6.9	2517	6	AR562413	AR562413 Sequence	ci087	92.5	6.9	3135	6	AX317578	Sequence
C 1015	92.5	6.9	2517	6	AX317066	AX317066 Sequence	ci088	92.5	6.9	4373	10	AK131166	Sequence
C 1016	92.5	6.9	2517	6	AX317125	AX317125 Sequence	ci089	92.5	6.9	5956	9	AB058752	Mus muscu
C 1017	92.5	6.9	2517	6	AX317481	AX317481 Sequence	ci090	92.5	6.9	5956	9	AB058752	Homo sapi
C 1018	92.5	6.9	2517	6	AX317492	AX317492 Sequence	ci091	92.5	6.9	6245	1	AF202779	Rhodobact
C 1019	92.5	6.9	2517	6	AX317498	AX317498 Sequence	ci092	92.5	6.9	7282	1	AF548455	Delfia a
C 1020	92.5	6.9	2517	6	AX317506	AX317506 Sequence	ci093	92.5	6.9	11159	1	AE012066	Xanthomon
C 1021	92.5	6.9	2517	6	AX317510	AX317510 Sequence	ci094	92.5	6.9	11267	1	AE004919	Pseudomon
C 1022	92.5	6.9	2517	6	AX317514	AX317514 Sequence	ci095	92.5	6.9	11791	1	AE004763	Pseudomon
C 1023	92.5	6.9	2517	6	AX317518	AX317518 Sequence	ci096	92.5	6.9	14253	1	AE015066	Shigella
C 1024	92.5	6.9	2517	6	AX317522	AX317522 Sequence	ci097	92.5	6.9	36078	2	AC151616	Emiliania
C 1025	92.5	6.9	2517	6	AX317526	AX317526 Sequence	ci098	92.5	6.9	39263	1	AY281354	Unculture
C 1026	92.5	6.9	2517	6	AX317530	AX317530 Sequence	ci099	92.5	6.9	54184	9	AL713889	Human DNA
									6.9	110000	1	AE016822_12	Continuation (13 o



1100	92.5	6.9	110000	1	BX571965_35	Continuation (36 o	cl173	91.5	6.8	2505	6	AR562433	Sequence
1101	92.5	6.9	110000	1	BX571966_26	Continuation (27 o	cl174	91.5	6.8	2505	6	AR562433	Sequence
1102	92.5	6.9	110000	1	BX571966_29	Continuation (30 o	cl175	91.5	6.8	2505	6	BD059335	FN-1 end
1103	92.5	6.9	110000	1	CP000010_25	Continuation (26 o	cl176	91.5	6.8	2511	6	AR309012	Sequence
1104	92.5	6.9	150372	2	AC150103	Gallus ga	cl177	91.5	6.8	2511	6	AR317143	Sequence
1105	92.5	6.9	189505	9	AC092138	Homo sapi	cl178	91.5	6.8	2511	6	AR410362	Sequence
1106	92.5	6.9	197815	5	BX470161	Zebrafish	cl179	91.5	6.8	2511	6	AR562251	Sequence
1107	92.5	6.9	203050	1	AL646071	Rattus no	cl180	91.5	6.8	2511	6	AR567943	Sequence
1108	92.5	6.9	241270	2	AC120095	Rattus no	cl181	91.5	6.8	2511	6	AR567943	Sequence
1109	92.5	6.9	250891	2	AC118119	Rattus no	cl182	91.5	6.8	2511	6	AX698678	Sequence
1110	92.5	6.9	262530	2	AC111916	Rattus no	cl183	91.5	6.8	2511	6	BD059335	FN-1 end
1111	92.5	6.9	265693	2	AC122319	Mus muscu	cl184	91.5	6.8	2640	6	BD155996	Primer 30
1112	92.5	6.9	292309	1	AE016979	Shigella	1185	91.5	6.8	2653	6	BD155996	Primer 30
1113	92.5	6.9	299450	1	AP006580	Gloeobact	1186	91.5	6.8	2653	6	AX544044	Sequence
1114	92.5	6.9	299925	1	AP005045	Streptomy	1187	91.5	6.8	2653	6	AX876185	Sequence
1115	92.5	6.9	301700	1	AP005948	Bradyrhiz	1188	91.5	6.8	2653	9	AK001186	Homo sapi
1116	92.5	6.9	301708	1	AE016792	Pseudomon	1189	91.5	6.8	2943	6	AR400590	Sequence
1117	92.5	6.9	304500	1	AP005953	Bradyrhiz	cl190	91.5	6.8	3221	1	TTHPOA	Thermus the
1118	92.5	6.9	305584	1	AP0016920	Chromobac	cl191	91.5	6.8	3221	6	E09501	DNA encodi
1119	92.5	6.9	338579	1	AP003004	AP003004	cl192	91.5	6.8	3488	8	AK101762	Oryza sat
1120	92.5	6.9	349061	1	NMA222491	AL162753	cl193	91.5	6.8	5022	1	AF112365	Streptomy
1121	92	6.9	1035	6	AX079056	Sequence	cl194	91.5	6.8	5260	12	AB025788	Expressio
1122	92	6.9	1987	1	PASSSDAPF	X78478	1195	91.5	6.8	7324	1	AF090329	Pseudomon
1123	92	6.9	2396	6	CQ581775	Sequence	1196	91.5	6.8	9972	1	AE003913	Xylella f
1124	92	6.9	2590	6	CQ599964	Sequence	cl197	91.5	6.8	10029	1	AE012481	Xanthomon
1125	92	6.9	2675	9	BC023554	Homo sapi	1198	91.5	6.8	10029	1	AE012523	Xanthomon
1126	92	6.9	2682	9	BC017210	Homo sapi	cl199	91.5	6.8	10087	1	AE004058	Xylella f
1127	92	6.9	2720	9	BC023551	Homo sapi	1200	91.5	6.8	10189	1	AE004715	Pseudomon
1128	92	6.9	2894	6	CQ599979	Sequence	cl201	91.5	6.8	10426	1	AE004699	Pseudomon
1129	92	6.9	2955	8	AK100088	AE004503	1202	91.5	6.8	11160	1	AE009150	Agrobacte
1130	92	6.9	4256	3	AY122355	Oryza sat	1203	91.5	6.8	11252	1	AE005760	Caulobact
1131	92	6.9	5008	6	CQ849971	AY122255	1204	91.5	6.8	11258	1	AE011803	Xanthomon
1132	92	6.9	5008	9	AK127044	Sequence	1205	91.5	6.8	11665	1	AE008115	Agrobacte
1133	92	6.9	5286	1	SCACTT6	X63449	1206	91.5	6.8	11786	1	AE004927	Pseudomon
1134	92	6.9	10369	1	AE005059	Halobacte	1207	91.5	6.8	12675	1	AE011822	Xanthomon
1135	92	6.9	13197	1	AE004503	Pseudomon	1208	91.5	6.8	20021	1	AE004730	Pseudomon
1136	92	6.9	14423	1	AE004532	AE004532	1209	91.5	6.8	35335	3	AC016161	Leishmani
1137	92	6.9	15280	9	AB107036	Homo sapi	cl210	91.5	6.8	61450	8	AP006556	Oryza sat
1138	92	6.9	24123	1	AF086815	Acidovora	cl211	91.5	6.8	76196	1	AY354515	Streptomy
1139	92	6.9	74542	1	BX571965_40	Continuation (41 o	cl212	91.5	6.8	101385	5	CNS09898	Tetradon
1140	92	6.9	102042	2	AC150097	Gallus ga	1213	91.5	6.8	110000	1	CP000010_06	Continuation (12 o
1141	92	6.9	106332	14	AY150217	AY150217	1214	91.5	6.8	110000	1	CP000010_06	Continuation (7 of
1142	92	6.9	110000	1	AE016822_15	Continuation (16 o	1215	91.5	6.8	140933	8	AP005063	Oryza sat
1143	92	6.9	110000	1	AE017282_24	Continuation (25 o	cl216	91.5	6.8	140933	8	AP005063	Oryza sat
1144	92	6.9	110000	1	AP006840_30	Continuation (31 o	1217	91.5	6.8	141166	10	AC122423	Mus muscu
1145	92	6.9	110000	1	AY316747_2	Continuation (3 of	1218	91.5	6.8	154019	9	AC151486	Pan trogl
1146	92	6.9	110000	1	CP000010_30	Continuation (31 o	1219	91.5	6.8	156840	2	AC146810	Zea mays
1147	92	6.9	110000	2	LMFLCHR12_00	Continuation (17 o	cl220	91.5	6.8	158749	8	AY360394	Oryza sat
1148	92	6.9	110000	2	LMFLCHR12_01	Continuation (2 of	1221	91.5	6.8	160541	8	AP004458	Oryza sat
1149	92	6.9	166421	8	AP003106	Continuation (17 o	cl222	91.5	6.8	160681	2	AC118586	Pan trogl
1150	92	6.9	244273	2	AC106167	Rattus no	cl223	91.5	6.8	163194	3	LMFP214	Leishmani
1151	92	6.9	245482	2	AC098630	Rattus no	1224	91.5	6.8	164901	8	AY360393	Oryza sat
1152	92	6.9	252109	2	AC150037	Rattus no	cl225	91.5	6.8	174714	9	AC025280	Homo sapi
1153	92	6.9	254439	2	AC150047	Gallus ga	cl226	91.5	6.8	180623	9	AC092341	Homo sapi
1154	92	6.9	269985	2	AC127669	Rattus no	1227	91.5	6.8	181161	2	AC092347	Homo sapi
1155	92	6.9	298300	1	AP005025	Streptomy	cl228	91.5	6.8	196204	9	AC073957	Homo sapi
1156	92	6.9	299350	1	SME591786	AY591786	1229	91.5	6.8	226460	2	AC114157	Rattus no
1157	92	6.9	300029	1	AE016787	Pseudomon	1230	91.5	6.8	247592	9	U52111	Homo sapien
1158	92	6.9	300550	1	AP005940	Bradyrhiz	1231	91.5	6.8	263875	2	AC094237	Rattus no
1159	92	6.8	1274	5	CR761306	Xenopus t	cl232	91.5	6.8	270418	1	AE017303	Thermus t
1160	91.5	6.8	1707	3	AF012276	Toxoplasma	1233	91.5	6.8	299925	1	AP005043	Streptomy
1161	91.5	6.8	1787	9	HSPG5UT	Z14129	1234	91.5	6.8	300425	1	AP005044	Streptomy
1162	91.5	6.8	2004	9	AY619993	H. sapiens p	cl235	91.5	6.8	300817	1	AE016756	Escherich
1163	91.5	6.8	2004	9	AY619993	Homo sapi	1236	91.5	6.8	313800	1	SC0939114	Streptomy
1164	91.5	6.8	2004	9	AY619993	Homo sapi	1237	91.5	6.8	314100	1	SC0939106	Streptomy
1165	91.5	6.8	2499	6	AR410430	Sequence	1238	91.5	6.8	325483	1	AP005050	Streptomy
1166	91.5	6.8	2499	6	AR562319	Sequence	cl239	91.5	6.8	333500	1	AP003590	Nostoc sp
1167	91.5	6.8	2499	6	AX317076	Sequence	1240	91	6.8	906	6	AR386351	Sequence
1168	91.5	6.8	2505	6	AR023938	Sequence	cl241	91	6.8	1092	12	AY659078	Synthetic
1169	91.5	6.8	2505	6	I15439	Sequence 9	1242	91	6.8	1125	12	AY659325	Synthetic
1170	91.5	6.8	2505	6	AR309011	Sequence	1243	91	6.8	1500	6	BD180484	Highly th
1171	91.5	6.8	2505	6	AR317142	Sequence	cl244	91	6.8	1509	6	AX751797	Sequence
1172	91.5	6.8	2505	6	AR410544	Sequence	1245	91	6.8	1906	6	E01303	cdna encodi

1246	91	6.8	2016	4	BOVMIS	M13151 Bovine Muel	c1319	90.5	6.7	3034	10	AK122327	Mus muscu
1247	91	6.8	2085	6	AX078521	AX078521 Sequence	c1320	90.5	6.7	3065	6	AR262597	Sequence
1248	91	6.8	2299	6	AX664177	AX664177 Sequence	c1321	90.5	6.7	3077	9	BC006278	Homo sapi
1249	91	6.8	2749	6	CQ767748	CQ767748 Sequence	c1322	90.5	6.7	3306	10	AB017609	Mus muscu
1250	91	6.8	2749	6	AR5252737	AR5252737 Sequence	c1323	90.5	6.7	3337	6	E30802	Novel prote
1251	91	6.8	2749	6	AR528644	AR528644 Sequence	c1324	90.5	6.7	3360	10	AB017608	Mus muscu
1252	91	6.8	2749	6	AX403629	AX403629 Sequence	c1325	90.5	6.7	3674	6	BC017126	Novel prote
1253	91	6.8	2749	6	AX454474	AX454474 Sequence	c1326	90.5	6.7	3680	10	BC017126	Mus muscu
1254	91	6.8	2749	6	AX464252	AX464252 Sequence	c1327	90.5	6.7	4449	10	CGU29946	U29946 Cricetus
1255	91	6.8	2749	6	AX490952	AX490952 Sequence	c1328	90.5	6.7	5054	1	AF042276	Pseudomon
1256	91	6.8	2749	9	AY358364	AY358364 Homo sapi	c1329	90.5	6.7	5054	6	AX105316	Sequence
1257	91	6.8	2873	1	SHU41627	SHU41627 Streptomyce	c1330	90.5	6.7	8775	3	AY061650	AY061650 Toxoplas
1258	91	6.8	3456	1	RSF543650	RSF543650 Rhodobact	c1331	90.5	6.7	10029	1	AE012488	Xanthomon
1259	91	6.8	6175	1	AF064527	AF064527 Rhodocist	c1332	90.5	6.7	10312	1	AE009781	Pyrobacul
1260	91	6.8	7312	9	HUMCACN11G	L29536 Homo sapien	c1333	90.5	6.7	10419	1	AE001865	Deinococc
1261	91	6.8	7417	9	HUMCACN11E	L29534 Homo sapien	c1334	90.5	6.7	10506	1	AE004806	Pseudomon
1262	91	6.8	7499	9	HUMLVDCCB	L29529 Homo sapien	c1335	90.5	6.7	10761	1	AE014547	Brucella
1263	91	6.8	8940	9	HUMLVDCCB	L04569 Homo sapien	c1336	90.5	6.7	10963	1	AE011744	Xanthomon
1264	91	6.8	10057	1	AE004871	AE004871 Pseudomon	c1337	90.5	6.7	11243	1	AE012067	Xanthomon
1265	91	6.8	10061	1	AE004314	AE004314 Vibrrio ch	c1338	90.5	6.7	12423	1	AE005155	Halobacte
1266	91	6.8	10429	1	AE004875	AE004875 Pseudomon	c1339	90.5	6.7	12985	1	AE009710	Brucella
1267	91	6.8	10518	1	AE012117	AE012117 Xanthomon	c1340	90.5	6.7	13341	1	AE003964	Xylella f
1268	91	6.8	10895	1	AE004521	AE004521 Pseudomon	c1341	90.5	6.7	14618	10	AF260753	Cricketulu
1269	91	6.8	10950	1	AE012119	AE012119 Xanthomon	c1342	90.5	6.7	43514	9	AC005545	Continuatio
1270	91	6.8	10958	1	AE004940	AE004940 Pseudomon	c1343	90.5	6.7	110000	1	BX571965_30	Continuatio
1271	91	6.8	11031	1	AE004648	AE004648 Pseudomon	c1344	90.5	6.7	110000	1	BX571966_13	Continuatio
1272	91	6.8	12201	1	AE012255	AE012255 Xanthomon	c1345	90.5	6.7	110000	2	CP000010_04	Continuatio
1273	91	6.8	13138	1	AE012166	AE012166 Xanthomon	c1346	90.5	6.7	110000	2	LMFLCHR33_08	Continuatio
1274	91	6.8	15446	1	AE000710	AE000710 Aquifex a	c1347	90.5	6.7	127952	8	OSJN000063	AL060706 Oryza sat
1275	91	6.8	110000	1	AE000516_31	Continuatio (32 o	c1348	90.5	6.7	135638	1	AF484556	AF484556 Streptomy
1276	91	6.8	110000	1	AE000516_32	Continuatio (33 o	c1349	90.5	6.7	156002	8	OSJN000050	AL060626 Oryza sat
1277	91	6.8	110000	1	AE016822_00	AE016822 Leifsonia	c1350	90.5	6.7	158170	9	AC016757	AC016757 Homo sapi
1278	91	6.8	110000	1	AE017282_13	Continuatio (14 o	c1351	90.5	6.7	184631	2	AC141913	AC141913 Rattus no
1279	91	6.8	110000	1	BX571965_30	Continuatio (31 o	c1352	90.5	6.7	191762	10	AC107770	AC107770 Mus muscu
1280	91	6.8	110000	1	CP000010_04	Continuatio (5 of	c1353	90.5	6.7	204050	1	AL646073	AL646073 Ralsconia
1281	91	6.8	110000	2	AP006494_7	Continuatio (8 of	c1354	90.5	6.7	210010	2	AB0146135	AB0146135 Pan trogl
1282	91	6.8	110000	2	AP006501_07	Continuatio (8 of	c1355	90.5	6.7	210614	1	AB088224	AB088224 Streptomy
1283	91	6.8	110000	2	LMFLCHR33_08	Continuatio (9 of	c1356	90.5	6.7	220622	2	AC118570	AC118570 Lemur cat
1284	91	6.8	138203	1	AY310323	AY310323 Streptomy	c1357	90.5	6.7	299800	1	AP005028	AP005028 Streptomy
1285	91	6.8	152881	10	AC124353	AC124353 Mus muscu	c1358	90.5	6.7	299800	1	AP005028	AP005028 Streptomy
1286	91	6.8	168916	10	AC124373	AC124373 Mus muscu	c1359	90.5	6.7	308050	1	SC0939124	SC0939124 Streptomy
1287	91	6.8	174139	2	AC116700	AC116700 Mus muscu	c1360	90.5	6.7	340000	1	AP005274	AP005274 Coryneb
1288	91	6.8	178376	2	AC125512	AC125512 Papio anu	c1361	90.5	6.7	346274	1	BX640443	BX640443 Bordetell
1289	91	6.8	193798	2	AC145535	AC145535 Lemur cat	c1362	90.5	6.7	346301	1	BX640432	BX640432 Bordetell
1290	91	6.8	196216	9	AC099343	AC099343 Homo sapi	c1363	90.5	6.7	348014	1	BX640430	BX640430 Bordetell
1291	91	6.8	202555	9	AC034159	AC034159 Homo sapi	c1364	90.5	6.7	348071	1	BX927148	BX927148 Coryneb
1292	91	6.8	255809	2	AC108312	AC108312 Rattus no	c1365	90.5	6.7	348676	1	BX842581	BX842581 Mycobacte
1293	91	6.8	272101	1	AE017302	AE017302 Therms t	c1366	90.5	6.7	349876	1	BX640442	BX640442 Bordetell
1294	91	6.8	299425	1	AP005037	AP005037 Streptomy	c1367	90.5	6.7	349980	6	AX120085	AX120085 Sequence
1295	91	6.8	299425	1	AP005049	AP005049 Streptomy	c1368	90.5	6.7	934	1	AY186970	AY186970 Geothermo
1296	91	6.8	299886	1	AE017240	AE017240 Mycobacte	c1369	90.5	6.7	1069	6	AR452916	AR452916 Sequence
1297	91	6.8	300550	1	AP005030	AP005030 Streptomy	c1370	90.5	6.7	1069	8	BT009567	BT009567 Trititicu
1298	91	6.8	300900	1	AP005939	AP005939 Bradyrhiz	c1371	90.5	6.7	1176	1	AB014153	AB014153 Micromono
1299	91	6.8	301482	1	AE016916	AE016916 Chromobac	c1372	90.5	6.7	1194	1	AB014944	AB014944 Rhodobact
1300	91	6.8	301995	1	AE016779	AE016779 Pseudomon	c1373	90.5	6.7	2016	6	AX653225	AX653225 Sequence
1301	91	6.8	303226	1	AE016774	AE016774 Pseudomon	c1374	90.5	6.7	2427	8	AF110494	AF110494 Neurospor
1302	91	6.8	307050	1	BX294140	BX294140 Pirellula	c1375	90.5	6.7	2451	8	AY604047	AY604047 Oryza sat
1303	91	6.8	329000	3	TBCHRI1A3	AX929605 trypanoso	c1376	90.5	6.7	2826	8	AK100795	AK100795 Oryza sat
1304	91	6.8	346362	1	BX640439	BX640439 Bordetell	c1377	90.5	6.7	3115	1	AF225972	AF225972 Ralsconia
1305	91	6.8	346510	1	AP003011	AP003011 Mesorhizo	c1378	90.5	6.7	3867	10	BC055076	BC055076 Mus muscu
1306	91	6.8	347894	1	BX640431	BX640431 Bordetell	c1379	90.5	6.7	6576	1	AF031590	AF031590 Streptomy
1307	91	6.8	348411	1	AP003007	AP003007 Mesorhizo	c1380	90.5	6.7	8651	1	AY124589	AY124589 Agromyces
1308	91	6.8	348642	1	BX640446	BX640446 Bordetell	c1381	90.5	6.7	9427	1	AE011711	AE011711 Xanthomon
1309	91	6.8	348676	1	BX842581	BX842581 Mycobacte	c1382	90.5	6.7	9589	1	SC0001205	SC0001205 Caulobact
1310	90.5	6.7	906	6	BD179555	BD179555 Highly th	c1383	90.5	6.7	10592	1	AE005729	AE005729 Xanthomon
1311	90.5	6.7	909	1	AB085185	AB085185 Thermus t	c1384	90.5	6.7	10901	1	AE012469	AE012469 Xanthomon
1312	90.5	6.7	1668	8	AD104988	AD104988 Oryza sat	c1385	90.5	6.7	11828	1	AF13561	AF13561 Methanosa
1313	90.5	6.7	1755	6	BD180277	BD180277 Highly th	c1386	90.5	6.7	12198	1	AF187159	AF187159 Streptomy
1314	90.5	6.7	1319	5	CR761885	CR761885 Xenopus t	c1387	90.5	6.7	12249	1	AE004632	AE004632 Pseudomon
1315	90.5	6.7	2377	1	AB108682	AB108682 Streptomy	c1388	90.5	6.7	12372	1	AE004670	AE004670 Pseudomon
1316	90.5	6.7	2526	6	AR410471	AR410471 Sequence	c1389	90.5	6.7	15816	1	AB091692	AB091692 Sphingomo
1317	90.5	6.7	2526	6	AR562360	AR562360 Sequence	c1390	90.5	6.7	21931	1	AY149472	AY149472 Acinetoba
1318	90.5	6.7	2526	6	AX317099	AX317099 Sequence	c1391	90.5	6.7	49999	6	AX015917	AX015917 Sequence

1392	90	6.7	79370	1	UNK4311260	AJ431260	Unculture	1465	89.5	6.7	2877	4	SSPHGPX	X76008 S. scrofa ph
1393	90	6.7	79506	9	AI137247	AI137247	Human DNA	1466	89.5	6.7	4740	1	SPU60417	U60417 Streptomyce
1394	90	6.7	87688	1	AY365053	AY365053	Wauteria	1467	89.5	6.7	4762	10	BC053083	BC053083 Mus muscu
1395	90	6.7	95437	3	AC139742	AC139742	Leishmani	1468	89.5	6.7	5540	1	RCNIFA	M86823 Rhodobacter
1396	90	6.7	110000	1	AE016822	AE016822	Continuation (18 o	1469	89.5	6.7	5823	9	HSN806092	BX537963 Homo sapi
1397	90	6.7	110000	1	AE017180	AE017180	Continuation (35 o	1470	89.5	6.7	6462	6	AX153794	AX153794 Sequence
1398	90	6.7	110000	1	BX571966	BX571966	Continuation (11 o	1471	89.5	6.7	10029	1	AE005827	AE005827 Caulobact
1399	90	6.7	110000	1	BX571966	BX571966	Continuation (12 o	1472	89.5	6.7	10176	1	AE014563	AE014563 Brucella
1400	90	6.7	110000	1	CP000010	CP000010	Continuation (23 o	1473	89.5	6.7	10667	1	AE002529	AE002529 Neisseria
1401	90	6.7	110000	8	CR382132	CR382132	Continuation (38 o	1474	89.5	6.7	10816	1	AE009191	AE009191 Agrobacte
1402	90	6.7	110000	8	CR382135	CR382135	Continuation (4 of	1475	89.5	6.7	10861	1	AE008157	AE008157 Agrobacte
1403	90	6.7	126928	2	AC096673	AC096673	Trypanoso	1476	89.5	6.7	11162	1	AE011767	AE011767 Xanthomon
1404	90	6.7	127403	2	AC098842	AC098842	Magnaport	1477	89.5	6.7	11601	8	AF335504	AF335504 Oryza sat
1405	90	6.7	134431	14	AY386265	AY386265	Bovine pa	1478	89.5	6.7	12010	1	AE005218	AE005218 Escherich
1406	90	6.7	138929	8	AP000616	AP000616	Oryza sat	1479	89.5	6.7	13393	1	AE011910	AE011910 Xanthomon
1407	90	6.7	139226	8	OSJN00374	AL731629	Oryza sat	1480	89.5	6.7	15470	1	AE004513	AE004513 Pseudomon
1408	90	6.7	143113	8	AP000559	AP000559	Oryza sat	1481	89.5	6.7	19771	1	PPEA3NIF	X96994 Plasmid pEA
1409	90	6.7	146366	2	AC091846	AC091846	Homo sapi	1482	89.5	6.7	34071	6	AX153790	AX153790 Sequence
1410	90	6.7	149270	9	AC091912	AC091912	Homo sapi	1483	89.5	6.7	39214	9	BX664700	BX664700 Human DNA
1411	90	6.7	153551	9	AC092675	AC092675	Homo sapi	1484	89.5	6.7	42559	9	AC005258	AC005258 Homo sapi
1412	90	6.7	155525	2	AP007206	AP007206	Oryza sat	1485	89.5	6.7	42717	6	AX153789	AX153789 Sequence
1413	90	6.7	156677	9	AC021087	AC021087	Homo sapi	1486	89.5	6.7	62709	2	AC117730	AC117730 Mus muscu
1414	90	6.7	161844	2	AC147451	AC147451	Orcolmur	1487	89.5	6.7	67480	7	AY129334	AY129334 Mycobacte
1415	90	6.7	163039	8	OSJN00156	AL662958	Oryza sat	1488	89.5	6.7	71120	2	AP005417	AP005417 Oryza sat
1416	90	6.7	164104	2	AC021571	AC021571	Homo sapi	1489	89.5	6.7	84371	2	AP001963	AP001963 Homo sapi
1417	90	6.7	169950	2	AC084049	AC084049	Homo sapi	1490	89.5	6.7	110000	1	AE016822	Continuation (6 of
1418	90	6.7	171280	2	AC024186	AC024186	Homo sapi	1491	89.5	6.7	110000	1	AP006618	Continuation (52 o
1419	90	6.7	171384	2	AC136212	AC136212	Gallus ga	1492	89.5	6.7	110000	1	AP006840	Continuation (32 o
1420	90	6.7	174839	9	AL157395	AL157395	Human DNA	1493	89.5	6.7	110000	1	CP000010	Continuation (19 o
1421	90	6.7	175231	10	AC034108	AC034108	Mus muscu	1494	89.5	6.7	110000	2	AC098940	Continuation (2 of
1422	90	6.7	178000	1	SC0590463	AL590463	Streptomy	1495	89.5	6.7	110000	2	LMFLCHR34	Continuation (3 of
1423	90	6.7	181105	2	AP002394	AP002394	Rattus no	1496	89.5	6.7	110000	2	AP006496	Continuation (13 o
1424	90	6.7	183349	2	AC027501	AC027501	Mus muscu	1497	89.5	6.7	110000	8	CR382131	Continuation (23 o
1425	90	6.7	191996	9	AC092275	AC092275	Thermus t	1498	89.5	6.7	116621	2	AC150102	AC150102 Gallus ga
1426	90	6.7	192366	10	AC068906	AC068906	Mus muscu	1499	89.5	6.7	123323	9	AP001816	AP001816 Homo sapi
1427	90	6.7	195791	2	AC018997	AC018997	Homo sapi	1500	89.5	6.7	123620	8	AC103891	AC103891 Oryza sat
1428	90	6.7	197635	2	AC019079	AC019079	Homo sapi							
1429	90	6.7	197701	9	AC091941	AC091941	Homo sapi							
1430	90	6.7	201050	1	AL646064	AL646064	Ralstonia							
1431	90	6.7	208524	1	AE016925	AE016925	Chromobac							
1432	90	6.7	210301	9	AF307337	AF307337	Homo sapi							
1433	90	6.7	225646	10	AC024915	AC024915	Mus muscu							
1434	90	6.7	227773	10	AC034109	AC034109	Mus muscu							
1435	90	6.7	230918	2	AC114190	AC114190	Rattus no							
1436	90	6.7	242808	10	AC024069	AC024069	Mus muscu							
1437	90	6.7	247910	1	AE017307	AE017307	Thermus t							
1438	90	6.7	260860	2	AC125982	AC125982	Rattus no							
1439	90	6.7	273785	1	SMES91793	AL591793	Sinorhizo							
1440	90	6.7	298550	1	AP005047	AP005047	Streptomy							
1441	90	6.7	300349	1	AE017319	AE017319	Desulfovi							
1442	90	6.7	303550	1	SC0939118	AL939118	Streptomy							
1443	90	6.7	308147	1	AE016915	AE016915	Chromobac							
1444	90	6.7	333800	1	SMES91792	AL591792	Sinorhizo							
1445	90	6.7	347365	1	BX569691	BX569691	Synechoco							
1446	90	6.7	347800	1	AP000060	AP000060	Myriophyrum							
1447	90	6.7	348247	1	BX842579	BX842579	Agrobacte							
1448	90	6.7	348706	1	BX640445	BX640445	Bordetelli							
1449	90	6.7	348764	1	BX569689	BX569689	Synechoco							
1450	90	6.7	348866	1	BX640426	BX640426	Bordetelli							
1451	89.5	6.7	660	6	CQ744105	CQ744105	Sequence							
1452	89.5	6.7	962	6	AR198362	AR198362	Sequence							
1453	89.5	6.7	1052	6	A37840	A37840	Sequence 10							
1454	89.5	6.7	1052	6	AR069878	AR069878	Sequence							
1455	89.5	6.7	1052	6	AR099274	AR099274	Sequence							
1456	89.5	6.7	1052	6	AR124159	AR124159	Sequence							
1457	89.5	6.7	1052	6	CQ761077	CQ761077	Sequence							
1458	89.5	6.7	1052	6	AR442766	AR442766	Sequence							
1459	89.5	6.7	1079	8	AF315118	AF315118	Populus e							
1460	89.5	6.7	1456	10	BC024087	BC024087	Mus muscu							
1461	89.5	6.7	1533	8	AK100881	AK100881	Oryza sat							
1462	89.5	6.7	1535	8	AK061493	AK061493	Oryza sat							
1463	89.5	6.7	1656	8	AK061220	AK061220	Oryza sat							
1464	89.5	6.7	2781	5	AY374500	AY374500	Tetraodon							

## ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	789 bp	DNA	linear	PAT 03-FEB-2004
CQ721501	CQ721501	Sequence 7435 from Patent WO02068579.				
DEFINITION	CQ721501	Sequence 7435 from Patent WO02068579.				
ACCESSION	CQ721501	Sequence 7435 from Patent WO02068579.				
VERSION	CQ721501.1	GI:42282358				
KEYWORDS	CQ721501.1	GI:42282358				
SOURCE	CQ721501	Sequence 7435 from Patent WO02068579.				
ORGANISM	CQ721501	Sequence 7435 from Patent WO02068579.				
REFERENCE	CQ721501	Sequence 7435 from Patent WO02068579.				
AUTHORS	CQ721501	Sequence 7435 from Patent WO02068579.				
TITLE	CQ721501	Sequence 7435 from Patent WO02068579.				
JOURNAL	CQ721501	Sequence 7435 from Patent WO02068579.				
FEATURES	CQ721501	Sequence 7435 from Patent WO02068579.				
source	CQ721501	Sequence 7435 from Patent WO02068579.				
Location/Qualifiers	CQ721501	Sequence 7435 from Patent WO02068579.				
ORIGIN	CQ721501	Sequence 7435 from Patent WO02068579.				
Alignment Scores:	CQ721501	Sequence 7435 from Patent WO02068579.				
Pred. No.:	CQ721501	Sequence 7435 from Patent WO02068579.				
Score:	CQ721501	Sequence 7435 from Patent WO02068579.				
Percent Similarity:	CQ721501	Sequence 7435 from Patent WO02068579.				
Best Local Similarity:	CQ721501	Sequence 7435 from Patent WO02068579.				
Query Match:	CQ721501	Sequence 7435 from Patent WO02068579.				
DB:	CQ721501	Sequence 7435 from Patent WO02068579.				

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Qy 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20
Db 1 ATGACCCAGCGGTGCCCCGGCTCTCGTCCCGCGCGCTGCGCTTGGCTCAGCGCA 60
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProTrpArgGly 40
Db 61 CTGGCGCGCCCTCGCCACTGCGCTTCTCTGGGAGGCGGTGCCCCCATGGCAGGC 120
Qy 41 ArgArgGluGlnCysLeuLeuProGluAAspSerArgLeuTrpGlnTrpLeuSer 60
Db 121 CGCGGAGAGCAGTCTGCTTCCCGCGAGCAGCGCTGTCGCGAGTATCTTCTGAGC 180
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuTrpGlnPro 80
Db 181 CGCTCCATCGGGAGACCCCGCGCTGCGAGCGCTGAGCTGCTGACCTGGAGCAGCG 240
Qy 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeu 120
Db 301 ATCCAGGCCAAGAAGCGCTGACCTTCCGCGGCTACTCCGCGCTTGGCGCTG 360
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPro 140
Db 361 GCCTTGGCGTCCCGCGAGCGGTGCTGACCTTCCGCGGCTACTCCGCGCTTGGCGCTG 420
Qy 141 GluLeuGlyArgProGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 601 CTGCTCGACCCGAGGATCTCTCGCGTCTCAGAGTCTGTCGCGCGGAGGAGTGTCTG 660
Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 661 CAACCTCCGAAAGGGAGCGTGGCGCGAGTGTGTGCGAAACCTAAACGAAACGATCCGG 720
Qy 261 LysIle 262
Db 781 AGATC 786
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## RESULT 2

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AX338456
LOCUS
DEFINITION
ACCESSION
VERSION
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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AX338456  
Sequence 3 from Patent WO0183719.  
AX338456  
AX338456.1 GI:18128895  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Meyers, R.A. and Williamson, M.  
25692, a novel human o-methyltransferase family member and uses thereof

JOURNAL Patent: WO 0183719-A 3 08-NOV-2001;  
Millennium Pharmaceuticals, Inc. (US)FEATURES  
source

1..789  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Alignment Scores:  
Pred. No.: 5,28e-95 Length: 789  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x AX338456 (1-789)

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Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 541 GTGGCGGTGGTGGATGCGGAGCAAGGAGAACTGCTCCGCTACTACGAGCGCTGCTGCGAG 600
Qy 201 LeuLeuArgProGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 601 CTGCTCGACCCGAGGATCTCTCGCGTCTCAGAGTCTGTCGCGCGGAGGAGTGTCTG 660
Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 661 CAACCTCCGAAAGGGAGCGTGGCGCGAGTGTGTGCGAAACCTAAACGAAACGATCCGG 720
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
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Db	781	AGATC 786	
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DEFINITION	Homo sapiens catechol-O-methyltransferase domain containing 1, mRNA (cdna clone MGC:29637 IMAGE:4897624), complete cds.		
ACCESSION	BC023663		
VERSION	BC023663.2	GI:40226187	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Strausberg, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Klauener, R.D., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Hopkins, K.F., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Diatchenko, L., Marusina, K., Bonaldo, M.F., Casavant, T.L., Stappleton, M., Soares, M.B., Udell, T.B., Toshikiyuki, S., Schetz, T.E., Brownstein, M.J., Udell, T.B., Toshikiyuki, S., Carninci, P., Prance, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worthy, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blackley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903 (2002)	
PUBMED	12477932		
REFERENCE	2	(bases 1 to 913)	
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	On Dec 19, 2003 this sequence version replaced gi:23959051.		
	Contact: MGC help desk		
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>		
	Tissue Procurement: ATCC		
	cdNA Library Preparation: Rubin Laboratory		
	cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;		
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>		
	Contact: <a href="mailto:nisc.mgc@nih.gov">nisc.mgc@nih.gov</a>		
	Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Akter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Series: IRAL Plate: 39 Row: j Column: 6		
	This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.		
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/lab_host="DH10B-R"		/note="Vector: pOTB7"	
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ORIGIN			
Alignment Scores:			
Pred. No.:	6 21e-95	Length:	913
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US-10-017-407A-306 (1-262) x BC023663 (1-913)			
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DB	66	CTGGCGCGCGCTTCGCCACTGCGCTCTTCTTCTGGGAGCGGTGCCCGCGAGGC	125
QY	41	ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTrpLeuLeuSer	60
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QY	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80
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DB	246	CAGGGGAGATTCTATGATGACCTCGAGCAGGCGCCAGCTCTTGGCCCAACCTGGCGGCTC	305
QY	101	IleGlnAlaLysValAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120
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QY	121	AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro	140
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QY	141	GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu	160
DB	426	GAGCTGGGACGGCCCTGTGGAGGCGAGCGCGAGCGAGCACAAAGATCGACCTCCGGCTG	485
QY	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp	180
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QY	201	LeuLeuArgProGlyGlyLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu	220
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QY	221	GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLys	240
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QY	241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe	260
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DEFINITION	Human signal peptide-containing protein.		
ACCESSION	BD222712		
VERSION	BD222712.1	GI:33032482	
SOURCE	JP 2002519030-A/58.		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 985)		
TITLE	Lal,P., Tang,X.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Reddy,R., Hillman,J.L. and Bandman,O.		
JOURNAL	Human signal peptide-containing protein Patent: JP 2002519030-A 58 02-JUL-2002; INCYTE PHARMACEUTICALS INC		
COMMENT	OS Homo sapiens (human) PN JP 2002519030-A/58 PD 02-JUL-2002 PF 25-JUN-1999 JP 2000557363 PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR 01-OCT-1998 US 60/103686 11-DEC-1998 US 60/112129 PI PREETI LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,PI MARIAH R BAUGHN,INGRID E AKERBLOW,JANICE AU YOUNG,HENRY YUE,PI CHANDRA PATTTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,PC A61P25/00,PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15,PC C12N1/19,PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08,PC C12N15/00,PC A61K37/02,C12N5/00CC Incyte Clone No: 2816821FT Key Location/QualifiersFT source 1..985/organism='Homo sapiens (human)'.FT Location/Qualifiers1..985/organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'		
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source			
ORIGIN			
Alignment Scores:			
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QY	21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly	40
Db	144	CTGGCGCCCGCTCTCGCACCTGCGCTCTTCTCTGGGGAGCGGTGCCCCCATGGCGAGGC	203
QY	41	ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrIleLeuSer	60
Db	204	CGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC	263
QY	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGluGlnPro	80
Db	264	CGCTCATCGGGAGACCCCGCGCTTGGAAACCTGAGGCTGCTGACCTGGAGCAGCGCG	323
QY	81	GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100
Db	324	CAGGGGGATTCATGATGACCTCGAGCGAGCGCCAGCTCTTGGCCAACTTGGCGGGCTC	383
QY	101	IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120
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Db	564	AAGCCCGCTTGGAGACCTTGGACGAGCTGTGGCGGCGGCGGAGCGCGCACCTTCGAC	623
QY	181	ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln	200
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QY	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu	220
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ACCESSION	AX201342		
VERSION	AX201342.1	GI:15391164	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V., Stone,D.M., Watanabe,C.K. and Wood,W.I.		

TITLE Compositions and methods for the treatment of tumour  
JOURNAL Patent: WO 0153486-A 21 26-JUL-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN  
Alignment Scores:  
Pred. No.: 6.79e-95 Length: 989  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-017-407A-306 (1-262) x AX201342 (1-989)  
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
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QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40  
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QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60  
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QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80  
DB 264 CGCTCCATCGCGAGCACCGCGCTGCGAAGCTCTGAGGCTGTGACCTTGGAGCAGCG 323  
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
DB 324 CAGGGGGATTCTATGATGACCTCGAGCAGCGCGCTGCGCGCGCGCGCGCGCTC 383  
QY 101 IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAla 120  
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QY 221 GlnProProIleGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArg 240  
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RESULT 6  
AX697237  
LOCUS AX697237  
DEFINITION Sequence 305 from Patent WO0078961.  
ACCESSION AX697237  
VERSION AX697237.1 GI:29498404  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ferrera,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,  
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,  
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0078961-A 305 28-DEC-2000;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN  
Alignment Scores:  
Pred. No.: 6.79e-95 Length: 989  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-017-407A-306 (1-262) x AX697237 (1-989)  
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
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QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
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DB 444 GCGCTTGGCGCTTCCCGCGAGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCG 503  
QY 141 GlnLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
DB 504 GAGCTGGAGCGGCGCTTGTGGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCTG 563  
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180





DEFINITION Sequence 1 from Patent WO0183719.  
ACCESSION AX338454  
VERSION AX338454.1 GI:18128893  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Meyers, R.A. and Williamson, M.  
TITLE 25692, a novel human o-methyltransferase family member and uses thereof  
JOURNAL Patent: WO 0183719-A 1 08-NOV-2001;  
FEATURES Millennium Pharmaceuticals, Inc. (US)  
source Location/Qualifiers  
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ORIGIN  
Alignment Scores:  
Pred. No.: 7.16e-95 Length: 1037  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
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QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80  
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QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
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BC047774  
LOCUS  
DEFINITION  
ACCESSION BC047774.1 GI:28839536  
VERSION BC047774.1  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1041)  
AUTHORS Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 1041)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mc@paxil.stanford.edu](mailto:mc@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 98 Row: 9 Column: 5  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

## FEATURES

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## ORIGIN

## Alignment Scores:

Pred. No.: 7,19e-95 Length: 1041  
 Score: 1343.00 Matches: 262  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 9 Gaps: 0

US-10-017-407A-306 (1-262) x BC047774 (1-1041)

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 DB 205 CGGCGAGAGCAGTGCCTGCTTCCCGCGAGGACAGCGCGCTGCGCGATCTTCTGAGC 264  
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## RESULT 10

AK074421

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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1. .988

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="KAT04516"

/cell\_line="KATO III"

/cell\_type="signet-ring cell carcinoma"

Location/Qualifiers

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- &amp; 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

Fax:81-3-5449-5416

(E-mail: [filedna@ims.u-tokyo.ac.jp](mailto:filedna@ims.u-tokyo.ac.jp), Tel:81-3-5449-5286,

Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan

Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,

University of Tokyo, Laboratory of Genome Structure, Human Genome

Direct Submission

Shibahara,T., Tanaka,T. and Nakamura,Y.

Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,

2 (bases 1 to 988)

Unpublished

NEDO human cDNA sequencing project

Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,

Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,

Nakamura,Y., Isogai,T. and Sugano,S.



## FEATURES

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## RESULT 13

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## LOCUS

## DEFINITION

## SEQUENCE, 28 unordered pieces.

## AC027393

## AC027393.3

## HTG; HTGS\_PHASE1; HTGS\_DRAFT.

## KEYWORDS

## SOURCE

## ORGANISM

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## 1 (bases 1 to 169612)

## Birren,B., Linton,L., Nusbaum,C. and Lander,E.

## Homo sapiens chromosome 10, clone RP11-770D23

## Unpublished

## 2 (bases 1 to 169612)

## Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

## Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

## Boguslavsky,L., Boukagater,B., Brown,A., Burkett,G.,

## Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

## Collimore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,

## Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

## Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

## Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

## Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

## Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,

## Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

## McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

## Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mieng,V., Morrow,J.,

## Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

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## Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

## Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

## Young,G., Zainoun,J., Zimmer,A. and Zody,M.

## Direct Submission

## Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome

## Research, 320 Charles Street, Cambridge, MA 02141, USA

## 3 (bases 1 to 169612)

## Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

## Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

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## Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

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## Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

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## Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

## Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

## Young,G., Zainoun,J., Zimmer,A. and Zody,M.

## Direct Submission

## Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome

## Research, 320 Charles Street, Cambridge, MA 02141, USA

## On May 25, 2000 this sequence version replaced gi:7652066.

## All repeats were identified using RepeatMasker:

## Smit, A.F.A. &amp; Green, P. (1996-1997)

## http://ftp.genome.washington.edu/RM/RepeatMasker.html

## ----- Genome Center

## Center: Whitehead Institute/ MIT Center for Genome Research

## Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L6572

Center clone name: 770\_D\_23

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 155213 bases at least Q40

Consensus quality: 162022 bases at least Q30

Consensus quality: 164973 bases at least Q20

Insert size: 179000; agarose-fp

Insert size: 166912; sum-of-contigs

Quality coverage: 4.1 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 1191: contig of 1191 bp in length

\* 1192 1291: gap of 100 bp

\* 1292 2404: contig of 1113 bp in length

\* 2405 2504: gap of 100 bp

\* 2505 3705: contig of 1201 bp in length

\* 3706 3805: gap of 100 bp

\* 3806 4734: contig of 929 bp in length

\* 4735 4834: gap of 100 bp

\* 4835 6570: contig of 1736 bp in length

\* 6571 8583: contig of 1913 bp in length

\* 8584 8683: gap of 100 bp

\* 8684 10290: contig of 1607 bp in length

\* 10291 10390: gap of 100 bp

\* 10391 11938: contig of 1548 bp in length

\* 11939 12038: gap of 100 bp

\* 12039 15839: contig of 3801 bp in length

\* 15840 19203: gap of 100 bp

\* 19204 19303: contig of 3264 bp in length

\* 19304 22581: contig of 3278 bp in length

\* 22582 22681: gap of 100 bp

\* 22682 24947: contig of 2266 bp in length

\* 24948 25047: gap of 100 bp

\* 25048 28267: gap of 100 bp

\* 28268 32083: contig of 3816 bp in length

\* 32084 32183: gap of 100 bp

\* 32184 35533: contig of 3350 bp in length

\* 35534 35633: gap of 100 bp

\* 35634 41517: contig of 5884 bp in length

\* 41518 41617: gap of 100 bp

\* 41618 47143: contig of 5526 bp in length

\* 47144 47243: gap of 100 bp

\* 47244 51694: contig of 4451 bp in length

\* 51695 51795: contig of 5776 bp in length

\* 51796 57570: gap of 100 bp

\* 57571 63190: contig of 5520 bp in length

\* 63191 63290: gap of 100 bp

\* 63291 70708: contig of 7418 bp in length

\* 70709 70808: gap of 100 bp

\* 70809 78988: contig of 8180 bp in length

\* 78989 79088: gap of 100 bp

\* 79089 86527: contig of 7439 bp in length

\* 86528 86628: gap of 100 bp

\* 86629 99114: contig of 12487 bp in length

\* 99115 99214: gap of 100 bp

\* 99215 110221: contig of 11007 bp in length  
 \* 110222 110321: gap of 100 bp  
 \* 120322 120327: contig of 12966 bp in length  
 \* 123288 123387: gap of 100 bp  
 \* 123388 147877: contig of 24490 bp in length  
 \* 147878 147977: gap of 100 bp  
 \* 147978 169612: contig of 21635 bp in length.

## FEATURES

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## Alignment Scores:

Pred. No.: 4 95e-68 Length: 169612  
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 Percent Similarity: 42.10% Conservative: 0  
 Best Local Similarity: 42.10% Mismatches: 1  
 Query Match: 76.55% Indels: 359  
 DB: 2 Gaps: 6

US-10-017-407A-306 (1-262) x AC027393 (1-169612)

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 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31  
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Db 142038 CTGGGCGCGCCCTTCGCCCACTGGCCCTCTTCCTGGGTGAGCAGACCTGGTCCCGCGCGGC 141979  
 QY 31 ----- 31  
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 QY 32 ---- GlyArgArgCysProProTrpArgGlyArgArgGluGlnCysLeuLeuProProG1 50  
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 Db 141858 GGACACCGCCCTGTGGCAGTAICTTCTGAGCCGCTCCATGCGGGAGCACCCCGCGCTGCG 141799  
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 QY 74 ----- 74  
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 QY 74 ----- 74  
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 QY 74 ----- 74  
 Db 141618 CGCCCTGGGGCTTGGGACCCCCCAGGGCGAAGGTGGGTGACCTGCATGGCTGGTGGCCACC 141559  
 QY 75 ----- LeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysG1 89  
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 QY 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysLeuAlaLeuHeptle 109  
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 Db 141498 GCAGGCCAGCTCTTGGCCAACCTGGCGGCTCATCCAGGCCCAAGAGCGCTGGACCT 141439  
 QY 109 u----- 109  
 Db 141438 GGGTAGGGCAGCGCGCGGGATCCCGGAGGGCGGAGTTTCCGGCGCCGACCCCACTCT 141379  
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 QY 149 ----- GlnAlaGluAlaGluHisIlyIleApp 157  
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 QY 158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167  
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 QY 167 ----- 167  
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 QY 167 ----- 167  
 Db 141019 GTTAAGGCGAGGCGCGTGTGTACAGAGCCCGGCGCGCTGGGAGGGGCTTCAGGGCGC 140960  
 QY 168 ----- AspGluLeuLeuAla 172  
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 Db 140959 CCGGGCGCGGAGTACAGCGCACCTGCTCCCTCCCTCCCCCGCAGACGAGCTGCTGGCG 140900

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QY 193 AlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyIleLeuAlaValLeuArg 212
Db 140839 GCCTACTACGAGCGCTCGCTGCAGCTGCTGCAGCCCGGAGGCATCTCGCGCTCCTCAGA 140780
QY 212 ----- 212
Db 140779 GTAAGGGATCACTGCGGGGAGGAGAAAGACCCCTGTCCGGCCGGTCCCAATCTTTTC 140720
QY 212 ----- 212
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QY 212 ----- 212
Db 140659 CCGGGGCTCCGGCCCGGTACCCAGGCTTTCTCCGCTTTGGTTCGTCTCCAGCTCTGG 140600
QY 212 ----- 212
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QY 212 ----- 212
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QY 212 ----- 212
Db 140479 CCCTCCAGTCCCGCCCTTCGCGCCGAGCACCTCCCTCCGAAGCCCGCCTCCCAACGGC 140420
QY 213 -----ValLeuTyrArgGlyIleValLeuGlnProProLys 224
Db 140419 CCGGTTGGCCCGCCCTCCCGCAGGTCCTGTGGCGCGGAAGGTGTGCAACCTCCGAAA 140360
QY 225 GlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArg 244
Db 140359 GGGGAGCTGGCGGCCGAGTGTGTGCGAACCCTTAACGAAAGCATCCGCGGGGACGTACAG 140300
QY 245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 140299 GTCTACATCAGCTCTCGCCCTCGCGCATGGACTCACCTTGGCCTTCAAGATC 140246

RESULT 14
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AY294423_1 10001 210000
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AY294423_3 30001 389888
Continuation (4 of 4) of AY294423 from base 300001 (AY294423 Mus musculus chromosome 17

Alignment Scores:
Pred. No.: 3,68e-56 Length: 89888
Score: 870.50 Matches: 223
Percent Similarity: 44.84% Conservative: 16
Best Local Similarity: 41.84% Mismatches: 23
Query Match: 64.82% Indels: 275
DB: 2 Gaps: 7

US-10-017-407A-306 (1-262) x AY294423_3 (1-89888)
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Db 78332 ATGGCTCAGCCGCTCCCTCGCTATCTATCCAGCGGCACCTGGCCTTGGCTCGGCGCG 78273
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGly----- 32
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QY 33 -----ArgArgCys----- 35
Db 78212 CCGGGNATGGGAGGAGGCGCGAGAGCCGAGAACCCGCTCAGAAA-TCAGGCCCC 78154
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QY 44 GlnCysLeuLeuProProGluAspSerArgLeuTyrGlnTyrLeuLeuSerArgSerMet 63
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QY 109 Leu----- 109
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Db 77614 CCTGAACTGAGCTTGACAGTGTCTCCCTTCCACAGGTACTTTCCAGGGCTACTCGGCCCTG 77555
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QY 139 ProProGluLeuGlyArgProLeuTyrArg----- 148
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QY 149 -----GlnAlaGluAlaGlu 153
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QY 154 HisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu----- 167
Db 77375 CAGAAATCGACCTTCGGCTGCGAGCCCGCTTCGAGACATT-GGGTGAGCACCATGGCGG 77317
QY 167 ----- 167
Db 77316 GAGGACCCAGACAGCACTGTCCAAACCCCGGGGAACAAACTGGGACCCCTGAGCAGCCC 77257
QY 168 -----AspGluLeuLeu 171
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Best Local Similarity: 41.84% Mismatches: 23  
Query Match: 64.82% Indels: 275  
DB: 10 Gaps: 7

US-10-017-407A-306 (1-262) x AC132590 (1-161371)

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QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGly----- 32  
Db 44970 CTGGCGCGCGCTTCGTACTGGTCTCTTGTCTGGGTGAGCTGGGTGGGCTGCTGCAGTC 45029  
QY 33 -----ArgArgCys----- 35  
Db 45030 CGGGGAATGGGAGGAGGGCGGAGAGCGGAGAACCCGGTCAGAAA-TGCAGGCC 45088  
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Db 45209 AGAGAGCACCCGCGCTGCGGAGCCTGCGACTGGTCACTAGTGGGACCGAGAACCGG 45268  
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QY 110 -----GlyThrPheThrGlyTrpSerAlaLeu 118  
Db 45628 CCTGAACCTGAGCTTGACAGTGTGTCCCTTTCCACAGGTACTTTTCACGGGCTACTCGGCCCTG 45687

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139 ProGluLeuGlyArgProLeuTyrArg- 148
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45748 CCCCCAAGCTGGGACGGCCCAATGTGGAA-GCAGGTGAGAGCCCCACACCTGCGGCGGTT 45806
QY 149 -----GlnAlaGluAlaGlu 153
Db |||||
45807 CGGGCTCCGGCTCGGGGGCTGCGGCTGACCGGCTCCTTCGCGAGGCGAGAAGTGGAG 45866
QY 154 HisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu- 167
Db |||||
45867 CAGAAGATCGACCTTCGGCTGCGAGCGCGCCCTGCAGACATT-GGGTGAGCACCAGTGGCG 45925
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45926 GAGGGACCCAGACAGCACTGTCCAACCCCGGGGAAACAAACTGGCGACCTGTAGCAGCCC 45985
QY 168 -----AspGluLeuLeu 171
Db |||||
45986 GCTGAGACCCCTAGCTCAGCCAGCGGCACATGCCCTCTGTCCCTGTTAAGATGAGCTCCTA 46045
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCys 191
Db |||||
46046 GCGCGGGGAGGCGCGAACCTTCGACATAGCGGTGGTGGACGCGGACAAAGAGAACTGT 46105
QY 192 SerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeu 211
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QY 212 Arg- 212
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46166 AGAGTAAGGACTAGCTAAGGCANAACTGTGTCTTCTTGTGGTGGGTACCCTCTTCTC 46225
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QY 212 ----- 212
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46286 CGCCCCCTCTGGCTAAAGCTCTGGGTGGCTACCCCCCACTTCCGACGGCCCCCGCCCTC 46345
QY 213 -----ValLeuTyrArgGlyLysValLeuGlnProProLysGlyAspValAlaAla 229
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QY 230 GluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeu 249
Db |||||
46406 GAATGTGTGGGAACCTGAACGAACGCATCTGAGGGAGCGCCAGGGTCTACATCAGCCTC 46465
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Job time : 4825 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 15:50:43 ; Search time 697 Seconds  
(without alignments)  
8608.289 Million cell updates/sec

Perfect score: 989  
Sequence: 1 gcggggccgcgagtcgagga.....caaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications NA.\*

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12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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39	989	100.0	989	16	US-10-013-909A-305
62	989	100.0	989	17	US-10-211-858-21
68	989	100.0	989	17	US-10-307-817-121
69	989	100.0	989	17	US-10-307-817-125
72	985.8	99.7	1037	9	US-09-844-468-1
73	938.2	94.9	967	15	US-10-106-698-521
74	789	79.8	789	9	US-09-844-468-3
75	583.6	59.0	787	17	US-10-307-817-123
c 76	548.6	55.5	620	17	US-10-240-435-182
77	422	42.7	474	10	US-09-918-995-22407
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					Sequence 121, Appl
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c 79	312	31.5	326	9	US-09-880-107-632	Sequence 632, Appl
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81	254.4	25.7	257	15	US-10-102-524-1452	Sequence 1452, Appl
c 82	185.8	18.8	84428	17	US-10-229-148B-1	Sequence 1, Appl
83	182.4	18.4	85692	17	US-10-461-194-1	Sequence 1, Appl
84	179.2	18.1	86941	17	US-10-461-194-2	Sequence 2, Appl
85	171.3	17.3	693	18	US-10-425-115-49671	Sequence 49671, A
86	161.8	16.4	953	9	US-09-452-239-43	Sequence 43, Appl
c 87	159.2	16.1	1049	9	US-09-452-239-45	Sequence 45, Appl
c 88	159.2	16.1	3759	18	US-10-437-963-23149	Sequence 23149, A
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91	157.2	15.9	1078	9	US-09-452-239-41	Sequence 41, Appl
92	155.6	15.7	1018	9	US-09-452-239-35	Sequence 35, Appl
93	154	15.6	891	9	US-09-452-239-1	Sequence 1, Appl
94	153.4	15.5	888	18	US-10-425-115-53820	Sequence 53820, A
95	153	15.5	77536	10	US-09-940-316B-1	Sequence 1, Appl
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98	152.4	15.4	1159	17	US-10-425-114-2777	Sequence 2777, Appl
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100	152.4	15.4	2381	18	US-10-425-115-138013	Sequence 138013, A
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103	149.6	15.1	1060	17	US-10-425-114-28379	Sequence 28379, A
104	149.6	15.1	1090	18	US-10-767-701-12827	Sequence 12827, A
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108	148	15.0	1097	17	US-10-425-114-3691	Sequence 3691, Appl
109	148	15.0	1097	17	US-10-425-114-3691	Sequence 3691, Appl
110	148	15.0	1118	9	US-09-452-239-37	Sequence 37, Appl
111	148	15.0	1146	9	US-09-452-239-3	Sequence 3, Appl
112	146.4	14.8	1160	16	US-10-361-460-31	Sequence 31, Appl
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122	143.2	14.5	1443	18	US-10-767-701-14336	Sequence 14336, A
123	143.2	14.4	1030	17	US-10-425-114-2377	Sequence 2377, Appl
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128	139.4	14.1	792	18	US-10-425-115-140246	Sequence 140246, A
129	135.4	13.7	1281	18	US-10-425-115-138015	Sequence 138015, A
130	134.6	13.6	1052	17	US-10-425-114-24738	Sequence 24738, A
131	134.6	13.6	1107	18	US-10-425-115-138003	Sequence 138003, A
132	129.6	13.1	1146	18	US-10-425-115-53825	Sequence 53825, A
133	129.6	13.1	985	17	US-10-425-114-23965	Sequence 23965, A
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135	127.4	12.9	109519	11	US-09-758-759-1	Sequence 1, Appl
136	126	12.7	923	9	US-09-452-239-7	Sequence 7, Appl
137	126	12.7	944	16	US-10-361-460-32	Sequence 32, Appl
138	126	12.7	1066	18	US-10-425-115-179664	Sequence 179664, A
139	125.4	12.7	1006	17	US-10-425-114-27818	Sequence 27818, A
140	125	12.6	1051	16	US-10-289-757-146	Sequence 146, Appl
141	123.4	12.5	1059	16	US-10-289-757-36	Sequence 36, Appl
142	122.6	12.4	1063	16	US-10-289-757-37	Sequence 37, Appl
143	122.2	12.4	1073	18	US-10-425-115-113171	Sequence 113171, A
144	113.4	11.5	781	18	US-10-425-115-53814	Sequence 53814, A
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c 146	103.6	10.5	343	9	US-09-917-800A-275	Sequence 275, Appl
c 147	103.6	10.5	343	17	US-10-152-319A-298	Sequence 298, Appl
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152	96.8	9.8	1026	15	US-10-174-693-6	Sequence 6, Appli	225	59.6	6.0	7185	16	US-10-329-079-48	Sequence 48, Appl
153	93	9.4	1257	18	US-10-425-115-66941	Sequence 66941, A	226	59.6	6.0	61944	16	US-10-329-079-34	Sequence 34, Appl
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155	88	8.9	1423	17	US-09-452-239-47	Sequence 47, Appl	228	59	6.0	3501	18	US-10-437-963-22161	Sequence 22161, A
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164	85.6	8.7	1512	18	US-10-739-930-3516	Sequence 3516, Ap	237	58.8	5.9	2487	18	US-10-437-963-10147	Sequence 10147, A
c 165	84	8.5	1072	9	US-09-770-443-132	Sequence 132, App	238	58.8	5.9	5858	19	US-10-488-056-14	Sequence 14, Appl
166	79.6	8.0	1233	18	US-10-767-795-6335	Sequence 6335, Ap	239	58.6	5.9	1257	15	US-10-156-761-5999	Sequence 5999, Ap
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168	79.2	8.0	1508	17	US-10-424-599-18320	Sequence 18320, A	241	58.4	5.9	1053	18	US-10-437-963-43823	Sequence 43823, A
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182	69.4	7.0	1311	13	US-10-087-192-1325	Sequence 1325, Ap	255	57	5.8	1671	15	US-10-156-761-2058	Sequence 2058, Ap
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185	68	6.9	749	18	US-10-767-795-6336	Sequence 6336, Ap	258	56.8	5.7	879	17	US-10-425-114-30199	Sequence 30199, A
186	67.2	6.8	969	18	US-10-437-963-21877	Sequence 21877, A	259	56.8	5.7	907	17	US-10-425-114-30210	Sequence 30210, A
187	67	6.8	1149	17	US-10-258-951-13	Sequence 13, Appl	260	56.8	5.7	1182	17	US-10-458-201-19	Sequence 19, Appl
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189	66.8	6.8	1075	15	US-10-174-693-55	Sequence 55, Appl	262	56.8	5.7	1486	17	US-10-425-114-3685	Sequence 3685, Ap
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194	66	6.7	1389	15	US-10-156-761-5082	Sequence 5082, Ap	267	56.8	5.7	22976	17	US-10-650-507-19	Sequence 19, Appl
195	65.8	6.7	575	18	US-10-425-115-140243	Sequence 140243, A	268	56.8	5.7	36401	19	US-10-925-357-1	Sequence 116, App
196	65	6.6	578	18	US-10-767-701-26345	Sequence 26345, A	269	56.8	5.7	41936	9	US-09-967-768A-116	Sequence 6261, Ap
197	64.6	6.5	553	17	US-10-264-049-1169	Sequence 1169, Ap	270	56.8	5.7	1190	18	US-10-437-963-36882	Sequence 36882, A
198	64.2	6.5	584	18	US-10-425-115-53810	Sequence 53810, A	271	56.8	5.7	1377	18	US-10-411-910A-228	Sequence 228, App
199	64.2	6.5	600	9	US-09-452-239-39	Sequence 39, Appl	272	56.6	5.7	1014	18	US-10-437-963-58666	Sequence 58666, A
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202	63.4	6.4	897	15	US-10-156-761-3542	Sequence 3542, Ap	275	56.6	5.7	25085	16	US-10-132-134-35	Sequence 35, Appl
203	63.2	6.4	966	15	US-10-156-761-4002	Sequence 4002, Ap	276	56.6	5.7	50543	16	US-10-132-134-25	Sequence 25, Appl
204	63.2	6.4	9025608	15	US-10-156-761-1	Sequence 1, Appli	277	56.6	5.7	3225	18	US-10-437-963-82422	Sequence 82422, A
c 205	63	6.4	135005	18	US-10-723-860-2320	Sequence 2320, Ap	278	56.4	5.7	3957	16	US-10-200-562-193	Sequence 193, App
206	62.8	6.3	75216	15	US-10-080-170-646	Sequence 646, App	279	56.4	5.7	15738	16	US-10-237-551-193	Sequence 193, App
207	62.8	6.3	75216	15	US-10-080-170-646	Sequence 646, App	280	56.4	5.7	15738	16	US-10-329-079-146	Sequence 46, Appl
c 208	62.8	6.3	75216	18	US-10-468-356-6740	Sequence 6740, Ap	281	56.4	5.7	154746	10	US-09-827-688-8	Sequence 8, Appli
209	61.8	6.2	1128	15	US-10-156-761-2740	Sequence 2740, Ap	282	56.4	5.7	154746	10	US-09-827-688-8	Sequence 8, Appli
210	61.6	6.2	1079	17	US-10-424-599-98070	Sequence 98070, A	283	56.4	5.7	426	15	US-10-156-761-4164	Sequence 4164, Ap
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212	61.6	6.2	3362	18	US-10-425-115-173652	Sequence 173652, A	285	56.2	5.7	1186	10	US-09-769-734-22	Sequence 22, Appl
213	61.4	6.2	775	18	US-10-425-115-65597	Sequence 65597, A	286	56.2	5.7	4421	17	US-10-107-431-280	Sequence 280, App
214	61	6.2	2117	18	US-10-437-963-97603	Sequence 97603, A	287	56.2	5.7	411	15	US-10-156-761-5439	Sequence 5439, Ap
215	60.6	6.1	2808	15	US-10-156-761-2021	Sequence 2021, Ap	288	56	5.7	494	10	US-09-918-995-32147	Sequence 32147, A
216	60.4	6.1	1544	18	US-10-437-963-72461	Sequence 72461, A	289	56	5.7	974	17	US-10-425-114-31148	Sequence 31148, A
217	60.4	6.1	2256646	18	US-10-470-565-1	Sequence 1, Appli	290	56	5.7	1189	18	US-10-437-963-45522	Sequence 45522, A
218	60	6.1	729	9	US-09-938-842A-2400	Sequence 2400, Ap	291	56	5.7	1403	17	US-10-437-963-19360	Sequence 19360, A
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220	60	6.1	966	18	US-10-739-930-382	Sequence 382, App	293	56	5.7	1658	18	US-10-646-664-6	Sequence 6, Appli
221	60	6.1	982	9	US-09-452-239-31	Sequence 31, Appl	294	56	5.7	2109	9	US-09-738-973-153	Sequence 153, App
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c 223	59.8	6.0	1041	18	US-10-437-963-8597	Sequence 8597, Ap	296	56	5.7	2109	9	US-09-854-133-153	Sequence 153, App

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303	5.7	13862	10	US-10-203-428-1003	Sequence 1003, Ap	376	54.2	5.5	3351	18	US-10-425-115-151164	Sequence 151164, A
304	5.7	15559	18	US-10-646-664-1	Sequence 1, Appl	377	54.2	5.5	11058	15	US-10-156-761-3629	Sequence 3629, Ap
305	5.7	43058	9	US-09-954-456-292	Sequence 292, App	378	54.2	5.5	65140	18	US-10-203-295-1	Sequence 1, Appl
306	5.7	43058	9	US-09-954-456-292	Sequence 292, App	379	54.2	5.5	125401	18	US-10-203-295-35	Sequence 35, Appl
307	5.7	43058	9	US-09-880-107-3950	Sequence 3950, Ap	380	54	5.5	897	17	US-10-282-122A-11524	Sequence 11524, A
308	5.7	43058	19	US-10-843-641A-3319	Sequence 3319, Ap	381	54	5.5	1118	15	US-10-180-375-101	Sequence 101, App
309	5.7	43058	19	US-10-843-641A-3556	Sequence 3556, Ap	382	54	5.5	1118	17	US-10-183-687-117	Sequence 117, App
310	5.8	1152	15	US-10-259-165-201	Sequence 201, App	383	54	5.5	1391	18	US-10-437-963-86834	Sequence 86834, A
311	5.8	1209	18	US-10-437-963-84053	Sequence 84053, A	384	54	5.5	1527	15	US-10-156-761-6634	Sequence 6634, Ap
312	5.8	16275	15	US-10-156-761-5927	Sequence 5927, Ap	385	54	5.5	2670	18	US-10-437-963-82460	Sequence 82460, A
313	5.8	16275	15	US-10-437-963-7695	Sequence 7695, Ap	386	54	5.5	2997	15	US-10-156-761-7034	Sequence 7034, Ap
314	5.8	1926	15	US-10-294-804-3	Sequence 3, Appl	387	54	5.5	4530	17	US-10-302-172-881	Sequence 881, App
315	5.8	1926	15	US-10-194-046-3	Sequence 3, Appl	388	53.8	5.4	451	14	US-10-062-727-457	Sequence 457, App
316	5.8	8705	15	US-10-291-230-14	Sequence 14, Appl	389	53.8	5.4	658	18	US-10-767-701-4204	Sequence 4204, Ap
317	5.8	8705	15	US-10-291-249-14	Sequence 14, Appl	390	53.8	5.4	1320	15	US-10-156-761-5076	Sequence 5076, Ap
318	5.8	8705	17	US-10-273-678-16	Sequence 16, Appl	391	53.8	5.4	2082	18	US-10-746-167-67	Sequence 67, Appl
319	5.8	9482	19	US-10-888-961-4	Sequence 4, Appl	392	53.8	5.4	3150	15	US-10-156-761-1266	Sequence 1266, Ap
320	5.8	9600	16	US-10-278-751-1	Sequence 1, Appl	393	53.8	5.4	64492	17	US-10-378-083-1	Sequence 1, Appl
321	5.8	10233	16	US-10-050-898-283	Sequence 283, App	394	53.8	5.4	114793	15	US-10-148-806-3	Sequence 3, Appl
322	5.8	10285	16	US-10-050-903-283	Sequence 283, App	395	53.6	5.4	822	15	US-10-156-761-4587	Sequence 4587, Ap
323	5.8	10330	18	US-10-656-263-24	Sequence 24, Appl	396	53.6	5.4	885	18	US-10-437-963-60765	Sequence 60765, A
324	5.8	10477	18	US-10-656-263-22	Sequence 22, Appl	397	53.6	5.4	935	17	US-10-425-114-23310	Sequence 23310, A
325	5.8	10516	18	US-10-656-263-20	Sequence 20, Appl	398	53.6	5.4	958	18	US-10-425-115-42563	Sequence 42563, A
326	5.8	10561	18	US-10-656-263-18	Sequence 18, Appl	399	53.6	5.4	1164	15	US-10-156-761-6517	Sequence 6517, Ap
327	5.8	10615	18	US-10-656-263-45	Sequence 45, Appl	400	53.6	5.4	1664	15	US-10-437-963-66411	Sequence 66411, A
328	5.8	10774	18	US-10-656-263-23	Sequence 23, Appl	401	53.6	5.4	2873	15	US-10-156-761-2660	Sequence 2660, Ap
329	5.8	10921	18	US-10-656-263-21	Sequence 21, Appl	402	53.6	5.4	28499	19	US-10-741-600-17869	Sequence 17869, A
330	5.8	10961	18	US-10-656-263-19	Sequence 19, Appl	403	53.6	5.4	38734	10	US-09-373-658-30	Sequence 30, Appl
331	5.8	11006	18	US-10-656-263-17	Sequence 17, Appl	404	53.6	5.4	38734	11	US-09-989-687-30	Sequence 30, Appl
332	5.8	11059	18	US-10-656-263-46	Sequence 46, Appl	405	53.4	5.4	707	18	US-10-437-963-91406	Sequence 91406, A
333	5.8	11924	18	US-10-678-816-7	Sequence 6, Appl	406	53.4	5.4	837	18	US-10-425-115-97779	Sequence 97779, A
334	5.8	12242	15	US-10-678-816-6	Sequence 6, Appl	407	53.4	5.4	2402	13	US-10-425-115-164051	Sequence 164051, A
335	5.6	1281	15	US-10-156-761-2031	Sequence 4135, Ap	408	53.4	5.4	4176	13	US-10-098-841-34	Sequence 34, Appl
336	5.4	659	18	US-10-767-701-4135	Sequence 1727, Ap	409	53.4	5.4	85915	18	US-10-647-196-1	Sequence 1, Appl
337	5.4	1035	15	US-10-156-761-1727	Sequence 1, Appl	410	53.2	5.4	900	17	US-10-282-122A-14712	Sequence 14712, A
338	5.4	84428	17	US-10-229-1488-1	Sequence 30211, A	411	53.2	5.4	972	17	US-10-424-539-133785	Sequence 133785, A
339	5.2	1161	17	US-10-425-114-30211	Sequence 1240, Ap	412	53.2	5.4	1400	18	US-10-437-963-19875	Sequence 19875, A
340	5.2	1182	15	US-10-156-761-1240	Sequence 13422, A	413	53.2	5.4	1431	18	US-10-437-963-73728	Sequence 73728, A
341	5.2	1203	17	US-10-425-114-13422	Sequence 30216, A	414	53.2	5.4	135638	16	US-10-314-657-1	Sequence 1, Appl
342	5.2	1344	17	US-10-425-114-30216	Sequence 85114, A	415	53	5.4	632	13	US-10-194-163-655	Sequence 655, App
343	5.2	1473	18	US-10-437-963-85114	Sequence 85114, A	416	53	5.4	797	17	US-10-424-539-78653	Sequence 78653, A
344	5.2	1885	17	US-10-183-687-149	Sequence 149, App	417	53	5.4	1068	15	US-10-156-761-5900	Sequence 5900, Ap
345	5.2	1887	17	US-10-282-122A-26004	Sequence 26004, A	418	53	5.4	1320	15	US-10-156-761-6285	Sequence 6285, Ap
346	5.2	21185	16	US-10-159-257A-2	Sequence 2, Appl	419	53	5.4	1699	18	US-10-369-493-40710	Sequence 40710, A
347	5.2	63158	16	US-10-293-198-1	Sequence 1, Appl	420	53	5.4	3444	17	US-10-425-115-149834	Sequence 149834, A
348	5.6	1875	18	US-10-437-963-33401	Sequence 33401, A	421	53	5.4	3444	17	US-10-369-493-40475	Sequence 40475, A
349	5.6	2559	18	US-10-723-860-2336	Sequence 2336, Ap	422	52.8	5.3	3444	17	US-10-425-115-138006	Sequence 138006, A
350	5.6	53799	19	US-10-042-665A-3	Sequence 3, Appl	423	52.8	5.3	956	17	US-10-425-114-24149	Sequence 24149, A
351	5.4	594	15	US-10-174-693-105	Sequence 105, App	424	52.8	5.3	984	18	US-10-425-115-118414	Sequence 118414, A
352	5.4	607	15	US-10-174-693-23	Sequence 23, Appl	425	52.8	5.3	1027	18	US-10-739-930-4902	Sequence 4902, Ap
353	5.4	820	18	US-10-767-701-9492	Sequence 9492, Ap	426	52.8	5.3	2712	17	US-10-282-122A-26256	Sequence 26256, A
354	5.4	1083	15	US-10-156-761-4116	Sequence 4116, Ap	427	52.8	5.3	2715	17	US-10-282-122A-28396	Sequence 28396, A
355	5.4	1188	18	US-10-437-963-65538	Sequence 65538, A	428	52.8	5.3	3858	15	US-10-156-761-6773	Sequence 6773, Ap
356	5.4	1683	15	US-10-156-761-5824	Sequence 5824, Ap	429	52.6	5.3	447	17	US-10-260-238-74	Sequence 74, Appl
357	5.4	1824	15	US-10-156-761-5824	Sequence 22350, A	430	52.6	5.3	513	18	US-10-437-963-77477	Sequence 77477, A
358	5.4	1824	15	US-10-156-761-5824	Sequence 41730, A	431	52.6	5.3	584	18	US-10-767-701-26823	Sequence 26823, A
359	5.4	1824	15	US-10-156-761-5824	Sequence 18, Appl	432	52.6	5.3	707	18	US-10-767-701-7590	Sequence 7590, Ap
360	5.4	1824	15	US-10-156-761-5824	Sequence 18, Appl	433	52.6	5.3	1155	15	US-10-156-761-7048	Sequence 7048, Ap
361	5.4	1824	15	US-10-156-761-5824	Sequence 3321, Ap	434	52.6	5.3	1275	15	US-10-190-435-55	Sequence 55, Appl
362	5.4	1824	15	US-10-156-761-5824	Sequence 2421, Ap	435	52.6	5.3	1275	15	US-10-190-305A-79	Sequence 79, Appl
363	5.4	1824	15	US-10-156-761-5824	Sequence 11714, A	436	52.6	5.3	1368	17	US-10-282-122A-25876	Sequence 25876, A
364	5.4	1824	15	US-10-156-761-5824	Sequence 55219, A	437	52.6	5.3	1605	17	US-10-425-114-19193	Sequence 19193, A
365	5.4	1824	15	US-10-156-761-5824	Sequence 86, Appl	438	52.6	5.3	2141	18	US-10-437-963-82757	Sequence 82757, A
366	5.4	1824	15	US-10-156-761-5824	Sequence 37276, A	439	52.6	5.3	2561	9	US-09-976-740-48	Sequence 48, Appl
367	5.4	1824	15	US-10-156-761-5824	Sequence 43079, A	440	52.6	5.3	2561	13	US-10-023-539-48	Sequence 48, Appl
368	5.4	1824	15	US-10-156-761-5824	Sequence 34784, A	441	52.6	5.3	2561	13	US-10-023-539-48	Sequence 48, Appl
369	5.4	1824	15	US-10-156-761-5824	Sequence 51013, A	442	52.6	5.3	2561	17	US-10-616-187-48	Sequence 48, Appl

c 443	52.6	5.3	2561	17	US-10-671-242-48	Sequence 48, Appl	516	51.8	5.2	2075	16	US-10-425-586-1	Sequence 1, Appli
444	52.6	5.3	3624	15	US-10-190-435-47	Sequence 47, Appl	517	51.8	5.2	2075	17	US-10-466-136-1	Sequence 1, Appli
445	52.6	5.3	3624	16	US-10-190-305A-41	Sequence 41, Appl	518	51.8	5.2	2145	17	US-10-282-122A-31855	Sequence 31855, A
446	52.4	5.3	867	15	US-10-156-761-2201	Sequence 2201, Ap	519	51.8	5.2	2322	18	US-10-739-930-2737	Sequence 2737, Ap
447	52.4	5.3	3671	15	US-10-437-963-74149	Sequence 74149, A	520	51.8	5.2	2847	15	US-10-156-761-2404	Sequence 2404, Ap
c 448	52.4	5.3	1071	18	US-10-156-761-7131	Sequence 7131, Ap	521	51.8	5.2	4462	9	US-09-974-298-28	Sequence 28, Appl
449	52.4	5.3	1142	18	US-10-425-115-165350	Sequence 165350,	522	51.8	5.2	4462	9	US-09-796-008-1	Sequence 1, Appli
450	52.4	5.3	1388	18	US-10-767-701-14298	Sequence 14298, A	523	51.8	5.2	4469	9	US-10-133-937-42	Sequence 42, Appl
451	52.4	5.3	1518	15	US-10-156-761-12280	Sequence 2280, Ap	524	51.8	5.2	4469	17	US-10-172-118-857	Sequence 857, App
452	52.4	5.3	1339	18	US-10-425-115-129809	Sequence 129809,	525	51.8	5.2	4469	17	US-10-159-563-42	Sequence 42, Appl
453	52.4	5.3	1891	9	US-09-969-708-146	Sequence 146, App	526	51.8	5.2	4469	17	US-10-342-887-857	Sequence 857, App
454	52.4	5.3	1891	15	US-10-007-926A-234	Sequence 234, App	527	51.8	5.2	4469	18	US-10-786-720-15	Sequence 15, Appl
455	52.4	5.3	1891	18	US-10-684-432-210	Sequence 210, App	528	51.8	5.2	4469	18	US-10-788-792-21	Sequence 21, Appl
456	52.4	5.3	1891	19	US-10-843-641A-7617	Sequence 7617, Ap	529	51.8	5.2	4469	18	US-10-473-974-203	Sequence 203, App
457	52.4	5.3	3114	18	US-10-437-963-28971	Sequence 28971, A	530	51.8	5.2	4469	18	US-10-817-525-1	Sequence 1, Appli
458	52.4	5.3	5117	17	US-10-172-118-24	Sequence 24, Appl	c 531	51.6	5.2	786	15	US-10-156-761-4529	Sequence 4529, Ap
459	52.4	5.3	5117	17	US-10-342-887-24	Sequence 24, Appl	532	51.6	5.2	893	15	US-10-180-375-107	Sequence 107, App
460	52.4	5.3	5204	17	US-10-037-417-7	Sequence 7, Appli	533	51.6	5.2	893	17	US-10-183-687-123	Sequence 123, App
461	52.4	5.3	5403	17	US-10-112-944-583	Sequence 583, App	534	51.6	5.2	1177	18	US-10-437-963-12093	Sequence 12093, A
462	52.4	5.3	5640	15	US-10-037-270-41	Sequence 41, Appl	535	51.6	5.2	1242	17	US-10-282-122A-25883	Sequence 25883, A
463	52.4	5.3	5640	17	US-10-117-722-41	Sequence 41, Appl	536	51.6	5.2	2055	17	US-10-369-493-35729	Sequence 35729, A
464	52.4	5.3	8296	14	US-10-037-182-35	Sequence 35, Appl	537	51.6	5.2	2211	18	US-10-437-963-63253	Sequence 63253, A
465	52.4	5.3	11091	17	US-10-312-088-9	Sequence 9, Appli	538	51.6	5.2	2241	15	US-10-156-761-4107	Sequence 4107, Ap
466	52.4	5.3	11118	17	US-10-312-088-8	Sequence 8, Appli	539	51.6	5.2	2853	17	US-10-282-122A-13968	Sequence 13968, A
467	52.4	5.3	11238	15	US-10-205-032-15	Sequence 15, Appl	c 540	51.6	5.2	2865	18	US-10-109-048-1143	Sequence 1143, Ap
468	52.4	5.3	11350	14	US-10-037-182-1	Sequence 1, Appli	541	51.6	5.2	2973	15	US-10-156-761-2660	Sequence 2660, Ap
469	52.4	5.3	11367	17	US-10-312-352-58	Sequence 58, Appl	542	51.6	5.2	9369	16	US-10-200-562-190	Sequence 190, App
470	52.4	5.3	11640	17	US-10-112-944-103	Sequence 103, App	543	51.6	5.2	9369	16	US-10-237-551-190	Sequence 190, App
471	52.4	5.3	14520	15	US-10-156-761-2885	Sequence 2885, Ap	544	51.6	5.2	9369	16	US-10-237-551-190	Sequence 190, App
472	52.4	5.3	60196	15	US-10-205-032-1	Sequence 1, Appli	545	51.6	5.2	77294	19	US-10-729-802-1	Sequence 247, App
473	52.4	5.3	125746	15	US-10-156-761-15102	Sequence 15102, A	c 546	51.6	5.2	218802	19	US-10-897-508-1	Sequence 1, Appli
474	52.2	5.3	897	18	US-10-437-963-54305	Sequence 54305, A	547	51.4	5.2	673	18	US-10-425-115-165006	Sequence 165006,
475	52.2	5.3	1126	18	US-10-767-701-13291	Sequence 13291, A	548	51.4	5.2	1130	18	US-10-437-963-79440	Sequence 79440, A
476	52.2	5.3	1193	17	US-10-425-114-24011	Sequence 24011, A	549	51.4	5.2	1230	15	US-10-156-761-5404	Sequence 5404, Ap
477	52.2	5.3	1308	18	US-10-425-115-49576	Sequence 49576, A	550	51.4	5.2	1359	15	US-10-156-761-6586	Sequence 6586, Ap
c 478	52.2	5.3	1671	18	US-10-437-963-65581	Sequence 65581, A	551	51.4	5.2	1359	15	US-10-156-761-6587	Sequence 6587, Ap
479	52.2	5.3	1687	18	US-10-425-115-71979	Sequence 71979, A	552	51.4	5.2	1510	18	US-10-437-963-60807	Sequence 60807, A
480	52.2	5.3	1746	15	US-10-156-761-4388	Sequence 4388, Ap	553	51.4	5.2	1629	15	US-10-156-761-3330	Sequence 3330, Ap
481	52.2	5.3	2505	17	US-10-369-493-31754	Sequence 31754, A	c 554	51.4	5.2	2021	18	US-10-437-963-99040	Sequence 99040, A
482	52.2	5.3	2757	17	US-10-282-122A-26027	Sequence 26027, A	c 555	51.4	5.2	2031	18	US-10-437-963-81510	Sequence 81510, A
483	52.2	5.3	6297	16	US-10-132-134-37	Sequence 37, Appl	556	51.4	5.2	2307	17	US-10-282-122A-11169	Sequence 11169, A
484	52	5.3	1062	18	US-10-767-701-9233	Sequence 9233, Ap	557	51.4	5.2	2526	18	US-10-723-860-818	Sequence 818, App
485	52	5.3	1065	15	US-10-156-761-6270	Sequence 6270, Ap	558	51.4	5.2	2652	18	US-10-723-860-5422	Sequence 5422, Ap
486	52	5.3	1159	18	US-10-437-963-54428	Sequence 54428, A	559	51.4	5.2	4725	15	US-10-205-032-17	Sequence 17, Appl
487	52	5.3	1218	16	US-10-214-446-37	Sequence 37, Appl	560	51.4	5.2	6891	17	US-10-437-963-54940	Sequence 54940, A
488	52	5.3	1230	15	US-10-156-761-6139	Sequence 6139, Ap	561	51.4	5.2	7847	17	US-10-302-172-591	Sequence 591, App
489	52	5.3	1449	18	US-10-425-115-161558	Sequence 161558,	562	51.4	5.2	11817	15	US-10-156-761-2884	Sequence 2884, Ap
490	52	5.3	1459	18	US-10-437-963-26984	Sequence 26984, A	563	51.4	5.2	30000	11	US-09-980-217-2	Sequence 2, Appli
491	52	5.3	1491	10	US-09-899-575-99	Sequence 99, Appl	564	51.2	5.2	447	11	US-09-732-627A-4334	Sequence 4334, Ap
492	52	5.3	1556	17	US-10-425-114-19808	Sequence 19808, A	565	51.2	5.2	507	18	US-10-437-963-12967	Sequence 12967, A
493	52	5.3	1586	17	US-10-425-114-14339	Sequence 14339, A	566	51.2	5.2	522	15	US-10-156-761-3105	Sequence 3105, Ap
c 494	52	5.3	1707	15	US-10-156-761-4723	Sequence 4723, Ap	567	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 1739, Ap
495	52	5.3	2367	15	US-10-156-761-1751	Sequence 1751, Ap	568	51.2	5.2	699	11	US-09-938-842A-1739	Sequence 841, App
496	52	5.3	3597	15	US-10-156-761-2534	Sequence 2534, Ap	c 569	51.2	5.2	792	9	US-09-770-445-841	Sequence 12968, A
497	51.8	5.2	672	15	US-10-156-761-1819	Sequence 1819, Ap	570	51.2	5.2	898	18	US-10-437-963-12968	Sequence 2043, Ap
498	51.8	5.2	918	15	US-10-156-761-6700	Sequence 6700, Ap	571	51.2	5.2	1002	15	US-10-156-761-2043	Sequence 14710, A
499	51.8	5.2	1227	17	US-10-282-122A-15076	Sequence 15076, A	572	51.2	5.2	1107	17	US-10-282-122A-14710	Sequence 3446, Ap
500	51.8	5.2	1253	13	US-10-087-192-1322	Sequence 1322, Ap	573	51.2	5.2	1134	15	US-10-156-761-3946	Sequence 421, App
501	51.8	5.2	1344	15	US-10-156-761-1108	Sequence 1108, Ap	574	51.2	5.2	1188	15	US-10-156-761-421	Sequence 421, App
502	51.8	5.2	1347	17	US-10-369-493-43202	Sequence 43202, A	575	51.2	5.2	1267	18	US-10-425-115-15750	Sequence 15750, A
503	51.8	5.2	1593	15	US-10-156-761-5226	Sequence 5226, Ap	576	51.2	5.2	1290	18	US-10-739-930-2596	Sequence 2596, Ap
504	51.8	5.2	1645	17	US-10-425-114-32254	Sequence 32254, A	577	51.2	5.2	1493	18	US-10-739-930-2577	Sequence 2577, Ap
505	51.8	5.2	1645	17	US-10-425-114-30266	Sequence 30266, A	578	51.2	5.2	1536	15	US-10-156-761-7115	Sequence 7115, Ap
506	51.8	5.2	1659	17	US-10-369-493-39901	Sequence 39901, A	579	51.2	5.2	1557	18	US-10-437-963-89570	Sequence 89570, A
507	51.8	5.2	1677	17	US-10-369-493-39150	Sequence 39150, A	580	51.2	5.2	1637	18	US-10-437-963-73981	Sequence 73981, A
508	51.8	5.2	1704	18	US-10-739-930-2739	Sequence 2739, Ap	c 581	51.2	5.2	1683	15	US-10-205-032-3	Sequence 3, Appli
509	51.8	5.2	1704	15	US-10-156-761-1559	Sequence 1559, Ap	582	51.2	5.2	1841	18	US-10-437-963-89571	Sequence 89571, A
510	51.8	5.2	1796	18	US-10-437-963-43317	Sequence 43317, A	583	51.2	5.2	1959	18	US-10-739-930-3025	Sequence 3025, Ap
511	51.8	5.2	1796	18	US-10-425-115-133999	Sequence 133999,	584	51.2	5.2	2034	9	US-09-815-242-8002	Sequence 8002, Ap
512	51.8	5.2	1803	18	US-10-437-963-23751	Sequence 23751, A	585	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6391, Ap
513	51.8	5.2	1880	18	US-10-437-963-23751	Sequence 23751, A	586	51.2	5.2	10000	15	US-10-156-761-15103	Sequence 15103, A
514	51.8	5.2	1894	18	US-10-437-963-89370	Sequence 89370, A	587	51	5.2	687	15	US-10-156-761-2253	Sequence 2253, Ap
515	51.8	5.2	2075	16	US-10-138-434A-2	Sequence 2, Appli	588	51	5.2	694	18	US-10-425-115-101015	Sequence 101015,



589	51	5.2	894	18	US-10-739-930-2948	Sequence 2948, Ap	662	50.4	5.1	45055	17	US-10-107-431-277	Sequence 277, App
590	51	5.2	1008	18	US-10-437-963-16086	Sequence 16086, A	663	50.2	5.1	595	17	US-10-260-238-3262	Sequence 3262, Ap
591	51	5.2	1160	17	US-10-425-114-2979	Sequence 2979, Ap	664	50.2	5.1	740	18	US-10-437-963-67956	Sequence 67956, A
592	51	5.2	1203	18	US-10-425-115-1045	Sequence 1045, Ap	665	50.2	5.1	841	17	US-10-282-122A-14618	Sequence 14618, A
593	51	5.2	1218	15	US-10-156-761-6041	Sequence 6041, Ap	666	50.2	5.1	1002	15	US-10-156-761-696	Sequence 696, App
594	51	5.2	1497	17	US-10-282-122A-25509	Sequence 25509, A	667	50.2	5.1	1093	18	US-10-425-115-106454	Sequence 106454, A
595	51	5.2	1503	17	US-10-260-238-1244	Sequence 1244, Ap	668	50.2	5.1	1426	18	US-10-437-963-1435	Sequence 1435, Ap
596	51	5.2	1632	16	US-10-132-350-39	Sequence 39, Appl	c 669	50.2	5.1	1856	18	US-10-437-963-59660	Sequence 59660, A
597	51	5.2	1755	17	US-10-369-493-32171	Sequence 32171, A	670	50.2	5.1	1896	15	US-10-156-761-5658	Sequence 5658, Ap
598	51	5.2	1803	16	US-10-132-350-37	Sequence 37, Appl	671	50.2	5.1	2856	18	US-10-437-963-61943	Sequence 61943, A
599	51	5.2	2878	18	US-10-437-963-42117	Sequence 42117, A	672	50.2	5.1	3032	18	US-10-437-963-16502	Sequence 16502, A
600	51	5.2	2220	15	US-10-156-761-5063	Sequence 5063, Ap	673	50.2	5.1	3039	17	US-10-369-493-42391	Sequence 42391, A
601	51	5.2	2266	18	US-10-425-115-130933	Sequence 130933, A	674	50.2	5.1	4826	9	US-09-772-304A-1	Sequence 1, Appl1
602	51	5.2	2370	15	US-10-156-761-4813	Sequence 4813, Ap	675	50.2	5.1	4826	18	US-10-717-381-1	Sequence 1, Appl1
603	51	5.2	2561	9	US-09-976-740-48	Sequence 48, Appl	c 676	50	5.1	390	9	US-09-960-352-14023	Sequence 14023, A
604	51	5.2	2561	13	US-10-023-529-48	Sequence 48, Appl	677	50	5.1	1020	17	US-10-437-963-98512	Sequence 98512, A
605	51	5.2	2561	13	US-10-023-523-48	Sequence 48, Appl	678	50	5.1	1057	17	US-10-425-114-24158	Sequence 24158, A
606	51	5.2	2561	17	US-10-616-187-48	Sequence 48, Appl	679	50	5.1	1213	18	US-10-425-115-122558	Sequence 122558, A
607	51	5.2	2561	17	US-10-671-242-48	Sequence 48, Appl	680	50	5.1	1272	18	US-10-437-963-37456	Sequence 37456, A
608	51	5.2	2601	18	US-10-437-963-72883	Sequence 72883, A	681	50	5.1	1317	17	US-10-369-493-31645	Sequence 31645, A
609	51	5.2	2710	17	US-10-250-613-33	Sequence 33, Appl	682	50	5.1	1337	17	US-10-369-493-42992	Sequence 42992, A
610	51	5.2	2765	18	US-10-437-963-2941	Sequence 2941, Ap	683	50	5.1	1365	17	US-10-282-122A-13750	Sequence 13750, A
611	51	5.2	3606	15	US-10-156-761-3063	Sequence 3063, Ap	c 684	50	5.1	1582	18	US-10-739-930-2333	Sequence 2333, Ap
612	50.8	5.1	819	15	US-10-156-761-4765	Sequence 4765, Ap	685	50	5.1	1806	16	US-10-329-079-38	Sequence 38, Appl
613	50.8	5.1	1125	17	US-10-282-122A-31378	Sequence 31378, A	686	50	5.1	1806	17	US-10-329-027-29	Sequence 29, Appl
614	50.8	5.1	1155	15	US-10-193-002-12	Sequence 12, Appl	687	50	5.1	1840	15	US-10-156-761-6889	Sequence 6889, Ap
615	50.8	5.1	1155	15	US-10-084-843-12	Sequence 12, Appl	688	50	5.1	2148	17	US-10-369-493-42943	Sequence 42943, A
616	50.8	5.1	1173	17	US-10-260-238-706	Sequence 706, App	689	50	5.1	3012	18	US-10-437-963-78726	Sequence 78726, A
617	50.8	5.1	1188	15	US-10-156-761-421	Sequence 421, App	690	50	5.1	3135	15	US-10-156-761-2721	Sequence 2721, Ap
618	50.8	5.1	1230	18	US-10-437-963-96421	Sequence 96421, A	691	50	5.1	3374	18	US-10-437-963-10004	Sequence 10004, A
619	50.8	5.1	1317	9	US-09-815-242-4148	Sequence 4148, Ap	c 692	50	5.1	5061	18	US-10-156-761-414	Sequence 414, App
620	50.8	5.1	1317	9	US-10-282-122A-7337	Sequence 7337, Ap	c 693	50	5.1	10692	15	US-10-437-963-9832	Sequence 9832, Ap
621	50.8	5.1	1551	15	US-10-156-761-1622	Sequence 1622, Ap	694	50	5.1	13842	9	US-09-861-289-30	Sequence 30, Appl
622	50.8	5.1	1622	18	US-10-476-638-10	Sequence 10, Appl	695	50	5.1	13842	10	US-09-860-846-30	Sequence 30, Appl
623	50.8	5.1	1682	18	US-10-156-761-65821	Sequence 65821, A	696	50	5.1	13842	10	US-09-988-384B-30	Sequence 30, Appl
624	50.8	5.1	2230	14	US-10-437-963-65821	Sequence 65821, A	697	50	5.1	13842	10	US-09-836-821-30	Sequence 30, Appl
625	50.8	5.1	5760	14	US-10-152-886-14	Sequence 14, Appl	698	50	5.1	13842	16	US-10-271-889-30	Sequence 30, Appl
c 626	50.8	5.1	100000	15	US-10-156-761-15103	Sequence 15103, A	699	50	5.1	15738	17	US-10-329-079-12	Sequence 12, Appl
627	50.6	5.1	940	9	US-09-452-239-15	Sequence 15, Appl	700	50	5.1	32329	17	US-10-374-903A-1	Sequence 1, Appl1
628	50.6	5.1	940	18	US-10-425-115-176490	Sequence 176490, A	701	50	5.1	36778	9	US-09-861-289-5	Sequence 5, Appl1
629	50.6	5.1	1032	15	US-10-425-115-176490	Sequence 36005, A	702	50	5.1	36778	9	US-09-860-846-5	Sequence 5, Appl1
630	50.6	5.1	1041	15	US-10-437-963-36005	Sequence 7418, Ap	703	50	5.1	36778	10	US-09-836-821-5	Sequence 5, Appl1
631	50.6	5.1	1371	17	US-10-282-122A-25436	Sequence 25436, A	704	50	5.1	36778	16	US-10-271-889-48	Sequence 48, Appl
632	50.6	5.1	1400	18	US-10-425-115-20597	Sequence 20597, A	705	50	5.1	37360	16	US-10-329-079-6	Sequence 6, Appl1
633	50.6	5.1	1449	18	US-10-437-963-64629	Sequence 64629, A	706	50	5.1	37948	10	US-09-988-384B-5	Sequence 5, Appl1
634	50.6	5.1	1695	15	US-10-156-761-3949	Sequence 3949, Ap	707	50	5.1	38506	10	US-09-793-708-19	Sequence 19, Appl
635	50.6	5.1	1848	18	US-10-437-963-22612	Sequence 22612, A	708	50	5.1	38506	15	US-10-201-385-1	Sequence 1, Appl1
636	50.6	5.1	2300	18	US-10-425-115-134362	Sequence 134362, A	709	50	5.1	38506	16	US-10-160-539-19	Sequence 19, Appl
637	50.6	5.1	2477	18	US-10-425-115-170055	Sequence 170055, A	710	50	5.1	38506	19	US-10-468-828-19	Sequence 19, Appl
638	50.6	5.1	2741	18	US-10-425-115-148395	Sequence 148395, A	711	49.8	5.0	856	9	US-09-823-245A-99	Sequence 99, Appl1
639	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, A	712	49.8	5.0	880	17	US-10-425-114-32836	Sequence 32836, A
640	50.6	5.1	4233	18	US-10-425-115-184346	Sequence 4143, Ap	713	49.8	5.0	915	15	US-10-156-761-2013	Sequence 2013, Ap
641	50.6	5.1	4244	18	US-10-723-860-8016	Sequence 8016, Ap	714	49.8	5.0	940	17	US-10-425-114-35300	Sequence 35300, A
c 642	50.4	5.1	549	17	US-10-260-238-239	Sequence 239, App	715	49.8	5.0	948	18	US-10-425-115-43218	Sequence 43218, A
643	50.4	5.1	645	15	US-10-156-761-6059	Sequence 6059, Ap	716	49.8	5.0	1227	15	US-10-156-761-6074	Sequence 6074, Ap
644	50.4	5.1	662	18	US-10-437-963-74146	Sequence 74146, A	717	49.8	5.0	1245	11	US-09-758-759-22	Sequence 22, Appl
645	50.4	5.1	669	17	US-10-107-431-166	Sequence 166, App	718	49.8	5.0	1372	17	US-10-107-431-32	Sequence 32, Appl
646	50.4	5.1	777	18	US-10-425-115-83763	Sequence 83763, A	719	49.8	5.0	1393	14	US-10-145-415-17	Sequence 17, Appl
647	50.4	5.1	838	18	US-10-425-115-127687	Sequence 127687, A	720	49.8	5.0	1374	17	US-10-282-122A-14455	Sequence 14455, A
648	50.4	5.1	891	18	US-10-437-963-41595	Sequence 41595, A	721	49.8	5.0	1410	18	US-10-437-963-97868	Sequence 97868, A
649	50.4	5.1	1062	18	US-10-437-963-34793	Sequence 34793, A	722	49.8	5.0	1440	15	US-10-156-761-5216	Sequence 5216, Ap
650	50.4	5.1	1159	17	US-10-374-780A-879	Sequence 879, App	723	49.8	5.0	1572	15	US-10-156-761-4159	Sequence 4159, Ap
651	50.4	5.1	1454	18	US-10-425-115-68094	Sequence 68094, A	724	49.8	5.0	1581	17	US-10-464-368-113	Sequence 113, App
652	50.4	5.1	1587	15	US-10-156-761-5134	Sequence 5134, Ap	725	49.8	5.0	1594	18	US-10-437-963-42666	Sequence 42666, A
653	50.4	5.1	1848	15	US-10-156-761-3850	Sequence 3850, Ap	726	49.8	5.0	1791	15	US-10-156-761-2352	Sequence 2352, Ap
654	50.4	5.1	1910	18	US-10-437-963-23941	Sequence 23941, A	727	49.8	5.0	1814	14	US-10-060-036-182	Sequence 182, App
655	50.4	5.1	1951	18	US-10-437-963-31078	Sequence 31078, A	728	49.8	5.0	1837	19	US-10-278-698-240	Sequence 240, App
656	50.4	5.1	2082	15	US-10-156-761-6082	Sequence 6082, Ap	729	49.8	5.0	1837	19	US-10-278-698-241	Sequence 241, App
657	50.4	5.1	3048	15	US-10-156-761-3146	Sequence 3146, Ap	730	49.8	5.0	1837	19	US-10-278-698-754	Sequence 754, App
658	50.4	5.1	3456	18	US-10-437-963-50711	Sequence 50711, A	731	49.8	5.0	1837	19	US-10-278-698-755	Sequence 755, App
c 659	50.4	5.1	5003	18	US-10-437-963-18350	Sequence 18350, A	732	49.8	5.0	1929	9	US-09-761-534A-9	Sequence 9, Appl1
660	50.4	5.1	6375	17	US-10-389-647-144	Sequence 144, App	733	49.8	5.0	1929	19	US-10-885-523-9	Sequence 9, Appl1
661	50.4	5.1	14427	15	US-10-156-761-1540	Sequence 1540, Ap	734	49.8	5.0	2031	15	US-10-156-761-2451	Sequence 2451, Ap

735	49.8	5.0	2115	15	US-10-156-761-5640	Sequence 5640, Ap	808	49.6	5.0	14023	19	US-10-741-600-17840	Sequence 17840, A
736	49.8	5.0	2136	18	US-10-437-963-49142	Sequence 49142, A	c 809	49.6	5.0	199130	19	US-10-741-600-17617	Sequence 17617, A
737	49.8	5.0	2220	10	US-09-873-367C-159	Sequence 159, App	810	49.4	5.0	426	18	US-10-437-963-99472	Sequence 99472, A
738	49.8	5.0	2320	19	US-10-843-641A-159	Sequence 159, App	811	49.4	5.0	843	15	US-10-156-761-1994	Sequence 1994, Ap
739	49.8	5.0	2335	18	US-10-437-963-11953	Sequence 11953, A	812	49.4	5.0	876	15	US-10-156-761-4743	Sequence 4743, Ap
740	49.8	5.0	2664	15	US-10-156-761-1241	Sequence 1241, Ap	813	49.4	5.0	951	15	US-10-259-165-313	Sequence 313, App
741	49.8	5.0	3066	15	US-10-156-761-1742	Sequence 1742, Ap	814	49.4	5.0	978	19	US-10-762-107-77	Sequence 77, Appl
742	49.8	5.0	3113	9	US-09-894-998-52	Sequence 52, Appl	c 815	49.4	5.0	1005	18	US-10-437-963-39562	Sequence 39562, A
743	49.8	5.0	3113	14	US-10-121-988-52	Sequence 52, Appl	816	49.4	5.0	1029	17	US-10-084-846A-87	Sequence 87, Appl
744	49.8	5.0	3113	16	US-10-200-562-52	Sequence 52, Appl	817	49.4	5.0	1173	17	US-10-282-122A-25963	Sequence 25963, A
745	49.8	5.0	3113	16	US-10-237-551-52	Sequence 52, Appl	818	49.4	5.0	1191	17	US-10-282-122A-15207	Sequence 15207, A
746	49.8	5.0	3345	9	US-09-894-998-49	Sequence 49, Appl	819	49.4	5.0	1281	15	US-10-156-761-2281	Sequence 2281, Ap
747	49.8	5.0	3345	14	US-10-121-988-49	Sequence 49, Appl	820	49.4	5.0	1385	17	US-10-425-114-26389	Sequence 26389, A
748	49.8	5.0	3345	16	US-10-200-562-49	Sequence 49, Appl	821	49.4	5.0	1401	18	US-10-437-963-95208	Sequence 95208, A
749	49.8	5.0	3345	16	US-10-200-562-189	Sequence 189, App	822	49.4	5.0	1557	17	US-10-425-114-18927	Sequence 18927, A
750	49.8	5.0	3345	16	US-10-237-551-49	Sequence 49, Appl	823	49.4	5.0	1587	17	US-10-282-122A-28573	Sequence 28573, A
751	49.8	5.0	3345	16	US-10-237-551-189	Sequence 189, App	824	49.4	5.0	1590	17	US-10-282-122A-26270	Sequence 26270, A
752	49.8	5.0	4323	17	US-10-282-122A-26577	Sequence 26577, A	c 825	49.4	5.0	1612	18	US-10-437-963-102480	Sequence 102480, A
753	49.8	5.0	37116	17	US-10-107-431-279	Sequence 279, App	826	49.4	5.0	1619	17	US-10-425-114-24202	Sequence 24202, A
754	49.8	5.0	65140	18	US-10-203-295-35	Sequence 1, Appli	827	49.4	5.0	1619	17	US-10-425-114-24326	Sequence 24326, A
755	49.8	5.0	125401	18	US-10-203-295-35	Sequence 35, Appl	828	49.4	5.0	1633	18	US-10-425-115-157740	Sequence 157740, A
756	49.6	5.0	242	9	US-09-823-876-781	Sequence 781, App	c 829	49.4	5.0	1697	17	US-10-425-114-29187	Sequence 29187, A
757	49.6	5.0	242	10	US-09-823-876-781	Sequence 781, App	830	49.4	5.0	1707	18	US-10-425-115-113441	Sequence 113441, A
758	49.6	5.0	746	17	US-10-425-114-12136	Sequence 12136, A	831	49.4	5.0	2091	14	US-10-121-988-78	Sequence 78, Appl
759	49.6	5.0	806	17	US-10-767-701-1614	Sequence 1614, Ap	832	49.4	5.0	2091	16	US-10-200-562-78	Sequence 78, Appl
760	49.6	5.0	876	18	US-10-425-115-55664	Sequence 55664, A	833	49.4	5.0	2091	16	US-10-237-551-78	Sequence 78, Appl
761	49.6	5.0	976	17	US-10-425-114-13780	Sequence 13780, A	834	49.4	5.0	2091	16	US-10-237-551-226	Sequence 226, App
762	49.6	5.0	978	15	US-10-156-761-6381	Sequence 6381, Ap	835	49.4	5.0	2118	14	US-10-121-988-87	Sequence 87, Appl
763	49.6	5.0	989	18	US-10-437-963-58326	Sequence 58326, A	836	49.4	5.0	2118	16	US-10-200-562-87	Sequence 87, Appl
764	49.6	5.0	1081	15	US-10-156-761-2655	Sequence 2655, Ap	837	49.4	5.0	2118	16	US-10-237-551-87	Sequence 87, Appl
765	49.6	5.0	1151	17	US-10-425-114-23539	Sequence 23539, A	838	49.4	5.0	2211	14	US-10-121-988-86	Sequence 86, Appl
766	49.6	5.0	1176	17	US-10-425-114-21556	Sequence 21556, A	839	49.4	5.0	2211	16	US-10-200-562-86	Sequence 86, Appl
767	49.6	5.0	1194	18	US-10-437-963-102262	Sequence 102262, A	840	49.4	5.0	2211	16	US-10-237-551-86	Sequence 86, Appl
768	49.6	5.0	1205	18	US-10-437-963-84924	Sequence 84924, A	c 841	49.4	5.0	2270	18	US-10-437-963-53336	Sequence 53336, A
769	49.6	5.0	1329	15	US-10-156-761-5851	Sequence 5851, Ap	842	49.4	5.0	2502	17	US-10-282-122A-17902	Sequence 17902, A
770	49.6	5.0	1362	17	US-10-282-122A-33594	Sequence 33594, A	843	49.4	5.0	2517	17	US-10-369-493-43222	Sequence 43222, A
771	49.6	5.0	1404	17	US-10-369-493-31750	Sequence 31750, A	844	49.4	5.0	3038	16	US-10-251-661-11	Sequence 11, Appl
772	49.6	5.0	1651	18	US-10-437-963-23386	Sequence 23386, A	845	49.4	5.0	3038	18	US-10-680-087-45	Sequence 45, Appl
773	49.6	5.0	1743	17	US-10-172-118-1387	Sequence 1387, Ap	846	49.4	5.0	3331	10	US-09-373-658-31	Sequence 31, Appl
774	49.6	5.0	1743	17	US-10-342-887-1387	Sequence 1387, Ap	847	49.4	5.0	3331	11	US-09-989-687-31	Sequence 31, Appl
775	49.6	5.0	1761	16	US-10-156-761-1503	Sequence 1503, Ap	848	49.4	5.0	3352	18	US-10-425-115-84048	Sequence 84048, A
776	49.6	5.0	1765	16	US-10-237-551-225	Sequence 225, App	c 849	49.4	5.0	3489	11	US-09-894-273-1	Sequence 1, Appli
777	49.6	5.0	1929	18	US-10-437-963-70663	Sequence 70663, A	850	49.4	5.0	3489	15	US-10-294-804-1	Sequence 1, Appli
778	49.6	5.0	1978	18	US-10-437-963-88743	Sequence 88743, A	c 851	49.4	5.0	3489	18	US-10-194-046-1	Sequence 1, Appli
779	49.6	5.0	2040	9	US-09-815-242-4027	Sequence 4027, Ap	852	49.4	5.0	4255	17	US-10-282-122A-14875	Sequence 14875, A
780	49.6	5.0	2040	17	US-10-282-122A-7316	Sequence 7316, Ap	853	49.4	5.0	4353	17	US-10-226-638A-15	Sequence 15, Appl
781	49.6	5.0	2059	18	US-10-437-963-59377	Sequence 59377, A	854	49.4	5.0	9762	19	US-10-762-107-73	Sequence 73, Appl
782	49.6	5.0	2065	18	US-10-437-963-31244	Sequence 31244, A	855	49.4	5.0	14061	17	US-10-093-463-73	Sequence 73, Appl
783	49.6	5.0	2218	17	US-10-108-260A-2174	Sequence 2174, Ap	c 856	49.4	5.0	30000	11	US-09-980-217-3	Sequence 3, Appli
784	49.6	5.0	2271	15	US-10-101-510-133	Sequence 133, App	857	49.4	5.0	32329	17	US-10-374-903A-1	Sequence 1, Appli
785	49.6	5.0	2471	18	US-10-437-963-62969	Sequence 62969, A	858	49.4	5.0	59816	17	US-10-084-846A-1	Sequence 1, Appli
786	49.6	5.0	2487	15	US-10-208-823-135	Sequence 135, App	c 859	49.4	5.0	59816	17	US-10-084-846A-2	Sequence 2, Appli
787	49.6	5.0	2487	17	US-10-172-118-1045	Sequence 1045, Ap	860	49.4	5.0	109519	11	US-09-758-759-1	Sequence 1, Appli
788	49.6	5.0	2487	17	US-10-342-887-1045	Sequence 1045, Ap	861	49.2	5.0	955	17	US-10-425-114-17203	Sequence 17203, A
789	49.6	5.0	2700	15	US-10-156-761-7310	Sequence 7310, Ap	862	49.2	5.0	972	18	US-10-425-115-150798	Sequence 32340, A
790	49.6	5.0	2742	9	US-09-815-242-4163	Sequence 4163, Ap	863	49.2	5.0	975	18	US-10-425-115-150798	Sequence 150798, A
791	49.6	5.0	2742	17	US-10-282-122A-7408	Sequence 7408, Ap	c 864	49.2	5.0	1004	17	US-10-332-859-324	Sequence 324, App
792	49.6	5.0	3459	17	US-10-369-493-31552	Sequence 31552, A	865	49.2	5.0	1051	18	US-10-425-115-173915	Sequence 173915, A
793	49.6	5.0	3729	17	US-10-671-403-86	Sequence 86, Appl	866	49.2	5.0	1155	18	US-10-437-963-94232	Sequence 94232, A
794	49.6	5.0	3729	17	US-10-671-419-86	Sequence 86, Appl	867	49.2	5.0	1296	18	US-10-437-963-82846	Sequence 82846, A
795	49.6	5.0	3729	17	US-10-670-844-86	Sequence 86, Appl	868	49.2	5.0	1317	15	US-10-156-761-3647	Sequence 3647, Ap
796	49.6	5.0	3729	17	US-10-671-138-86	Sequence 86, Appl	869	49.2	5.0	1357	18	US-10-437-963-18242	Sequence 18242, A
797	49.6	5.0	3729	17	US-10-673-098-86	Sequence 86, Appl	870	49.2	5.0	1493	17	US-10-425-114-3264	Sequence 3264, Ap
798	49.6	5.0	3729	17	US-10-673-638-86	Sequence 86, Appl	871	49.2	5.0	1587	15	US-10-156-761-4508	Sequence 4508, Ap
799	49.6	5.0	3729	17	US-10-673-127-86	Sequence 86, Appl	c 872	49.2	5.0	1602	9	US-09-833-790-417	Sequence 417, App
800	49.6	5.0	3729	18	US-10-670-817-86	Sequence 86, Appl	c 873	49.2	5.0	1602	16	US-10-293-582-15	Sequence 15, Appli
801	49.6	5.0	3729	18	US-10-673-119-86	Sequence 86, Appl	c 874	49.2	5.0	1602	17	US-10-761-169-5	Sequence 5, Appli
802	49.6	5.0	3729	18	US-10-671-207-86	Sequence 86, Appl	875	49.2	5.0	1613	17	US-10-425-114-3572	Sequence 3572, Ap
803	49.6	5.0	3729	19	US-10-673-120-86	Sequence 86, Appl	876	49.2	5.0	1679	18	US-10-437-963-32154	Sequence 32154, A
804	49.6	5.0	3942	11	US-10-156-761-5692	Sequence 86, Appl	877	49.2	5.0	1908	15	US-10-437-963-32154	Sequence 32154, A
805	49.6	5.0	5181	11	US-09-968-007A-802	Sequence 802, App	878	49.2	5.0	2331	18	US-10-156-761-260	Sequence 260, App
806	49.6	5.0	5181	19	US-10-843-641A-7272	Sequence 7272, Ap	879	49.2	5.0	2455	9	US-09-917-800A-1386	Sequence 1386, Ap
807	49.6	5.0	12591	19	US-10-741-600-17855	Sequence 17855, A	880	49.2	5.0	2455	16	US-10-316-253-77	Sequence 27, Appl

881	49.2	5.0	2455	17	US-10-388-934-21	Sequence 21, Appl	954	48.8	4.9	4322	18	US-10-425-115-15092	Sequence 15092, A
882	49.2	5.0	2455	17	US-10-152-319A-1964	Sequence 1964, Ap	955	48.8	4.9	7897	17	US-10-359-120-161	Sequence 161, App
883	49.2	5.0	2607	16	US-10-247-671-13	Sequence 13, Appl	956	48.8	4.9	9166	17	US-10-359-120-168	Sequence 168, App
C 884	49.2	5.0	2717	17	US-10-723-860-8011	Sequence 8011, Ap	957	48.8	4.9	9167	17	US-10-359-120-171	Sequence 171, App
885	49.2	5.0	3540	17	US-10-369-493-32003	Sequence 32003, A	958	48.8	4.9	9169	17	US-10-359-120-169	Sequence 169, App
886	49.2	5.0	4161	15	US-10-156-761-5450	Sequence 5450, Ap	959	48.8	4.9	9170	17	US-10-359-120-166	Sequence 166, App
887	49.2	5.0	137560	18	US-10-481-111-1	Sequence 1, Appl	960	48.8	4.9	9189	17	US-10-359-120-159	Sequence 159, App
888	49.2	5.0	339	15	US-10-174-693-193	Sequence 193, App	961	48.8	4.9	9194	17	US-10-359-120-163	Sequence 163, App
889	49.2	5.0	1011	17	US-10-282-122A-25697	Sequence 25697, A	962	48.8	4.9	9194	17	US-10-359-120-164	Sequence 164, App
C 891	49.2	5.0	1261	18	US-10-156-761-7058	Sequence 7058, Ap	963	48.8	4.9	9407	17	US-10-359-120-175	Sequence 175, App
892	49.2	5.0	1226	18	US-10-437-963-70724	Sequence 70724, A	964	48.8	4.9	9782	17	US-10-359-120-173	Sequence 173, App
893	49.2	5.0	1236	18	US-10-437-963-27235	Sequence 27235, A	965	48.8	4.9	9783	17	US-10-359-120-172	Sequence 172, App
894	49.2	5.0	1355	17	US-10-437-963-23001	Sequence 23001, A	966	48.8	4.9	9783	17	US-10-359-120-176	Sequence 176, App
895	49.2	5.0	1400	17	US-10-458-108-6	Sequence 6, Appl	967	48.8	4.9	9788	17	US-10-359-120-174	Sequence 174, App
896	49.2	5.0	1462	14	US-10-437-963-2506	Sequence 2506, Ap	968	48.8	4.9	9792	17	US-10-359-120-170	Sequence 170, App
897	49.2	5.0	1473	18	US-10-175-523-163	Sequence 163, App	969	48.8	4.9	10035	17	US-10-107-431-282	Sequence 282, App
C 898	49.2	5.0	1473	18	US-10-411-910A-261	Sequence 261, App	970	48.8	4.9	12411	17	US-10-107-431-282	Sequence 165, App
899	49.2	5.0	1614	9	US-09-976-740-45	Sequence 45, Appl	971	48.8	4.9	18435	15	US-10-359-120-165	Sequence 165, App
C 900	49.2	5.0	1614	13	US-10-023-529-45	Sequence 45, Appl	972	48.8	4.9	18435	15	US-10-156-761-412	Sequence 412, App
C 901	49.2	5.0	1614	13	US-10-023-529-45	Sequence 45, Appl	972	48.8	4.9	13538	16	US-10-314-657-1	Sequence 1, Appl
C 902	49.2	5.0	1614	17	US-10-616-187-45	Sequence 45, Appl	974	48.6	4.9	396	18	US-10-767-701-30763	Sequence 30763, A
903	49.2	5.0	1614	17	US-10-671-242-45	Sequence 45, Appl	975	48.6	4.9	528	9	US-09-452-239-33	Sequence 33, Appl
904	49.2	5.0	1797	18	US-10-437-963-28602	Sequence 28602, A	976	48.6	4.9	528	9	US-10-437-963-5272	Sequence 5272, Ap
C 905	49.2	5.0	1852	9	US-09-969-852-4	Sequence 4, Appl	976	48.6	4.9	668	18	US-10-767-701-11523	Sequence 11523, A
C 906	49.2	5.0	1852	17	US-10-310-151-280	Sequence 280, App	977	48.6	4.9	687	17	US-10-282-122A-26299	Sequence 26299, A
907	49.2	5.0	1946	18	US-10-437-963-22064	Sequence 22064, A	978	48.6	4.9	690	17	US-10-282-122A-28509	Sequence 28509, A
908	49.2	5.0	1974	18	US-10-437-963-87831	Sequence 87831, A	979	48.6	4.9	761	18	US-10-425-115-127921	Sequence 127921, A
909	49.2	5.0	2067	18	US-10-437-963-18405	Sequence 18405, A	980	48.6	4.9	796	18	US-10-767-701-7856	Sequence 7856, Ap
C 910	49.2	5.0	2143	17	US-10-425-114-23617	Sequence 23617, A	981	48.6	4.9	847	18	US-10-425-115-17266	Sequence 17266, A
C 911	49.2	5.0	2204	18	US-10-437-963-11022	Sequence 11022, A	982	48.6	4.9	934	17	US-10-425-114-17266	Sequence 17266, A
912	49.2	5.0	2239	17	US-10-425-114-5232	Sequence 5232, Ap	983	48.6	4.9	974	17	US-10-425-114-18881	Sequence 18881, A
C 913	49.2	5.0	2271	18	US-10-437-963-74809	Sequence 74809, A	984	48.6	4.9	1107	18	US-10-425-115-161174	Sequence 161174, A
914	49.2	5.0	2436	15	US-10-156-761-2569	Sequence 2569, Ap	985	48.6	4.9	1143	15	US-10-156-761-6453	Sequence 6453, Ap
C 915	49.2	5.0	2539	18	US-10-425-115-91117	Sequence 91117, A	986	48.6	4.9	1170	18	US-10-425-115-162747	Sequence 162747, A
C 916	49.2	5.0	2939	9	US-10-437-963-58050	Sequence 58050, A	987	48.6	4.9	1203	17	US-10-369-493-34414	Sequence 34414, A
C 917	49.2	5.0	12425	13	US-09-976-740-50	Sequence 50, Appl	988	48.6	4.9	1302	18	US-10-425-115-164928	Sequence 164928, A
C 918	49.2	5.0	12425	13	US-10-023-529-50	Sequence 50, Appl	989	48.6	4.9	1366	18	US-10-425-115-28293	Sequence 28293, A
C 919	49.2	5.0	12425	17	US-10-616-187-50	Sequence 50, Appl	990	48.6	4.9	1453	18	US-10-437-963-78719	Sequence 78719, A
C 920	49.2	5.0	12425	17	US-10-616-187-50	Sequence 50, Appl	991	48.6	4.9	1461	13	US-10-156-761-2205	Sequence 2205, Ap
C 921	49.2	5.0	77536	10	US-09-940-3158-1	Sequence 50, Appl	992	48.6	4.9	1479	13	US-10-016-283-35	Sequence 35, Appl
922	48.8	4.9	363	15	US-10-156-761-5224	Sequence 1, Appl	993	48.6	4.9	1533	18	US-09-814-353-20197	Sequence 20197, A
923	48.8	4.9	389	18	US-10-425-115-179802	Sequence 179802, A	994	48.6	4.9	1617	18	US-10-425-115-164014	Sequence 164014, A
C 924	48.8	4.9	459	18	US-10-437-963-3398	Sequence 3398, Ap	995	48.6	4.9	1685	17	US-10-425-114-27558	Sequence 27558, A
925	48.8	4.9	513	15	US-10-156-761-5057	Sequence 5057, Ap	996	48.6	4.9	1783	18	US-10-437-963-340	Sequence 340, App
926	48.8	4.9	516	18	US-10-437-963-75898	Sequence 75898, A	997	48.6	4.9	1839	11	US-09-758-759-150	Sequence 150, App
927	48.8	4.9	602	18	US-10-425-115-12234	Sequence 12234, A	998	48.6	4.9	1962	18	US-10-437-963-89753	Sequence 89753, A
928	48.8	4.9	618	15	US-10-156-761-4061	Sequence 172234, A	999	48.6	4.9	2040	9	US-09-874-923-5	Sequence 5, Appl
929	48.8	4.9	728	17	US-10-425-114-14002	Sequence 14002, A	1000	48.6	4.9	2040	9	US-09-991-496-5	Sequence 5, Appl
930	48.8	4.9	827	17	US-10-425-114-18832	Sequence 18832, A	1001	48.6	4.9	2040	16	US-10-098-732A-72	Sequence 72, Appl
931	48.8	4.9	828	15	US-10-156-761-1422	Sequence 1422, Ap	1002	48.6	4.9	2238	18	US-10-437-963-35019	Sequence 35019, A
932	48.8	4.9	933	15	US-10-156-761-1758	Sequence 1758, Ap	1003	48.6	4.9	2279	16	US-10-021-660-68	Sequence 68, Appl
933	48.8	4.9	1068	15	US-10-156-761-1861	Sequence 1861, Ap	1005	48.6	4.9	2279	17	US-10-211-462-212	Sequence 212, App
934	48.8	4.9	1085	17	US-10-425-114-3	Sequence 3, Appl	1006	48.6	4.9	2577	18	US-10-332-413-9	Sequence 9, Appl
935	48.8	4.9	1094	18	US-10-767-701-13435	Sequence 13435, A	1007	48.6	4.9	2712	9	US-09-748-033-4	Sequence 4, Appl
936	48.8	4.9	1125	17	US-10-425-114-14054	Sequence 14054, A	1008	48.6	4.9	3298	17	US-10-362-247-4	Sequence 4, Appl
C 937	48.8	4.9	1149	18	US-10-425-115-109968	Sequence 109968, A	1009	48.6	4.9	3298	17	US-10-437-963-57556	Sequence 57556, A
938	48.8	4.9	1164	18	US-10-767-701-12837	Sequence 12837, A	1010	48.6	4.9	3375	15	US-10-156-761-4112	Sequence 4112, Ap
939	48.8	4.9	1194	16	US-10-214-446-33	Sequence 12837, A	1011	48.6	4.9	5065	14	US-10-067-457-4	Sequence 4, Appl
940	48.8	4.9	1224	17	US-10-425-114-21138	Sequence 33, Appl	1012	48.4	4.9	5499	17	US-10-276-774-973	Sequence 973, App
941	48.8	4.9	1272	17	US-10-107-431-262	Sequence 2138, A	1013	48.4	4.9	562	15	US-10-174-693-53	Sequence 53, Appl
942	48.8	4.9	1290	18	US-10-767-701-9008	Sequence 9008, Ap	1014	48.4	4.9	642	15	US-10-156-761-6149	Sequence 6149, Ap
943	48.8	4.9	1335	15	US-10-156-761-7202	Sequence 7202, Ap	1015	48.4	4.9	651	15	US-10-156-761-6890	Sequence 6890, Ap
944	48.8	4.9	1392	15	US-10-156-761-4350	Sequence 4350, Ap	1016	48.4	4.9	800	18	US-10-425-115-25676	Sequence 25676, A
945	48.8	4.9	1463	17	US-10-425-114-18406	Sequence 31249, A	1017	48.4	4.9	819	18	US-10-425-115-151084	Sequence 151084, A
946	48.8	4.9	1463	17	US-10-425-114-18406	Sequence 31249, A	1018	48.4	4.9	819	18	US-10-259-165-215	Sequence 215, App
947	48.8	4.9	1743	18	US-10-425-115-85293	Sequence 85293, A	1019	48.4	4.9	1164	17	US-10-425-114-21717	Sequence 21717, A
948	48.8	4.9	2017	17	US-10-425-114-32728	Sequence 32728, A	1020	48.4	4.9	1264	18	US-10-425-115-36748	Sequence 36748, A
949	48.8	4.9	2135	18	US-10-425-115-169676	Sequence 169676, A	1021	48.4	4.9	1395	18	US-10-437-963-27475	Sequence 27475, A
C 950	48.8	4.9	2391	18	US-10-425-115-86864	Sequence 86864, A	1022	48.4	4.9	1558	17	US-10-437-963-38959	Sequence 38959, A
951	48.8	4.9	2671	18	US-10-425-115-158863	Sequence 158863, A	1023	48.4	4.9	1650	17	US-10-425-114-1638	Sequence 1638, Ap
952	48.8	4.9	2771	18	US-10-425-115-167636	Sequence 167636, A	1024	48.4	4.9	1872	18	US-10-282-122A-25691	Sequence 25691, A
953	48.8	4.9	3657	18	US-10-437-963-26197	Sequence 26197, A	1025	48.4	4.9	1974	18	US-10-437-963-86467	Sequence 86467, A
							1026	48.4	4.9	1974	18	US-10-437-963-78147	Sequence 78147, A
							1027	48.4	4.9	1809	18	US-10-437-963-86462	Sequence 86462, A

1027	48.4	4.9	2019	15	US-10-156-761-3693	Sequence 3693, Ap	1100	48.2	4.9	9579	16	US-10-132-134-11	Sequence 11, Appl
c1028	48.4	4.9	2523	17	US-10-282-122A-15228	Sequence 15228, A	1101	48.2	4.9	20322	10	US-09-942-025-14	Sequence 14, Appl
c1029	48.4	4.9	2862	15	US-10-437-963-96575	Sequence 96575, A	1102	48.2	4.9	27541	18	US-10-203-235-2	Sequence 2, Appl
1030	48.4	4.9	2892	18	US-10-156-761-3066	Sequence 3066, Ap	1103	48.2	4.9	27705	10	US-09-942-025-12	Sequence 12, Appl
1031	48.4	4.9	3377	17	US-10-437-963-92668	Sequence 92668, A	1104	48.2	4.9	52101	16	US-10-132-134-1	Sequence 1, Appl
1032	48.4	4.9	4751	17	US-10-311-795-5	Sequence 5, Appl	1105	48.2	4.9	67311	10	US-09-942-025-1	Sequence 1, Appl
1033	48.4	4.9	4833	17	US-10-287-123A-25605	Sequence 25605, A	1106	48.2	4.9	70383	15	US-10-283-247-3	Sequence 3, Appl
c1034	48.4	4.9	6779	18	US-10-437-963-29812	Sequence 29812, A	c1107	48.2	4.9	86941	17	US-10-461-194-2	Sequence 2, Appl
c1035	48.4	4.9	24081	16	US-10-132-134-13	Sequence 13, Appl	1108	48	4.9	353	18	US-10-425-115-98452	Sequence 98452, A
1036	48.4	4.9	31263	17	US-10-282-122A-25447	Sequence 25447, A	1109	48	4.9	489	15	US-10-156-761-4741	Sequence 4741, Ap
c1037	48.4	4.9	52101	16	US-10-132-134-1	Sequence 1, Appl	1110	48	4.9	579	11	US-09-758-759-174	Sequence 174, Ap
1038	48.2	4.9	480	18	US-10-437-963-48143	Sequence 48143, A	1111	48	4.9	652	18	US-10-767-701-5497	Sequence 5497, Ap
c1039	48.2	4.9	553	18	US-10-425-115-82149	Sequence 82149, A	c1112	48	4.9	712	18	US-10-363-345A-27449	Sequence 27449, A
1040	48.2	4.9	618	17	US-10-425-114-6672	Sequence 6672, Ap	1113	48	4.9	712	18	US-10-363-345A-27450	Sequence 27450, A
1041	48.2	4.9	729	18	US-10-425-115-154823	Sequence 154823, A	c1114	48	4.9	712	18	US-10-363-483A-27449	Sequence 27449, A
1042	48.2	4.9	738	17	US-10-425-114-19698	Sequence 19698, A	1115	48	4.9	712	19	US-10-363-483A-27450	Sequence 27450, A
c1043	48.2	4.9	786	17	US-10-260-238-458	Sequence 458, App	1116	48	4.9	753	11	US-09-758-759-193	Sequence 193, App
1044	48.2	4.9	789	17	US-10-425-114-27917	Sequence 27917, A	1117	48	4.9	756	17	US-10-107-431-132	Sequence 132, App
1045	48.2	4.9	811	18	US-10-489-372-40	Sequence 40, Appl	1118	48	4.9	768	17	US-10-369-493-33233	Sequence 33233, A
1046	48.2	4.9	823	14	US-10-153-668-54	Sequence 54, Appl	1119	48	4.9	833	17	US-10-425-114-24992	Sequence 24992, A
1047	48.2	4.9	823	14	US-10-153-668-56	Sequence 56, Appl	1120	48	4.9	833	18	US-10-425-115-24687	Sequence 24687, A
1048	48.2	4.9	825	17	US-10-282-122A-25820	Sequence 25820, A	1121	48	4.9	888	18	US-10-437-963-98299	Sequence 98299, A
1049	48.2	4.9	852	18	US-10-437-963-89306	Sequence 89306, A	1122	48	4.9	954	15	US-10-156-761-4757	Sequence 4757, Ap
1050	48.2	4.9	861	15	US-10-156-761-3921	Sequence 3921, Ap	1123	48	4.9	1128	10	US-09-875-076-15	Sequence 875, Ap
1051	48.2	4.9	920	15	US-10-037-270-132	Sequence 132, App	1124	48	4.9	1128	10	US-09-875-252-17	Sequence 15, Appl
1052	48.2	4.9	920	17	US-10-117-722-132	Sequence 132, App	1125	48	4.9	1128	14	US-10-318-142-1	Sequence 1, Appl
c1053	48.2	4.9	930	17	US-10-282-122A-30550	Sequence 30550, A	1126	48	4.9	1128	15	US-10-225-567A-493	Sequence 493, App
1054	48.2	4.9	956	18	US-10-437-963-95323	Sequence 95323, A	1127	48	4.9	1128	15	US-10-272-983-15	Sequence 15, Appl
1055	48.2	4.9	969	9	US-09-789-836-3	Sequence 3, Appl	1128	48	4.9	1128	16	US-10-393-807-15	Sequence 15, Appl
1056	48.2	4.9	969	9	US-09-789-836-3	Sequence 3, Appl	1129	48	4.9	1128	17	US-10-417-820A-17	Sequence 17, Appl
1057	48.2	4.9	1038	9	US-09-789-831-3	Sequence 2, Appl	1130	48	4.9	1128	17	US-10-295-027-1121	Sequence 1121, Ap
1058	48.2	4.9	1038	10	US-09-789-831-2	Sequence 2, Appl	1131	48	4.9	1128	18	US-10-723-955-17	Sequence 17, Appl
1059	48.2	4.9	1038	16	US-10-251-661-9	Sequence 9, Appl	1132	48	4.9	1128	18	US-10-782-596-15	Sequence 15, Appl
1060	48.2	4.9	1038	17	US-10-410-888-3	Sequence 3, Appl	1133	48	4.9	1128	19	US-10-898-329-16	Sequence 16, Appl
1061	48.2	4.9	1038	17	US-10-159-563-166	Sequence 166, App	1134	48	4.9	1128	19	US-10-898-329-16	Sequence 16, Appl
1062	48.2	4.9	1038	18	US-10-415-325-17	Sequence 22, Appl	1135	48	4.9	1155	17	US-10-369-493-42888	Sequence 42888, A
1063	48.2	4.9	1042	10	US-09-789-831-21	Sequence 21, Appl	1136	48	4.9	1158	17	US-10-425-114-22632	Sequence 22632, A
1064	48.2	4.9	1059	17	US-10-389-647-304	Sequence 304, App	c1137	48	4.9	1164	17	US-10-425-114-21171	Sequence 21171, A
1065	48.2	4.9	1151	18	US-10-425-115-175028	Sequence 175028, A	c1138	48	4.9	1175	17	US-10-425-114-1930	Sequence 1930, Ap
1066	48.2	4.9	1215	15	US-10-156-761-2811	Sequence 2811, Ap	1139	48	4.9	1186	18	US-10-425-115-84443	Sequence 84443, A
1067	48.2	4.9	1336	19	US-10-488-056-9	Sequence 9, Appl	c1140	48	4.9	1188	16	US-10-246-330-9	Sequence 9, Appl
1068	48.2	4.9	1347	15	US-10-156-761-6038	Sequence 6038, Ap	1141	48	4.9	1232	17	US-10-425-114-17219	Sequence 17219, A
1069	48.2	4.9	1566	18	US-10-817-483-30	Sequence 30, Appl	1142	48	4.9	1236	18	US-10-437-963-95996	Sequence 95996, A
1070	48.2	4.9	1638	18	US-10-437-963-82416	Sequence 82416, A	1143	48	4.9	1257	18	US-10-767-701-11943	Sequence 11943, A
1071	48.2	4.9	1670	18	US-10-767-701-33989	Sequence 13989, A	1144	48	4.9	1275	17	US-10-282-122A-25779	Sequence 25779, A
1072	48.2	4.9	1710	15	US-10-156-761-2318	Sequence 2318, Ap	c1145	48	4.9	1297	17	US-10-425-115-14015	Sequence 14015, A
1073	48.2	4.9	1818	18	US-10-437-963-55757	Sequence 55757, A	1146	48	4.9	1313	17	US-10-425-114-33638	Sequence 33638, A
1074	48.2	4.9	1827	17	US-10-425-114-28744	Sequence 28744, A	1147	48	4.9	1332	17	US-10-156-761-2601	Sequence 2601, Ap
1075	48.2	4.9	1830	17	US-10-425-115-41313	Sequence 41313, A	1148	48	4.9	1437	17	US-10-369-493-42370	Sequence 42370, A
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1078	48.2	4.9	1910	18	US-10-415-325-18	Sequence 18, Appl	1151	48	4.9	1644	18	US-10-437-963-97070	Sequence 97070, A
1079	48.2	4.9	1941	15	US-10-156-761-3418	Sequence 3418, Ap	1152	48	4.9	1677	17	US-10-369-493-43031	Sequence 43031, A
1080	48.2	4.9	1975	10	US-09-972-607-10	Sequence 10, Appl	1153	48	4.9	1782	17	US-10-282-122A-13824	Sequence 13824, A
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1083	48.2	4.9	1994	10	US-09-972-607-3	Sequence 3, Appl	1156	48	4.9	2431	18	US-10-437-963-17818	Sequence 17818, A
1084	48.2	4.9	1994	17	US-09-851-673-1	Sequence 3, Appl	1157	48	4.9	2488	18	US-10-739-930-2308	Sequence 2308, Ap
1085	48.2	4.9	1994	17	US-10-628-841-3	Sequence 3, Appl	1158	48	4.9	2583	15	US-10-156-761-3778	Sequence 3778, Ap
1086	48.2	4.9	1997	18	US-10-425-115-11418	Sequence 11418, A	1159	48	4.9	2632	18	US-10-437-963-26695	Sequence 26695, A
1087	48.2	4.9	2009	18	US-10-761-370-1	Sequence 1, Appl	1160	48	4.9	3435	11	US-09-758-759-166	Sequence 166, App
1088	48.2	4.9	2034	18	US-10-761-370-2	Sequence 2, Appl	c1161	48	4.9	3489	9	US-09-815-242-7731	Sequence 7731, Ap
1089	48.2	4.9	2035	10	US-09-863-049A-3	Sequence 3, Appl	c1162	48	4.9	3489	17	US-10-282-122A-30110	Sequence 30110, A
1090	48.2	4.9	2130	18	US-10-425-115-114288	Sequence 114288, A	c1163	48	4.9	42152	11	US-09-758-759-182	Sequence 182, App
1091	48.2	4.9	2595	17	US-10-282-122A-14998	Sequence 14998, A	1164	48	4.9	37116	17	US-10-107-431-279	Sequence 279, App
c1092	48.2	4.9	3350	9	US-09-894-998-48	Sequence 48, Appl	1165	48	4.9	43623	19	US-10-741-600-17818	Sequence 17818, A
c1093	48.2	4.9	3350	14	US-10-121-988-48	Sequence 48, Appl	1166	48	4.9	77294	19	US-10-729-802-1	Sequence 1, Appl
c1094	48.2	4.9	3350	16	US-10-200-562-48	Sequence 48, Appl	c1167	47.8	4.8	487	17	US-10-374-780A-1253	Sequence 1253, Ap
c1095	48.2	4.9	3350	16	US-10-237-551-48	Sequence 48, Appl	1168	47.8	4.8	579	18	US-10-437-963-87078	Sequence 87078, A
c1096	48.2	4.9	4025	18	US-10-437-963-97674	Sequence 97674, A	1169	47.8	4.8	627	15	US-10-156-761-6579	Sequence 6579, Ap
c1097	48.2	4.9	4146	17	US-10-282-122A-28711	Sequence 28711, A	1170	47.8	4.8	702	18	US-10-437-963-14724	Sequence 14724, A
1098	48.2	4.9	4542	17	US-10-282-122A-28674	Sequence 28674, A	1171	47.8	4.8	717	17	US-10-425-114-18216	Sequence 18216, A
1099	48.2	4.9	6591	15	US-10-301-822-3	Sequence 3, Appl	1172	47.8	4.8	777	17	US-10-332-947-28	Sequence 28, Appl

1173	47.8	4.8	888	15	US-10-156-761-5898	Sequence 5898, Ap	1258	47.6	4.8	2305	17	US-10-387-336-80	Sequence 80, Appl
1174	47.8	4.8	982	17	US-10-767-701-8931	Sequence 8931, Ap	1259	47.6	4.8	2306	17	US-10-387-336-82	Sequence 82, Appl
1175	47.8	4.8	1029	17	US-10-282-122A-25590	Sequence 25590, A	1260	47.6	4.8	2337	17	US-10-282-122A-25485	Sequence 25485, A
1176	47.8	4.8	1037	17	US-10-425-114-23005	Sequence 23005, A	1261	47.6	4.8	2424	17	US-10-282-122A-15037	Sequence 15037, A
1177	47.8	4.8	1075	18	US-10-425-115-5563	Sequence 5563, Ap	1262	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl
1178	47.8	4.8	1173	18	US-10-425-115-5563	Sequence 5563, Ap	1263	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl
1179	47.8	4.8	1173	18	US-10-425-115-5563	Sequence 5563, Ap	1264	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl
1180	47.8	4.8	1179	17	US-10-425-114-1395	Sequence 14395, A	1265	47.6	4.8	2466	16	US-09-899-575-31	Sequence 31, Appl
1181	47.8	4.8	1191	18	US-10-425-115-7975	Sequence 7975, A	1266	47.6	4.8	2466	16	US-10-241-009-31	Sequence 31, Appl
1182	47.8	4.8	1287	17	US-10-282-122A-14756	Sequence 14756, A	1267	47.6	4.8	2466	16	US-10-190-434B-31	Sequence 31, Appl
1183	47.8	4.8	1329	18	US-10-437-963-32214	Sequence 32214, A	1268	47.6	4.8	2466	16	US-10-190-434B-31	Sequence 31, Appl
1184	47.8	4.8	1401	15	US-10-156-761-6597	Sequence 6597, Ap	1269	47.6	4.8	2481	9	US-09-894-998-35	Sequence 35, Appl
1185	47.8	4.8	1404	17	US-10-282-122A-25706	Sequence 25706, A	1270	47.6	4.8	2481	14	US-10-121-988-35	Sequence 35, Appl
1186	47.8	4.8	1428	18	US-10-437-963-48509	Sequence 48509, A	1271	47.6	4.8	2481	16	US-10-200-562-35	Sequence 35, Appl
1187	47.8	4.8	1471	18	US-10-425-115-82155	Sequence 82155, A	1272	47.6	4.8	2481	16	US-10-237-551-35	Sequence 35, Appl
1188	47.8	4.8	1527	17	US-10-282-122A-25749	Sequence 25749, A	1273	47.6	4.8	2552	17	US-10-369-493-42921	Sequence 42921, A
1189	47.8	4.8	1531	18	US-10-425-115-37426	Sequence 37426, A	1274	47.6	4.8	3066	14	US-10-121-988-152	Sequence 152, App
1190	47.8	4.8	1612	18	US-10-437-963-15030	Sequence 15030, A	1275	47.6	4.8	3066	16	US-10-200-562-152	Sequence 152, App
1191	47.8	4.8	1671	11	US-09-758-759-102	Sequence 102, App	1276	47.6	4.8	3066	16	US-10-237-551-152	Sequence 152, App
1192	47.8	4.8	1711	18	US-10-425-115-58741	Sequence 58741, A	1277	47.6	4.8	3090	17	US-10-369-493-40513	Sequence 40513, A
1193	47.8	4.8	1771	9	US-09-874-923-7	Sequence 7, Appl	1278	47.6	4.8	3783	16	US-10-316-253-96	Sequence 96, Appl
1194	47.8	4.8	1771	9	US-09-991-496-7	Sequence 7, Appl	1279	47.6	4.8	3783	16	US-10-316-253-96	Sequence 96, Appl
1195	47.8	4.8	2256	18	US-10-437-963-86656	Sequence 86656, A	1280	47.6	4.8	5802	14	US-10-152-886-84	Sequence 84, Appl
1196	47.8	4.8	2387	18	US-10-437-963-38072	Sequence 38072, A	1281	47.6	4.8	5886	18	US-10-798-037-3	Sequence 3, Appl
1197	47.8	4.8	2556	18	US-10-437-963-29317	Sequence 29317, A	1282	47.6	4.8	6008	17	US-10-336-472-21	Sequence 21, Appl
1198	47.8	4.8	2556	18	US-10-437-963-29317	Sequence 29317, A	1283	47.6	4.8	6008	17	US-10-336-472-21	Sequence 21, Appl
1199	47.8	4.8	3824	17	US-10-116-275-197	Sequence 66971, A	1284	47.6	4.8	6008	17	US-10-717-597-197	Sequence 197, App
1200	47.8	4.8	3824	17	US-10-159-563-307	Sequence 307, App	1285	47.6	4.8	10692	15	US-10-156-761-414	Sequence 414, App
1201	47.8	4.8	3824	18	US-10-723-860-2600	Sequence 2600, Ap	1286	47.6	4.8	12801	18	US-10-798-037-5	Sequence 5, Appl
1202	47.8	4.8	3824	18	US-10-723-860-2600	Sequence 2600, Ap	1287	47.6	4.8	12801	18	US-10-798-037-5	Sequence 5, Appl
1203	47.8	4.8	7201	18	US-10-600-790-20	Sequence 7201, Ap	1288	47.6	4.8	27541	18	US-10-203-295-2	Sequence 2, Appl
1204	47.8	4.8	7429	19	US-10-873-332-61	Sequence 61, Appl	1289	47.6	4.8	349	18	US-10-425-115-40892	Sequence 40892, A
1205	47.8	4.8	71989	9	US-09-727-889-2	Sequence 2, Appl	1290	47.6	4.8	414	15	US-10-259-165-779	Sequence 779, App
1206	47.8	4.8	71989	18	US-10-849-463-2	Sequence 873, App	1291	47.6	4.8	463	18	US-10-767-701-559	Sequence 559, App
1207	47.6	4.8	524	18	US-10-437-963-873	Sequence 873, App	1292	47.6	4.8	497	18	US-10-425-115-51767	Sequence 51767, A
1208	47.6	4.8	633	17	US-10-369-493-41491	Sequence 41491, A	1293	47.6	4.8	504	17	US-10-260-238-5853	Sequence 5853, Ap
1209	47.6	4.8	780	15	US-10-156-761-6288	Sequence 6288, Ap	1294	47.6	4.8	601	18	US-10-767-701-4418	Sequence 4418, Ap
1210	47.6	4.8	825	19	US-10-762-107-43	Sequence 43, Appl	1295	47.6	4.8	670	16	US-10-132-350-29	Sequence 29, Appl
1211	47.6	4.8	878	17	US-10-425-114-15378	Sequence 15378, A	1296	47.6	4.8	670	16	US-10-132-350-29	Sequence 29, Appl
1212	47.6	4.8	891	15	US-10-156-761-7285	Sequence 7285, Ap	1297	47.6	4.8	693	15	US-10-156-761-1183	Sequence 1183, Ap
1213	47.6	4.8	921	17	US-10-282-122A-7524	Sequence 7524, Ap	1298	47.6	4.8	862	18	US-10-767-701-10425	Sequence 10425, A
1214	47.6	4.8	967	18	US-10-425-115-66497	Sequence 66497, A	1299	47.6	4.8	862	18	US-10-767-701-10425	Sequence 10425, A
1215	47.6	4.8	968	17	US-10-425-114-19397	Sequence 19397, A	1300	47.6	4.8	951	18	US-10-437-963-91705	Sequence 91705, A
1216	47.6	4.8	1026	17	US-10-259-194A-618	Sequence 618, App	1301	47.6	4.8	951	18	US-10-437-963-91705	Sequence 91705, A
1217	47.6	4.8	1026	17	US-10-259-194A-618	Sequence 618, App	1302	47.6	4.8	996	15	US-10-156-761-7396	Sequence 7396, Ap
1218	47.6	4.8	1036	14	US-10-085-783A-53529	Sequence 53529, A	1303	47.6	4.8	1050	18	US-10-767-701-12642	Sequence 12642, A
1219	47.6	4.8	1036	14	US-10-123-155-358	Sequence 358, App	1304	47.6	4.8	1050	18	US-10-767-701-12642	Sequence 12642, A
1220	47.6	4.8	1060	18	US-10-425-115-134347	Sequence 134347, A	1305	47.6	4.8	1195	18	US-10-425-115-172335	Sequence 172335, A
1221	47.6	4.8	1110	15	US-10-156-761-4246	Sequence 4246, Ap	1306	47.6	4.8	1203	15	US-10-156-761-4664	Sequence 4664, Ap
1222	47.6	4.8	1176	17	US-10-369-493-40494	Sequence 40494, A	1307	47.6	4.8	1203	15	US-10-156-761-4664	Sequence 4664, Ap
1223	47.6	4.8	1203	17	US-10-282-122A-25722	Sequence 25722, A	1308	47.6	4.8	12356	18	US-10-425-115-73921	Sequence 73921, A
1224	47.6	4.8	1203	17	US-10-437-963-64185	Sequence 64185, A	1309	47.6	4.8	12356	18	US-10-425-115-73921	Sequence 73921, A
1225	47.6	4.8	1257	18	US-10-437-963-64185	Sequence 64185, A	1310	47.6	4.8	1345	17	US-10-425-114-24692	Sequence 24692, A
1226	47.6	4.8	1282	17	US-10-425-114-23644	Sequence 23644, A	1311	47.6	4.8	1345	17	US-10-425-114-24692	Sequence 24692, A
1227	47.6	4.8	1329	15	US-10-156-761-1297	Sequence 1297, Ap	1312	47.6	4.8	1404	17	US-10-282-122A-15189	Sequence 15189, A
1228	47.6	4.8	1344	17	US-10-425-114-16346	Sequence 16346, A	1313	47.6	4.8	1420	17	US-10-425-114-21968	Sequence 21968, A
1229	47.6	4.8	1376	18	US-10-437-963-10544	Sequence 10544, A	1314	47.6	4.8	1438	18	US-10-425-115-84149	Sequence 84149, A
1230	47.6	4.8	1403	18	US-10-425-115-68130	Sequence 68130, A	1315	47.6	4.8	1443	15	US-10-156-761-3397	Sequence 3397, Ap
1231	47.6	4.8	1410	17	US-10-369-493-42819	Sequence 42819, A	1316	47.6	4.8	1468	18	US-10-425-115-115629	Sequence 115629, A
1232	47.6	4.8	1469	17	US-10-425-114-31292	Sequence 31292, A	1317	47.6	4.8	1649	18	US-10-437-963-89113	Sequence 89113, A
1233	47.6	4.8	1527	17	US-10-369-493-31928	Sequence 31928, A	1318	47.6	4.8	1672	18	US-10-437-963-81182	Sequence 81182, A
1234	47.6	4.8	1644	18	US-10-425-115-14950	Sequence 14950, A	1319	47.6	4.8	1695	18	US-10-437-963-76703	Sequence 76703, A
1235	47.6	4.8	1661	18	US-10-437-963-12797	Sequence 12797, A	1320	47.6	4.8	1723	17	US-10-437-963-11515	Sequence 11515, A
1236	47.6	4.8	1689	17	US-10-425-114-17162	Sequence 17162, A	1321	47.6	4.8	1734	18	US-10-282-122A-25721	Sequence 25721, A
1237	47.6	4.8	1713	18	US-10-324-967-33	Sequence 33, Appl	1322	47.6	4.8	1741	15	US-10-425-114-17536	Sequence 17536, A
1238	47.6	4.8	1956	15	US-10-156-761-5591	Sequence 5591, Ap	1323	47.6	4.8	1848	15	US-10-156-761-3041	Sequence 3041, Ap
1239	47.6	4.8	1970	17	US-10-425-114-22993	Sequence 22993, A	1324	47.6	4.8	1848	15	US-10-156-761-3041	Sequence 3041, Ap
1240	47.6	4.8	1971	16	US-10-190-435-49	Sequence 49, Appl	1325	47.6	4.8	1900	18	US-10-437-963-28228	Sequence 28228, A
1241	47.6	4.8	1971	16	US-10-241-009-38	Sequence 38, Appl	1326	47.6	4.8	1992	17	US-10-425-114-28230	Sequence 28230, A
1242	47.6	4.8	1971	16	US-10-190-434B-38	Sequence 38, Appl	1327	47.6	4.8	2041	18	US-10-425-115-41669	Sequence 41669, A
1243	47.6	4.8	1971	16	US-10-190-305A-48	Sequence 48, Appl	1328	47.6	4.8	2076	15	US-10-156-761-5585	Sequence 5585, Ap
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135	55.6	5.6	1164	4	US-09-902-540-5610	Sequence 5610, Ap	C 208	52.8	5.3	1080	4	US-09-902-540-5147	Sequence 5147, Ap
136	55.6	5.6	11812	4	US-09-902-540-1041	Sequence 1041, Ap	C 209	52.8	5.3	1236	1	US-08-440-856A-1	Sequence 1, Appl
137	55.4	5.6	774	4	US-09-252-991A-9665	Sequence 9665, Ap	C 210	52.8	5.3	26659	4	US-09-902-540-1237	Sequence 1237, Ap
138	55.4	5.6	3033	4	US-09-724-797-81	Sequence 81, Appl	C 211	52.8	5.3	29559	4	US-09-902-540-1254	Sequence 1254, Ap
139	55.2	5.6	1794	4	US-09-902-540-6985	Sequence 6985, Ap	C 212	52.6	5.3	888	4	US-09-902-540-7561	Sequence 7561, Ap
140	55.2	5.6	2010	4	US-09-902-540-9587	Sequence 9587, Ap	C 213	52.6	5.3	1446	4	US-09-902-540-8541	Sequence 8541, Ap
141	55.2	5.6	4042	4	US-09-902-540-609	Sequence 609, App	C 214	52.6	5.3	1458	4	US-09-902-540-5187	Sequence 5187, Ap
142	55.2	5.6	14807	4	US-09-902-540-1085	Sequence 1085, Ap	C 215	52.6	5.3	2561	4	US-09-616-289-48	Sequence 48, Appl
143	55	5.6	2358	4	US-09-902-540-2632	Sequence 2632, Ap	C 216	52.6	5.3	7295	4	US-09-902-540-924	Sequence 924, App
144	55	5.6	2559	4	US-09-657-013-40	Sequence 40, Appl	C 217	52.6	5.3	7713	4	US-09-902-540-900	Sequence 900, App
145	55	5.6	2559	4	US-09-949-016-1791	Sequence 1791, Ap	C 218	52.6	5.3	34199	4	US-09-902-540-1255	Sequence 1255, Ap
146	55	5.6	2567	4	US-09-949-016-567	Sequence 567, App	C 219	52.4	5.3	549	4	US-09-902-540-6777	Sequence 6777, Ap
147	55	5.6	17173	4	US-09-902-540-1122	Sequence 1122, Ap	C 220	52.4	5.3	591	4	US-09-902-540-6057	Sequence 6057, Ap
148	54.8	5.5	594	3	US-09-615-192A-105	Sequence 105, App	C 221	52.4	5.3	1591	4	US-09-902-540-250	Sequence 250, App
149	54.8	5.5	594	2	US-09-169-789-105	Sequence 105, App	C 222	52.4	5.3	3653	4	US-09-902-540-555	Sequence 555, App
150	54.8	5.5	607	2	US-08-975-316-23	Sequence 23, Appl	C 223	52.4	5.3	3978	3	US-08-726-214-1	Sequence 1, Appl
151	54.8	5.5	607	3	US-09-615-192A-23	Sequence 23, Appl	C 224	52.4	5.3	5640	4	US-09-620-312D-41	Sequence 41, Appl
152	54.8	5.5	607	4	US-09-169-789-23	Sequence 23, Appl	C 225	52.4	5.3	11220	4	US-09-949-016-5061	Sequence 5061, Ap
153	54.8	5.5	1350	4	US-09-902-540-8483	Sequence 8483, Ap	C 226	52.2	5.3	4296	4	US-09-902-540-3291	Sequence 3291, Ap
154	54.8	5.5	5673	4	US-09-902-540-8259	Sequence 8259, Ap	C 227	52.2	5.3	4455	4	US-09-902-540-7119	Sequence 7119, Ap
155	54.8	5.5	7513	4	US-09-902-540-892	Sequence 892, App	C 228	52.2	5.3	4458	4	US-09-902-540-650	Sequence 650, App
156	54.8	5.5	8704	4	US-09-902-540-854	Sequence 854, App	C 229	52.2	5.3	17727	4	US-09-902-540-1152	Sequence 1152, Ap
157	54.6	5.5	474	4	US-09-902-540-5898	Sequence 5898, Ap	C 230	52	5.3	693	4	US-09-902-540-9571	Sequence 9571, Ap
158	54.6	5.5	1257	4	US-09-902-540-8550	Sequence 8550, App	C 231	52	5.3	1152	4	US-09-902-540-5580	Sequence 5580, Ap
159	54.6	5.5	1258	4	US-09-902-540-166	Sequence 166, App	C 232	52	5.3	1209	4	US-09-902-540-147	Sequence 147, App
160	54.6	5.5	1308	3	US-08-937-067-18	Sequence 18, Appl	C 233	52	5.3	1248	4	US-09-252-991A-1681	Sequence 1681, Ap
161	54.6	5.5	2830	2	US-09-010-928B-1	Sequence 1, Appl	C 234	52	5.3	1302	4	US-09-252-991A-1437	Sequence 1437, Ap
162	54.6	5.5	3077	4	US-09-902-540-495	Sequence 495, App	C 235	52	5.3	1956	4	US-09-252-991A-1494	Sequence 1494, Ap
163	54.6	5.5	7562	4	US-09-902-540-902	Sequence 902, App	C 236	52	5.3	2586	4	US-09-902-540-5619	Sequence 5619, Ap
164	54.4	5.5	843	4	US-09-902-540-3428	Sequence 3428, Ap	C 237	52	5.3	14555	4	US-09-902-540-1096	Sequence 1096, Ap
165	54.4	5.5	2022	4	US-09-902-540-5510	Sequence 5510, Ap	C 238	52	5.3	4225	4	US-09-902-540-1269	Sequence 1269, Ap
166	54.4	5.5	2712	4	US-09-902-540-4301	Sequence 4301, Ap	C 239	51.8	5.2	498	4	US-09-252-991A-10389	Sequence 10389, A
167	54.4	5.5	18192	4	US-09-902-540-1162	Sequence 1162, Ap	C 240	51.8	5.2	561	4	US-09-252-991A-10580	Sequence 10580, A
168	54.4	5.5	41768	4	US-09-902-540-1266	Sequence 1266, Ap	C 241	51.8	5.2	1053	4	US-09-252-991A-10684	Sequence 10684, A
169	54.2	5.5	1374	4	US-09-902-540-4587	Sequence 4587, Ap	C 242	51.8	5.2	1149	4	US-09-902-540-6250	Sequence 6250, Ap
170	54.2	5.5	1689	4	US-09-902-540-3347	Sequence 3347, Ap	C 243	51.8	5.2	1233	4	US-09-902-540-3104	Sequence 3104, Ap
171	54.2	5.5	1824	4	US-09-902-540-6709	Sequence 6709, Ap	C 244	51.8	5.2	1272	4	US-09-902-540-5243	Sequence 5243, Ap
172	54.2	5.5	4234	4	US-09-902-540-534	Sequence 534, App	C 245	51.8	5.2	1386	4	US-09-252-991A-2867	Sequence 2867, Ap
173	54.2	5.5	18537	4	US-09-902-540-1157	Sequence 1157, Ap	C 246	51.8	5.2	1581	4	US-09-902-540-9170	Sequence 9170, Ap

C 247	51.8	5.2	1926	3	US-09-249-585A-4	Sequence 4, Appli	Sequence 4, Appli	320	50.4	5.1	1404	4	US-09-902-540-7362	Sequence 7362, Ap
C 248	51.8	5.2	1931	2	US-09-130-114-2	Sequence 2, Appli	Sequence 2, Appli	321	50.4	5.1	1818	4	US-09-902-540-5126	Sequence 5126, Ap
C 249	51.8	5.2	2075	5.1	US-09-087-031B-2	Sequence 2, Appli	Sequence 2, Appli	C 322	50.4	5.1	5121	4	US-09-902-540-704	Sequence 704, App
250	51.8	5.2	2075	4	US-09-546-043-1	Sequence 1, Appli	Sequence 1, Appli	323	50.4	5.1	23673	3	US-09-773-816-1	Sequence 1, Appli
251	51.8	5.2	2075	4	US-09-514-885-2	Sequence 2, Appli	Sequence 2, Appli	324	50.2	5.1	825	4	US-09-902-540-2941	Sequence 2941, Ap
252	51.8	5.2	2351	4	US-09-902-540-344	Sequence 144, App	Sequence 144, App	325	50.2	5.1	864	4	US-09-252-991A-10932	Sequence 10932, A
253	51.8	5.2	2469	4	US-09-949-016-428	Sequence 428, App	Sequence 428, App	326	50.2	5.1	930	4	US-09-902-540-3946	Sequence 3946, Ap
254	51.8	5.2	5097	4	US-09-902-540-5555	Sequence 5555, App	Sequence 5555, App	C 327	50.2	5.1	1587	4	US-09-902-540-3702	Sequence 3702, Ap
C 255	51.8	5.2	11612	4	US-09-902-540-981	Sequence 981, App	Sequence 981, App	C 328	50.2	5.1	2211	4	US-09-252-991A-11256	Sequence 11256, A
C 256	51.8	5.2	34316	4	US-09-902-540-1257	Sequence 1257, App	Sequence 1257, App	329	50.2	5.1	2289	4	US-09-252-991A-10995	Sequence 10995, A
C 257	51.8	5.2	41170	4	US-09-902-540-1267	Sequence 1267, App	Sequence 1267, App	330	50.2	5.1	2589	4	US-09-902-540-4601	Sequence 4601, Ap
C 258	51.6	5.2	591	4	US-09-902-540-4984	Sequence 4984, App	Sequence 4984, App	331	50.2	5.1	4826	4	US-09-772-304A-1	Sequence 1, Appli
C 259	51.6	5.2	1026	4	US-09-902-540-6694	Sequence 6694, App	Sequence 6694, App	C 332	50.2	5.1	12173	4	US-09-902-540-1022	Sequence 1022, Ap
C 260	51.6	5.2	1065	4	US-09-902-540-4327	Sequence 4327, App	Sequence 4327, App	C 333	50.2	5.1	21295	4	US-09-902-540-1194	Sequence 1194, Ap
C 261	51.6	5.2	1311	4	US-09-252-991A-14065	Sequence 14065, A	Sequence 14065, A	C 334	50.2	5.1	23417	4	US-09-902-540-1207	Sequence 1207, Ap
C 262	51.6	5.2	1581	4	US-09-902-540-3972	Sequence 3972, App	Sequence 3972, App	335	50.2	5.1	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 263	51.6	5.2	2850	4	US-09-252-991A-14205	Sequence 14205, A	Sequence 14205, A	336	50	5.1	636	4	US-09-902-540-4812	Sequence 4812, Ap
C 264	51.6	5.2	4353	4	US-09-902-540-529	Sequence 529, App	Sequence 529, App	337	50	5.1	888	4	US-09-311-021-155	Sequence 155, App
C 265	51.6	5.2	9369	4	US-10-237-551-190	Sequence 190, App	Sequence 190, App	338	50	5.1	1272	4	US-09-902-540-8799	Sequence 8799, Ap
C 266	51.6	5.2	9369	4	US-10-237-551-247	Sequence 247, App	Sequence 247, App	339	50	5.1	1365	4	US-09-902-540-5489	Sequence 5489, Ap
C 267	51.6	5.2	18324	4	US-09-902-540-1196	Sequence 1196, App	Sequence 1196, App	340	50	5.1	1579	4	US-09-902-540-4020	Sequence 4020, Ap
C 268	51.6	5.2	23951	4	US-09-902-540-1245	Sequence 1245, App	Sequence 1245, App	C 341	50	5.1	1619	4	US-09-902-540-331	Sequence 331, App
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C 270	51.4	5.2	1368	4	US-09-902-540-9337	Sequence 9337, App	Sequence 9337, App	343	50	5.1	1702	4	US-09-902-540-8057	Sequence 8057, Ap
C 271	51.4	5.2	7847	4	US-09-799-451-591	Sequence 591, App	Sequence 591, App	344	50	5.1	2073	4	US-09-902-540-2661	Sequence 2661, Ap
C 272	51.4	5.2	8604	4	US-09-902-540-5331	Sequence 5331, App	Sequence 5331, App	345	50	5.1	2193	4	US-09-902-540-4585	Sequence 4585, Ap
C 273	51.4	5.2	10486	4	US-09-902-540-997	Sequence 997, App	Sequence 997, App	346	50	5.1	2190	4	US-09-902-540-8946	Sequence 8946, Ap
C 274	51.4	5.2	35399	4	US-09-902-540-1260	Sequence 1260, App	Sequence 1260, App	C 347	50	5.1	2319	4	US-09-902-540-2035	Sequence 2035, Ap
C 275	51.2	5.2	762	4	US-09-902-540-5117	Sequence 5117, App	Sequence 5117, App	348	50	5.1	2699	4	US-09-902-540-6501	Sequence 6501, Ap
C 276	51.2	5.2	1395	4	US-09-902-540-3473	Sequence 3473, App	Sequence 3473, App	349	50	5.1	2700	4	US-09-902-540-467	Sequence 467, App
C 277	51.2	5.2	2277	1	US-08-676-967-5	Sequence 5, Appli	Sequence 5, Appli	350	50	5.1	2733	4	US-09-902-540-3104	Sequence 3104, Ap
C 278	51.2	5.2	2277	1	US-08-676-974-5	Sequence 5, Appli	Sequence 5, Appli	351	50	5.1	7160	4	US-09-902-540-821	Sequence 821, App
C 279	51.2	5.2	2277	2	US-09-908-487-5	Sequence 5, Appli	Sequence 5, Appli	C 352	50	5.1	8967	4	US-09-902-540-935	Sequence 935, App
C 280	51.2	5.2	2757	4	US-09-902-540-5701	Sequence 5701, App	Sequence 5701, App	353	50	5.1	10096	4	US-09-902-540-935	Sequence 935, App
C 281	51.2	5.2	3699	4	US-09-902-540-3731	Sequence 3731, App	Sequence 3731, App	C 354	50	5.1	12730	4	US-09-902-540-1029	Sequence 1029, Ap
C 282	51.2	5.2	17188	4	US-09-902-540-1166	Sequence 1166, App	Sequence 1166, App	355	50	5.1	13842	3	US-09-105-537-30	Sequence 30, Appli
C 283	51.2	5.2	19112	4	US-09-902-540-1181	Sequence 1181, App	Sequence 1181, App	356	50	5.1	15499	4	US-09-902-540-1140	Sequence 1140, Ap
C 284	51.2	5.2	28058	4	US-09-902-540-1252	Sequence 1252, App	Sequence 1252, App	C 357	50	5.1	19068	4	US-09-902-540-1123	Sequence 1123, Ap
C 285	51.2	5.2	50725	4	US-09-902-540-1271	Sequence 1271, App	Sequence 1271, App	C 358	50	5.1	26533	4	US-09-902-540-1199	Sequence 1199, Ap
C 286	51	5.2	501	4	US-09-252-991A-11947	Sequence 11947, A	Sequence 11947, A	359	50	5.1	36778	3	US-09-105-537-5	Sequence 5, Appli
C 287	51	5.2	600	4	US-09-902-540-4489	Sequence 4489, App	Sequence 4489, App	360	50	5.1	38506	4	US-09-320-878-19	Sequence 19, Appli
C 288	51	5.2	1341	4	US-09-902-540-6300	Sequence 6300, App	Sequence 6300, App	361	50	5.1	38506	4	US-09-141-908-1	Sequence 1, Appli
C 289	51	5.2	1344	4	US-09-902-540-381	Sequence 381, App	Sequence 381, App	362	50	5.1	38506	4	US-09-657-440-19	Sequence 19, Appli
C 290	51	5.2	1500	4	US-09-252-991A-11907	Sequence 11907, A	Sequence 11907, A	C 363	50	5.1	229354	4	US-09-705-400-64	Sequence 64, Appli
C 291	51	5.2	2118	4	US-09-902-540-3960	Sequence 3960, App	Sequence 3960, App	364	49.8	5.0	1644	4	US-09-902-540-4613	Sequence 4613, Ap
C 292	51	5.2	2561	4	US-09-616-289-48	Sequence 48, Appli	Sequence 48, Appli	365	49.8	5.0	3003	4	US-09-252-991A-14790	Sequence 14790, A
C 293	51	5.2	3381	4	US-09-902-540-7493	Sequence 7493, App	Sequence 7493, App	366	49.8	5.0	3113	4	US-09-894-988A-52	Sequence 52, Appli
C 294	51	5.2	6269	4	US-09-902-540-726	Sequence 726, App	Sequence 726, App	367	49.8	5.0	3113	4	US-10-237-551-52	Sequence 52, Appli
C 295	51	5.2	8438	1	US-07-945-283-1	Sequence 1, Appli	Sequence 1, Appli	368	49.8	5.0	3132	4	US-09-252-991A-14540	Sequence 14540, A
C 296	51	5.2	10593	4	US-09-902-540-1030	Sequence 1030, App	Sequence 1030, App	369	49.8	5.0	3147	2	US-08-781-802-7	Sequence 7, Appli
C 297	51	5.2	18324	4	US-09-902-540-1196	Sequence 1196, App	Sequence 1196, App	370	49.8	5.0	3147	3	US-08-694-078-7	Sequence 7, Appli
C 298	50.8	5.1	741	4	US-09-724-797-73	Sequence 73, Appli	Sequence 73, Appli	371	49.8	5.0	3147	3	US-09-058-260-7	Sequence 7, Appli
C 299	50.8	5.1	1047	4	US-09-902-540-9236	Sequence 9236, App	Sequence 9236, App	372	49.8	5.0	3345	4	US-09-894-988A-49	Sequence 49, Appli
C 300	50.8	5.1	1155	3	US-08-818-112-12	Sequence 12, Appli	Sequence 12, Appli	373	49.8	5.0	3345	4	US-10-237-551-49	Sequence 49, Appli
C 301	50.8	5.1	1155	3	US-08-818-111-12	Sequence 12, Appli	Sequence 12, Appli	374	49.8	5.0	3345	4	US-10-237-551-189	Sequence 189, App
C 302	50.8	5.1	1155	3	US-09-056-556-12	Sequence 12, Appli	Sequence 12, Appli	C 375	49.8	5.0	3411	4	US-09-252-991A-14823	Sequence 14823, A
C 303	50.8	5.1	1155	3	US-09-072-596-12	Sequence 12, Appli	Sequence 12, Appli	376	49.8	5.0	9521	4	US-09-902-540-953	Sequence 953, App
C 304	50.8	5.1	1155	4	US-09-072-967-12	Sequence 12, Appli	Sequence 12, Appli	C 377	49.8	5.0	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 305	50.8	5.1	1380	4	US-09-902-540-3259	Sequence 3259, App	Sequence 3259, App	C 378	49.6	5.0	678	4	US-09-252-991A-2221	Sequence 2221, Ap
C 306	50.8	5.1	1350	4	US-09-902-540-3982	Sequence 3982, App	Sequence 3982, App	C 379	49.6	5.0	753	4	US-09-252-991A-2382	Sequence 2382, Ap
C 307	50.8	5.1	2032	4	US-09-902-540-8077	Sequence 8077, App	Sequence 8077, App	380	49.6	5.0	789	4	US-09-902-540-7266	Sequence 7266, Ap
C 308	50.8	5.1	7811	4	US-09-902-540-824	Sequence 824, App	Sequence 824, App	381	49.6	5.0	831	4	US-09-902-540-5618	Sequence 5618, Ap
C 309	50.8	5.1	9818	4	US-09-902-540-987	Sequence 987, App	Sequence 987, App	382	49.6	5.0	831	4	US-09-902-540-8404	Sequence 8404, Ap
C 310	50.8	5.1	19954	4	US-09-902-540-1150	Sequence 1150, App	Sequence 1150, App	383	49.6	5.0	867	4	US-09-902-540-7887	Sequence 7887, Ap
C 311	50.8	5.1	20232	4	US-09-902-540-1197	Sequence 1197, App	Sequence 1197, App	384	49.6	5.0	1137	4	US-09-902-540-3757	Sequence 3757, Ap
C 312	50.8	5.1	72704	4	US-09-902-540-1273	Sequence 1273, App	Sequence 1273, App	385	49.6	5.0	1743	4	US-09-949-016-945	Sequence 945, App
C 313	50.6	5.1	508	3	US-09-452-239-15	Sequence 15, Appli	Sequence 15, Appli	386	49.6	5.0	1743	4	US-09-949-016-2709	Sequence 2709, Ap
C 314	50.6	5.1	1011	4	US-09-902-540-5491	Sequence 5491, App	Sequence 5491, App	387	49.6	5.0	1752	4	US-09-902-540-8626	Sequence 8626, Ap
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C 316	50.6	5.1	2448	4	US-09-902-540-5509	Sequence 5509, App	Sequence 5509, App	389	49.6	5.0	1929	4	US-09-902-540-9129	Sequence 9129, Ap
C 317	50.6	5.1	3588	4	US-09-902-540-4681	Sequence 4681, App	Sequence 4681, App	390	49.6	5.0	2814	4	US-09-252-991A-2537	Sequence 2537, Ap
C 318	50.6	5.1	14467	4	US-09-902-540-1058	Sequence 1058, App	Sequence 1058, App	391	49.6	5.0	4324	4	US-09-902-540-684	Sequence 684, App
C 319	50.6	5.1	24754	4	US-09-902-540-1230	Sequence 1230, App	Sequence 1230, App	392	49.6	5.0	5743	4	US-09-949-016-12687	Sequence 12687, A

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C 394	49.6	5.0	5808	4	US-09-902-540-794	Sequence 794, App	467	48.8	4.9	531	4	US-09-902-540-7089	Sequence 7089, Ap
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C 398	49.6	5.0	10216	4	US-09-902-540-976	Sequence 976, App	C 471	48.8	4.9	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
C 399	49.6	5.0	11612	4	US-09-902-540-981	Sequence 981, App	472	48.8	4.9	1194	4	US-09-902-540-4954	Sequence 4954, Ap
C 400	49.6	5.0	17897	4	US-09-902-540-1182	Sequence 1182, Ap	473	48.8	4.9	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
C 401	49.6	5.0	22156	4	US-09-902-540-1195	Sequence 1195, Ap	474	48.8	4.9	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
C 402	49.6	5.0	134890	4	US-09-949-016-15602	Sequence 15602, A	475	48.8	4.9	1403	4	US-09-902-540-163	Sequence 163, App
C 403	49.4	5.0	552	4	US-09-902-540-3608	Sequence 3608, Ap	476	48.8	4.9	1415	4	US-09-902-540-5962	Sequence 5962, Ap
C 404	49.4	5.0	1419	4	US-09-252-991A-152	Sequence 152, App	477	48.8	4.9	1495	4	US-09-902-540-203	Sequence 203, App
C 405	49.4	5.0	1692	4	US-09-252-991A-157	Sequence 157, App	478	48.8	4.9	1542	4	US-09-902-540-5690	Sequence 5690, Ap
C 406	49.4	5.0	1698	4	US-09-252-991A-186	Sequence 186, App	479	48.8	4.9	1782	4	US-09-902-540-5356	Sequence 5356, Ap
C 407	49.4	5.0	2091	4	US-10-237-551-78	Sequence 78, Appl	480	48.8	4.9	2232	4	US-09-252-991A-11756	Sequence 11756, A
C 408	49.4	5.0	2091	4	US-10-237-551-226	Sequence 226, App	C 481	48.8	4.9	2274	4	US-09-252-991A-11609	Sequence 11609, A
C 409	49.4	5.0	2118	4	US-10-237-551-87	Sequence 87, Appl	482	48.8	4.9	2613	4	US-09-252-991A-11836	Sequence 11836, A
C 410	49.4	5.0	2211	4	US-10-237-551-86	Sequence 86, Appl	C 483	48.8	4.9	2715	4	US-09-252-991A-8715	Sequence 8715, A
C 411	49.4	5.0	2214	3	US-08-864-038A-1	Sequence 1, Appli	C 484	48.8	4.9	4992	4	US-09-902-540-6335	Sequence 635, App
C 412	49.4	5.0	2244	4	US-09-902-540-3217	Sequence 3217, Ap	485	48.8	4.9	8829	4	US-09-902-540-2387	Sequence 2387, Ap
C 413	49.4	5.0	2745	1	US-08-363-255-1	Sequence 1, Appli	486	48.8	4.9	15644	4	US-09-902-540-1133	Sequence 1133, Ap
C 414	49.4	5.0	2745	1	US-08-363-255-13	Sequence 13, Appl	C 487	48.8	4.9	17315	4	US-09-902-540-1103	Sequence 1103, Ap
C 415	49.4	5.0	2754	4	US-09-902-540-5587	Sequence 5587, Ap	488	48.8	4.9	18848	4	US-09-902-540-1174	Sequence 1174, Ap
C 416	49.4	5.0	3331	3	US-08-864-038A-2	Sequence 2, Appli	489	48.8	4.9	27219	4	US-09-902-540-1244	Sequence 1244, Ap
C 417	49.4	5.0	3331	3	US-08-864-038A-4	Sequence 4, Appli	C 490	48.8	4.9	34662	4	US-09-902-540-1261	Sequence 1261, Ap
C 418	49.4	5.0	3489	2	US-08-728-123A-1	Sequence 1, Appli	C 491	48.6	4.9	528	3	US-09-453-239-33	Sequence 33, Appl
C 419	49.4	5.0	3489	2	US-09-298-568-1	Sequence 1, Appli	492	48.6	4.9	1278	4	US-09-902-540-8457	Sequence 8457, Ap
C 420	49.4	5.0	3489	4	US-09-410-399-1	Sequence 1, Appli	493	48.6	4.9	1320	4	US-09-724-797-85	Sequence 85, Appl
C 421	49.4	5.0	3489	4	US-09-894-273-1	Sequence 1, Appli	494	48.6	4.9	1410	4	US-09-902-540-3735	Sequence 3735, Ap
C 422	49.4	5.0	8144	4	US-09-902-540-820	Sequence 820, App	495	48.6	4.9	1479	1	US-08-644-271-31	Sequence 31, Appl
C 423	49.4	5.0	17726	4	US-09-902-540-1148	Sequence 1148, Ap	496	48.6	4.9	1479	3	US-09-077-955-35	Sequence 35, Appl
C 424	49.4	5.0	20113	4	US-09-902-540-1173	Sequence 1173, Ap	497	48.6	4.9	1575	4	US-09-252-991A-11212	Sequence 11212, A
C 425	49.4	5.0	32207	2	US-08-770-379-20	Sequence 20, Appl	498	48.6	4.9	1620	4	US-09-252-991A-11146	Sequence 11146, A
C 426	49.4	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appl	499	48.6	4.9	1893	4	US-09-902-540-4291	Sequence 4291, Ap
C 427	49.4	5.0	41927	3	US-09-230-371A-20	Sequence 20, Appl	500	48.6	4.9	2040	2	US-08-533-669A-5	Sequence 5, Appli
C 428	49.4	5.0	789	4	US-09-902-540-1268	Sequence 1268, Ap	501	48.6	4.9	2040	3	US-09-183-861-5	Sequence 5, Appli
C 429	49.2	5.0	789	4	US-09-252-991A-15913	Sequence 15913, A	502	48.6	4.9	2040	3	US-09-022-765-5	Sequence 5, Appli
C 430	49.2	5.0	795	4	US-09-252-991A-11852	Sequence 11852, A	503	48.6	4.9	2040	4	US-09-551-974A-5	Sequence 5, Appli
C 431	49.2	5.0	861	4	US-09-902-540-188	Sequence 188, App	504	48.6	4.9	2040	4	US-09-565-501A-5	Sequence 5, Appli
C 432	49.2	5.0	888	4	US-09-252-991A-16512	Sequence 16512, A	505	48.6	4.9	2040	4	US-09-639-206A-5	Sequence 5, Appli
C 433	49.2	5.0	1221	4	US-09-252-991A-11531	Sequence 11531, A	506	48.6	4.9	2040	4	US-08-874-923-5	Sequence 5, Appli
C 434	49.2	5.0	1263	4	US-09-252-991A-13467	Sequence 13467, A	507	48.6	4.9	2040	4	US-08-798-841-5	Sequence 5, Appli
C 435	49.2	5.0	1263	4	US-09-252-991A-13658	Sequence 13658, A	508	48.6	4.9	2274	4	US-09-902-540-4081	Sequence 4081, Ap
C 436	49.2	5.0	1512	4	US-09-252-991A-16092	Sequence 16092, A	509	48.6	4.9	2472	4	US-09-252-991A-11043	Sequence 11043, A
C 437	49.2	5.0	1521	4	US-09-252-991A-15778	Sequence 15778, A	C 510	48.6	4.9	2712	3	US-09-025-691-4	Sequence 4, Appli
C 438	49.2	5.0	1569	4	US-09-252-991A-15857	Sequence 15857, A	511	48.6	4.9	4276	4	US-09-949-016-4900	Sequence 4900, Ap
C 439	49.2	5.0	2133	4	US-09-902-540-8854	Sequence 8854, Ap	512	48.6	4.9	5065	4	US-09-949-016-744	Sequence 744, App
C 440	49.2	5.0	2401	4	US-09-902-540-15991	Sequence 15991, A	513	48.6	4.9	7190	4	US-09-902-540-843	Sequence 843, App
C 441	49.2	5.0	2481	4	US-09-902-540-1867	Sequence 1867, Ap	C 514	48.6	4.9	7686	4	US-09-949-016-13489	Sequence 13489, A
C 442	49.2	5.0	2541	4	US-09-902-540-8123	Sequence 8123, Ap	C 515	48.6	4.9	8590	4	US-09-902-540-889	Sequence 889, App
C 443	49.2	5.0	3318	3	US-09-593-589-3	Sequence 3, Appli	516	48.6	4.9	20113	4	US-09-902-540-1173	Sequence 1173, Ap
C 444	49.2	5.0	7325	4	US-09-949-016-13839	Sequence 13839, A	517	48.6	4.9	20250	4	US-09-902-540-1213	Sequence 1213, Ap
C 445	49.2	5.0	7846	4	US-09-902-540-830	Sequence 830, App	C 518	48.6	4.9	23847	4	US-09-902-540-1202	Sequence 1202, Ap
C 446	49.2	5.0	9993	4	US-09-902-540-942	Sequence 942, App	519	48.6	4.9	24602	4	US-09-902-540-1307	Sequence 1307, Ap
C 447	49	5.0	399	3	US-09-615-192A-193	Sequence 193, App	520	48.6	4.9	50453	4	US-09-949-016-15642	Sequence 15642, A
C 448	49	5.0	678	4	US-09-902-540-6290	Sequence 6290, Ap	521	48.6	4.9	51242	4	US-09-949-016-12486	Sequence 12486, A
C 449	49	5.0	843	4	US-09-724-797-33	Sequence 33, Appl	C 522	48.6	4.9	152132	4	US-09-949-016-13845	Sequence 13845, A
C 450	49	5.0	1011	4	US-09-902-540-3362	Sequence 3362, Ap	C 523	48.6	4.9	15145	4	US-09-949-016-12371	Sequence 12371, A
C 451	49	5.0	1355	3	US-08-415-655-14	Sequence 14, Appl	524	48.4	4.9	562	2	US-08-973-316-53	Sequence 53, Appl
C 452	49	5.0	1614	4	US-09-616-289-45	Sequence 45, Appl	525	48.4	4.9	562	3	US-09-615-192A-53	Sequence 53, Appl
C 453	49	5.0	1731	4	US-09-902-540-6944	Sequence 6944, Ap	526	48.4	4.9	562	4	US-09-169-789-53	Sequence 53, Appl
C 454	49	5.0	1811	4	US-09-902-540-375	Sequence 375, App	C 527	48.4	4.9	756	1	US-08-642-255-50	Sequence 50, Appl
C 455	49	5.0	1899	4	US-09-902-540-4564	Sequence 4564, Ap	528	48.4	4.9	1116	4	US-09-902-540-2568	Sequence 2568, Ap
C 456	49	5.0	3270	4	US-09-902-540-4814	Sequence 4814, Ap	529	48.4	4.9	1350	4	US-09-902-540-5939	Sequence 5939, Ap
C 457	49	5.0	3810	4	US-09-902-540-3021	Sequence 3021, Ap	C 530	48.4	4.9	1351	4	US-09-902-540-132	Sequence 132, App
C 458	49	5.0	3812	4	US-09-902-540-600	Sequence 600, App	531	48.4	4.9	1407	4	US-09-902-540-4833	Sequence 4833, Ap
C 459	49	5.0	4587	4	US-09-902-540-600	Sequence 600, App	532	48.4	4.9	1935	4	US-09-902-540-7710	Sequence 7710, Ap
C 460	49	5.0	6935	4	US-09-902-540-865	Sequence 865, App	C 533	48.4	4.9	6611	4	US-09-902-540-762	Sequence 762, App
C 461	49	5.0	9125	4	US-09-902-540-959	Sequence 959, App	534	48.4	4.9	6975	4	US-09-902-540-2386	Sequence 2386, Ap
C 462	49	5.0	12425	4	US-09-616-289-50	Sequence 50, Appl	535	48.4	4.9	13706	4	US-09-902-540-1124	Sequence 1124, Ap
C 463	49	5.0	17125	4	US-09-902-540-1158	Sequence 1158, Ap	536	48.4	4.9	13855	4	US-09-902-540-1117	Sequence 1117, Ap
C 464	49	5.0	24905	4	US-09-902-540-1225	Sequence 1225, Ap	537	48.2	4.9	822	4	US-09-252-991A-11707	Sequence 11707, A
C 465	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appli	538	48.2	4.9	920	4	US-09-620-312D-132	Sequence 132, App

539	48.2	4.9	957	4	US-09-902-540-4213	Sequence 4213, Ap	612	47.8	4.8	1771	4	US-09-551-974A-7	Sequence 7, Appli
540	48.2	4.9	1035	1	US-07-601-094-30	Sequence 30, Appl	613	47.8	4.8	1771	4	US-09-565-501A-7	Sequence 7, Appli
541	48.2	4.9	1035	1	US-08-012-735-30	Sequence 30, Appl	614	47.8	4.8	1771	4	US-09-639-206A-7	Sequence 7, Appli
542	48.2	4.9	1306	4	US-09-902-540-8937	Sequence 8937, Ap	615	47.8	4.8	1771	4	US-09-874-923-7	Sequence 7, Appli
543	48.2	4.9	1701	4	US-09-949-016-1139	Sequence 1139, Ap	616	47.8	4.8	1771	4	US-08-798-841-7	Sequence 7, Appli
544	48.2	4.9	1701	4	US-09-949-016-2634	Sequence 2634, Ap	617	47.8	4.8	1962	4	US-09-252-991A-16037	Sequence 16037, A
545	48.2	4.9	1910	3	US-09-593-711A-3	Sequence 3, Appli	618	47.8	4.8	2526	4	US-09-252-991A-18563	Sequence 18563, A
546	48.2	4.9	1914	1	US-07-601-094-1	Sequence 1, Appli	619	47.8	4.8	2526	4	US-09-902-540-2500	Sequence 2500, Ap
547	48.2	4.9	1914	1	US-08-012-735-1	Sequence 1, Appli	620	47.8	4.8	3126	4	US-09-252-991A-9066	Sequence 9066, Ap
548	48.2	4.9	2009	4	US-09-646-403-1	Sequence 1, Appli	621	47.8	4.8	4410	4	US-09-902-540-673	Sequence 673, App
549	48.2	4.9	2023	3	US-09-491-522-6	Sequence 6, Appli	622	47.8	4.8	4524	2	US-08-845-998-7	Sequence 7, Appli
550	48.2	4.9	2034	4	US-09-646-403-2	Sequence 2, Appli	623	47.8	4.8	4524	3	US-09-206-537-7	Sequence 7, Appli
551	48.2	4.9	2035	4	US-09-863-049B-3	Sequence 3, Appli	624	47.8	4.8	4524	3	US-09-430-854-7	Sequence 7, Appli
552	48.2	4.9	2450	3	US-09-491-522-2	Sequence 2, Appli	625	47.8	4.8	4991	4	US-09-902-540-719	Sequence 719, App
553	48.2	4.9	3350	4	US-09-894-998A-48	Sequence 48, Appl	626	47.8	4.8	5121	4	US-09-252-991A-15189	Sequence 15189, A
554	48.2	4.9	3350	4	US-10-237-551-48	Sequence 48, Appl	627	47.8	4.8	6327	4	US-09-252-991A-14931	Sequence 14931, A
555	48.2	4.9	3636	4	US-09-949-016-5530	Sequence 5530, Ap	628	47.8	4.8	10871	4	US-09-902-540-1025	Sequence 1025, Ap
556	48.2	4.9	4761	4	US-09-902-540-739	Sequence 739, App	629	47.8	4.8	12950	4	US-09-902-540-1036	Sequence 1036, Ap
557	48.2	4.9	6692	3	US-09-491-522-1	Sequence 1, Appli	630	47.8	4.8	15382	4	US-09-902-540-1121	Sequence 1121, Ap
558	48.2	4.9	17639	4	US-09-902-540-1153	Sequence 1153, Ap	631	47.8	4.8	15782	4	US-09-902-540-1094	Sequence 1094, Ap
559	48.2	4.9	21330	4	US-09-902-540-1209	Sequence 1209, Ap	632	47.8	4.8	16833	4	US-09-902-540-1112	Sequence 1112, Ap
560	48	4.9	465	4	US-09-252-991A-2233	Sequence 2233, Ap	633	47.8	4.8	24459	4	US-09-902-540-5004	Sequence 5004, Ap
561	48	4.9	561	4	US-09-902-540-3942	Sequence 3942, Ap	634	47.8	4.8	32241	4	US-09-902-540-1247	Sequence 1247, Ap
562	48	4.9	822	4	US-09-252-991A-7080	Sequence 7080, Ap	635	47.8	4.8	71989	3	US-09-443-501A-2	Sequence 2, Appli
563	48	4.9	822	4	US-09-252-991A-2447	Sequence 2447, Ap	636	47.6	4.8	687	4	US-09-902-540-6345	Sequence 6345, Ap
564	48	4.9	933	4	US-09-902-540-6632	Sequence 6632, Ap	637	47.6	4.8	720	4	US-09-902-540-7501	Sequence 7501, Ap
565	48	4.9	1071	4	US-09-252-991A-1635	Sequence 1635, Ap	638	47.6	4.8	924	4	US-09-902-540-3612	Sequence 3612, Ap
566	48	4.9	1128	4	US-09-622-439-1	Sequence 1, Appli	639	47.6	4.8	930	4	US-09-252-991A-15663	Sequence 15663, A
567	48	4.9	1128	4	US-10-318-142-1	Sequence 1, Appli	640	47.6	4.8	1248	4	US-09-252-991A-2635	Sequence 2635, Ap
568	48	4.9	1161	4	US-09-902-540-3053	Sequence 3053, Ap	641	47.6	4.8	1278	4	US-09-252-991A-3896	Sequence 3896, Ap
569	48	4.9	1341	4	US-09-902-540-5533	Sequence 5533, Ap	642	47.6	4.8	1365	4	US-09-902-540-6352	Sequence 6352, Ap
570	48	4.9	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	643	47.6	4.8	1646	4	US-09-902-540-402	Sequence 402, App
571	48	4.9	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	644	47.6	4.8	1667	4	US-09-902-540-407	Sequence 407, App
572	48	4.9	1677	4	US-09-902-540-7773	Sequence 7773, Ap	645	47.6	4.8	1971	4	US-09-252-991A-2197	Sequence 2197, Ap
573	48	4.9	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	646	47.6	4.8	1977	4	US-09-902-540-3924	Sequence 3924, Ap
574	48	4.9	1701	4	US-09-902-540-9608	Sequence 9608, Ap	647	47.6	4.8	2091	4	US-09-252-991A-4016	Sequence 4016, Ap
575	48	4.9	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	648	47.6	4.8	2211	4	US-09-252-991A-2477	Sequence 2477, Ap
576	48	4.9	1806	4	US-09-252-991A-1931	Sequence 1931, Ap	649	47.6	4.8	2305	4	US-09-475-515-80	Sequence 80, Appl
577	48	4.9	1834	4	US-09-252-991A-7017	Sequence 7017, Ap	650	47.6	4.8	2306	4	US-09-475-515-82	Sequence 82, Appl
578	48	4.9	1917	4	US-09-252-991A-7111	Sequence 7111, Ap	651	47.6	4.8	2481	4	US-09-894-998A-35	Sequence 35, Appl
579	48	4.9	2230	4	US-09-902-540-6807	Sequence 6807, Ap	652	47.6	4.8	2481	4	US-10-237-551-35	Sequence 35, Appl
580	48	4.9	2253	4	US-09-252-991A-7191	Sequence 7191, Ap	653	47.6	4.8	2670	4	US-09-902-540-8525	Sequence 8525, Ap
581	48	4.9	2403	4	US-09-252-991A-7253	Sequence 7253, Ap	654	47.6	4.8	3066	4	US-10-237-551-152	Sequence 152, App
582	48	4.9	2490	4	US-09-252-991A-7447	Sequence 7447, Ap	655	47.6	4.8	3390	4	US-09-902-540-6647	Sequence 6647, Ap
583	48	4.9	3492	4	US-09-949-016-837	Sequence 837, App	656	47.6	4.8	3393	4	US-09-902-540-514	Sequence 514, App
584	48	4.9	4800	4	US-09-902-540-562	Sequence 562, App	657	47.6	4.8	5001	4	US-09-902-540-8618	Sequence 8618, Ap
585	48	4.9	6250	4	US-09-902-540-773	Sequence 773, App	658	47.6	4.8	5481	4	US-09-902-540-7351	Sequence 7351, Ap
586	48	4.9	6713	4	US-09-902-540-793	Sequence 793, App	659	47.6	4.8	5618	4	US-09-902-540-728	Sequence 728, App
587	48	4.9	9165	4	US-09-902-540-1050	Sequence 1050, Ap	660	47.6	4.8	6008	4	US-09-949-016-5058	Sequence 5058, App
588	48	4.9	12194	4	US-09-902-540-1091	Sequence 1091, Ap	661	47.6	4.8	6402	4	US-09-902-540-702	Sequence 702, App
589	48	4.9	15482	4	US-09-902-540-1067	Sequence 1067, Ap	662	47.6	4.8	9321	4	US-09-902-540-898	Sequence 898, App
590	48	4.9	22431	4	US-09-949-016-14099	Sequence 14099, A	663	47.6	4.8	9360	3	US-08-822-586-46	Sequence 46, Appl
591	48	4.9	24509	4	US-09-949-016-12612	Sequence 12612, A	664	47.6	4.8	13299	4	US-09-902-540-968	Sequence 968, App
592	48	4.9	24509	4	US-09-949-016-13687	Sequence 13687, A	665	47.6	4.8	14158	4	US-09-902-540-1069	Sequence 1069, App
593	48	4.9	33529	3	US-09-144-085-3	Sequence 3, Appli	666	47.4	4.8	411	4	US-09-902-540-5862	Sequence 5862, Ap
594	48	4.9	41170	4	US-09-902-540-1267	Sequence 1267, Ap	667	47.4	4.8	789	4	US-09-902-540-3137	Sequence 3137, Ap
595	47.8	4.8	309	4	US-09-252-991A-6725	Sequence 6725, Ap	668	47.4	4.8	918	4	US-09-252-991A-8762	Sequence 8762, Ap
596	47.8	4.8	468	4	US-09-902-540-2625	Sequence 2625, Ap	669	47.4	4.8	948	4	US-09-252-991A-9192	Sequence 9192, Ap
597	47.8	4.8	482	4	US-09-902-540-7213	Sequence 7213, Ap	670	47.4	4.8	954	4	US-09-252-991A-5807	Sequence 5807, Ap
598	47.8	4.8	801	4	US-09-252-991A-15941	Sequence 15941, A	671	47.4	4.8	1023	4	US-09-902-540-3025	Sequence 3025, Ap
599	47.8	4.8	819	4	US-09-252-991A-14581	Sequence 14581, A	672	47.4	4.8	1116	4	US-09-252-991A-10924	Sequence 10924, A
600	47.8	4.8	896	4	US-09-902-540-7446	Sequence 7446, Ap	673	47.4	4.8	1149	4	US-09-252-991A-8983	Sequence 8983, Ap
601	47.8	4.8	966	4	US-09-252-991A-6895	Sequence 6895, Ap	674	47.4	4.8	1209	4	US-09-252-991A-11138	Sequence 11138, A
602	47.8	4.8	1218	4	US-09-252-991A-16453	Sequence 16453, A	675	47.4	4.8	1245	4	US-09-902-540-4829	Sequence 4829, Ap
603	47.8	4.8	1485	4	US-09-252-991A-6815	Sequence 6815, Ap	676	47.4	4.8	1248	4	US-09-724-797-23	Sequence 23, Appl
604	47.8	4.8	1509	4	US-09-252-991A-6930	Sequence 6930, Ap	677	47.4	4.8	1251	4	US-09-252-991A-5844	Sequence 5844, Ap
605	47.8	4.8	1652	4	US-09-902-540-9646	Sequence 9646, Ap	678	47.4	4.8	1332	4	US-09-902-540-9176	Sequence 9176, Ap
606	47.8	4.8	1671	4	US-09-902-540-4098	Sequence 4098, Ap	679	47.4	4.8	1413	4	US-09-902-540-5411	Sequence 5411, Ap
607	47.8	4.8	1708	4	US-09-902-540-5058	Sequence 5058, Ap	680	47.4	4.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap
608	47.8	4.8	1771	2	US-08-533-669A-7	Sequence 7, Appli	681	47.4	4.8	1812	4	US-09-902-540-2482	Sequence 2482, Ap
609	47.8	4.8	1771	2	US-08-511-872-1	Sequence 1, Appli	682	47.4	4.8	1869	4	US-09-252-991A-3231	Sequence 3231, Ap
610	47.8	4.8	1771	3	US-09-183-861-7	Sequence 7, Appli	683	47.4	4.8	1881	4	US-09-252-991A-11264	Sequence 11264, A
611	47.8	4.8	1771	3	US-09-022-765-7	Sequence 7, Appli	684	47.4	4.8	1977	4	US-09-902-540-7785	Sequence 7785, Ap

685	47.4	4.8	1986	4	US-09-252-991A-5767	Sequence 5767, Ap	758	47	4.8	4377	3	US-08-911-853-28	Sequence 28, Appl
686	47.4	4.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	759	47	4.8	4377	3	US-09-479-409-28	Sequence 28, Appl
687	47.4	4.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	760	47	4.8	4377	3	US-09-479-453-28	Sequence 28, Appl
688	47.4	4.8	2634	1	US-08-196-218-31	Sequence 31, Appl	761	47	4.8	13434	4	US-09-902-540-1003	Sequence 1003, Ap
689	47.4	4.8	2634	1	US-08-681-953-31	Sequence 31, Appl	762	47	4.8	18469	4	US-09-902-540-1205	Sequence 1205, Ap
690	47.4	4.8	3073	4	US-09-302-540-643	Sequence 643, Ap	763	47	4.8	24986	4	US-09-902-540-1200	Sequence 1200, Ap
691	47.4	4.8	3099	4	US-09-302-540-5065	Sequence 5065, Ap	c 764	47	4.8	26659	4	US-09-902-540-1237	Sequence 1237, Ap
692	47.4	4.8	3333	4	US-09-302-540-1965	Sequence 1965, Ap	765	47	4.8	80161	3	US-09-036-987A-1	Sequence 1, Appli
693	47.4	4.8	5175	4	US-09-302-540-774	Sequence 774, Ap	766	47	4.8	80161	3	US-09-370-700-1	Sequence 1, Appli
694	47.4	4.8	8820	4	US-09-302-540-974	Sequence 974, Ap	767	47	4.8	80161	3	US-09-603-207-1	Sequence 1, Appli
695	47.4	4.8	17938	4	US-09-302-540-1111	Sequence 1111, Ap	768	46.8	4.7	296	4	US-09-615-192A-195	Sequence 195, App
696	47.4	4.8	19598	4	US-09-302-540-1143	Sequence 1143, Ap	769	46.8	4.7	687	4	US-09-902-540-7361	Sequence 7361, Ap
697	47.4	4.8	28194	4	US-09-302-540-1143	Sequence 1250, Ap	770	46.8	4.7	792	4	US-09-252-991A-4971	Sequence 4971, Ap
698	47.4	4.8	34953	4	US-09-302-540-1250	Sequence 1263, Ap	771	46.8	4.7	801	2	US-08-770-379-16	Sequence 16, Appl
699	47.4	4.8	50397	3	US-09-428-517-1	Sequence 1, Appli	772	46.8	4.7	801	3	US-08-757-669A-16	Sequence 16, Appl
700	47.4	4.8	50397	3	US-09-428-517-1	Sequence 1, Appli	773	46.8	4.7	801	3	US-09-298-568-3	Sequence 3, Appli
701	47.4	4.8	767677	4	US-09-949-016-12147	Sequence 12147, A	774	46.8	4.7	801	3	US-09-230-371A-16	Sequence 16, Appl
702	47.4	4.8	767677	4	US-09-949-016-17361	Sequence 17361, A	775	46.8	4.7	801	4	US-09-894-273-3	Sequence 3, Appli
703	47.2	4.8	519	4	US-09-302-540-6955	Sequence 6955, Ap	776	46.8	4.7	1071	4	US-09-252-991A-4955	Sequence 4955, Ap
704	47.2	4.8	714	4	US-09-302-540-16021	Sequence 16021, A	777	46.8	4.7	1131	4	US-09-252-991A-4994	Sequence 4994, Ap
705	47.2	4.8	864	4	US-09-302-540-8350	Sequence 8350, Ap	c 778	46.8	4.7	1215	4	US-09-252-991A-4984	Sequence 4984, Ap
706	47.2	4.8	888	3	US-08-765-907A-2	Sequence 2, Appli	779	46.8	4.7	2592	4	US-09-902-540-3407	Sequence 3407, Ap
707	47.2	4.8	888	4	US-09-987-614A-2	Sequence 2, Appli	780	46.8	4.7	2811	4	US-09-902-540-2406	Sequence 2406, Ap
708	47.2	4.8	897	4	US-09-302-540-2413	Sequence 2413, Ap	781	46.8	4.7	2962	4	US-09-902-540-6991	Sequence 6991, Ap
709	47.2	4.8	899	4	US-09-252-991A-970	Sequence 970, Ap	782	46.8	4.7	3171	4	US-09-252-991A-7591	Sequence 7591, Ap
710	47.2	4.8	1110	4	US-09-252-991A-1014	Sequence 1014, Ap	783	46.8	4.7	3210	4	US-09-252-991A-7962	Sequence 7962, Ap
711	47.2	4.8	1194	4	US-09-724-797-25	Sequence 25, Appli	784	46.8	4.7	4532	4	US-09-902-540-8368	Sequence 8368, Ap
712	47.2	4.8	1231	4	US-09-302-540-3596	Sequence 3596, Ap	785	46.8	4.7	4873	4	US-09-902-540-610	Sequence 610, App
c 713	47.2	4.8	1275	4	US-09-252-991A-1080	Sequence 1080, Ap	786	46.8	4.7	10182	4	US-09-902-540-1049	Sequence 1049, Ap
714	47.2	4.8	1335	4	US-09-302-540-5111	Sequence 5111, Ap	787	46.8	4.7	17654	4	US-09-902-540-1161	Sequence 1161, Ap
715	47.2	4.8	1347	4	US-09-724-797-43	Sequence 43, Appl	788	46.6	4.7	270	4	US-09-252-991A-14378	Sequence 14378, A
716	47.2	4.8	1818	4	US-09-302-540-4685	Sequence 4685, Ap	c 789	46.6	4.7	489	4	US-09-252-991A-452	Sequence 452, App
717	47.2	4.8	1869	4	US-09-302-540-8930	Sequence 8930, Ap	790	46.6	4.7	741	4	US-09-902-540-8930	Sequence 8930, Ap
718	47.2	4.8	1902	4	US-09-302-540-8930	Sequence 8930, Ap	c 791	46.6	4.7	777	4	US-09-252-991A-12568	Sequence 12568, A
719	47.2	4.8	1944	4	US-09-252-991A-16245	Sequence 16245, A	792	46.6	4.7	780	4	US-09-902-540-5800	Sequence 5800, Ap
720	47.2	4.8	2065	4	US-09-302-540-7188	Sequence 7188, Ap	793	46.6	4.7	786	4	US-09-252-991A-13239	Sequence 13239, A
721	47.2	4.8	2133	4	US-09-252-991A-5907	Sequence 5907, Ap	794	46.6	4.7	932	4	US-09-902-540-8519	Sequence 8519, Ap
722	47.2	4.8	212	4	US-09-475-515-84	Sequence 84, Appl	c 795	46.6	4.7	981	4	US-09-252-991A-431	Sequence 431, App
723	47.2	4.8	2406	4	US-09-302-540-5545	Sequence 5545, Ap	796	46.6	4.7	981	4	US-09-252-991A-10487	Sequence 10487, A
724	47.2	4.8	2808	4	US-09-252-991A-16466	Sequence 16466, A	797	46.6	4.7	1032	4	US-09-902-540-6426	Sequence 6426, Ap
c 725	47.2	4.8	2862	4	US-09-252-991A-10659	Sequence 10659, A	798	46.6	4.7	1062	4	US-09-252-991A-6751	Sequence 6751, Ap
726	47.2	4.8	2888	3	US-08-765-907A-1	Sequence 1, Appli	799	46.6	4.7	1206	4	US-09-302-540-3165	Sequence 3165, Ap
727	47.2	4.8	2888	4	US-09-987-614A-1	Sequence 1, Appli	800	46.6	4.7	1320	4	US-09-902-540-7649	Sequence 7649, Ap
728	47.2	4.8	2910	4	US-09-252-991A-10414	Sequence 10414, A	801	46.6	4.7	1380	4	US-09-252-991A-3550	Sequence 3550, Ap
729	47.2	4.8	3111	4	US-09-252-991A-10504	Sequence 10504, A	c 802	46.6	4.7	1530	4	US-09-252-991A-6874	Sequence 6874, Ap
730	47.2	4.8	3335	4	US-09-252-991A-5922	Sequence 5922, Ap	803	46.6	4.7	1770	4	US-09-902-540-7504	Sequence 7504, Ap
731	47.2	4.8	4319	4	US-09-475-515-6	Sequence 6, Appli	804	46.6	4.7	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
c 732	47.2	4.8	4604	4	US-09-302-540-602	Sequence 602, Ap	805	46.6	4.7	2247	4	US-09-902-540-3294	Sequence 3294, Ap
733	47.2	4.8	5033	4	US-09-302-540-670	Sequence 670, Ap	806	46.6	4.7	2295	4	US-09-902-540-7287	Sequence 7287, Ap
734	47.2	4.8	5051	4	US-09-302-540-667	Sequence 667, Ap	807	46.6	4.7	2325	4	US-09-252-991A-12916	Sequence 12916, A
c 735	47.2	4.8	9556	4	US-09-902-540-929	Sequence 929, Ap	808	46.6	4.7	2632	4	US-09-902-540-6888	Sequence 688, App
c 736	47.2	4.8	9992	4	US-09-902-540-952	Sequence 952, Ap	809	46.6	4.7	4487	4	US-09-902-540-6888	Sequence 688, App
737	47.2	4.8	11220	3	US-09-105-537-32	Sequence 32, Appl	810	46.6	4.7	5411	4	US-09-902-540-8809	Sequence 8809, Ap
738	47.2	4.8	11812	4	US-09-302-540-1041	Sequence 1041, Ap	c 811	46.6	4.7	5618	4	US-09-902-540-7028	Sequence 7028, App
c 739	47.2	4.8	16782	4	US-09-302-540-1105	Sequence 1105, Ap	812	46.6	4.7	6594	4	US-09-902-540-752	Sequence 752, App
740	47.2	4.8	28058	4	US-09-302-540-1252	Sequence 1252, Ap	c 813	46.6	4.7	7419	4	US-09-252-991A-481	Sequence 481, App
c 741	47	4.8	441	4	US-09-252-991A-14658	Sequence 14658, A	814	46.6	4.7	7449	4	US-09-252-991A-396	Sequence 396, App
742	47	4.8	758	4	US-09-302-331B-5	Sequence 5, Appli	815	46.6	4.7	8310	4	US-09-902-540-1001	Sequence 1001, Ap
743	47	4.8	936	4	US-09-902-540-4133	Sequence 4133, Ap	c 816	46.6	4.7	8765	4	US-09-902-540-939	Sequence 939, App
c 744	47	4.8	1260	4	US-09-252-991A-14526	Sequence 14526, A	817	46.6	4.7	9880	4	US-09-902-540-8196	Sequence 8196, Ap
745	47	4.8	1260	4	US-09-252-991A-14838	Sequence 14838, A	c 818	46.6	4.7	16350	4	US-09-902-540-1144	Sequence 1144, Ap
c 746	47	4.8	1320	2	US-08-461-775-8	Sequence 8, Appli	c 819	46.6	4.7	19862	4	US-09-902-540-1198	Sequence 1198, Ap
c 747	47	4.8	1320	3	US-09-031-606-8	Sequence 3, Appli	820	46.4	4.7	475	4	US-09-902-540-6044	Sequence 6044, Ap
748	47	4.8	1416	3	US-08-911-853-3	Sequence 3, Appli	821	46.4	4.7	525	4	US-09-902-540-6280	Sequence 6280, Ap
749	47	4.8	1416	3	US-09-479-409-3	Sequence 3, Appli	822	46.4	4.7	819	4	US-09-902-540-8196	Sequence 8196, Ap
750	47	4.8	1416	3	US-09-479-453-3	Sequence 3, Appli	823	46.4	4.7	876	4	US-09-902-540-5288	Sequence 5288, Ap
c 751	47	4.8	1620	2	US-08-461-775-10	Sequence 10, Appl	c 824	46.4	4.7	981	4	US-09-252-991A-14299	Sequence 14299, A
c 752	47	4.8	1620	3	US-09-031-606-10	Sequence 10, Appl	825	46.4	4.7	1072	3	US-09-088-549-2	Sequence 2, Appli
753	47	4.8	1707	4	US-09-724-797-15	Sequence 15, Appl	826	46.4	4.7	1263	4	US-09-252-991A-14349	Sequence 14349, A
c 754	47	4.8	2223	4	US-09-902-540-3967	Sequence 3967, Ap	827	46.4	4.7	1296	4	US-09-902-540-4063	Sequence 4063, Ap
c 755	47	4.8	2724	4	US-09-302-540-1968	Sequence 1968, Ap	828	46.4	4.7	1551	4	US-09-902-540-9008	Sequence 9008, Ap
c 756	47	4.8	2745	4	US-09-902-540-4835	Sequence 4835, Ap	829	46.4	4.7	1553	4	US-09-902-540-245	Sequence 245, App
757	47	4.8	2946	4	US-09-902-540-2504	Sequence 2504, Ap	c 830	46.4	4.7	1644	4	US-09-902-540-371	Sequence 371, App

831	46.4	4.7	2187	4	US-09-902-540-9583	Sequence 9583, Ap	C 904	46	4.7	11358	4	US-09-902-540-1075	Sequence 1075, Ap
832	46.4	4.7	2196	4	US-09-902-540-6529	Sequence 6529, Ap	905	46	4.7	12323	4	US-09-949-016-16703	Sequence 16703, A
833	46.4	4.7	2235	4	US-09-252-991A-14374	Sequence 14374, A	906	46	4.7	17228	4	US-09-902-540-11703	Sequence 1170, Ap
834	46.4	4.7	3147	4	US-09-902-540-476	Sequence 476, App	907	46	4.7	17612	3	US-08-911-853-29	Sequence 29, Appl
835	46.4	4.7	3768	4	US-09-902-540-5368	Sequence 5368, Ap	908	46	4.7	17612	3	US-09-479-409-29	Sequence 29, Appl
836	46.4	4.7	11566	4	US-09-902-540-1088	Sequence 1088, Ap	909	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl
837	46.4	4.7	12849	4	US-09-902-540-963	Sequence 963, App	C 910	46	4.7	19394	4	US-09-902-540-1172	Sequence 1172, Ap
838	46.4	4.7	21511	4	US-09-902-540-1201	Sequence 1201, Ap	C 911	46	4.7	19954	4	US-09-902-540-1150	Sequence 1150, Ap
839	46.4	4.7	30783	4	US-09-902-540-1258	Sequence 1258, Ap	C 912	46	4.7	34552	4	US-09-902-540-1262	Sequence 1262, Ap
840	46.4	4.7	41927	4	US-09-902-540-1268	Sequence 1268, Ap	C 913	46	4.7	41768	4	US-09-902-540-1266	Sequence 1266, Ap
841	46.2	4.7	432	1	US-08-642-255-48	Sequence 48, Appl	914	45.8	4.6	549	4	US-09-902-540-5246	Sequence 5246, Ap
842	46.2	4.7	465	4	US-09-902-540-6929	Sequence 6929, Ap	915	45.8	4.6	557	4	US-09-252-991A-4833	Sequence 4833, Ap
843	46.2	4.7	822	4	US-08-893-737-227	Sequence 227, App	C 916	45.8	4.6	774	3	US-08-956-307B-12	Sequence 12, Appl
844	46.2	4.7	1050	4	US-09-902-540-3534	Sequence 3534, Ap	C 917	45.8	4.6	778	3	US-08-956-307B-11	Sequence 11, Appl
845	46.2	4.7	1086	4	US-09-902-540-5546	Sequence 5546, Ap	C 918	45.8	4.6	960	4	US-09-534-229C-8	Sequence 8, Appl
846	46.2	4.7	1362	4	US-09-724-797-31	Sequence 31, Appl	919	45.8	4.6	1140	4	US-09-902-540-2965	Sequence 2965, Ap
847	46.2	4.7	1396	4	US-09-902-540-2306	Sequence 2306, Ap	920	45.8	4.6	1245	4	US-09-252-991A-13463	Sequence 13463, A
848	46.2	4.7	1401	4	US-09-902-540-6962	Sequence 6962, Ap	921	45.8	4.6	1284	4	US-09-902-540-8320	Sequence 8320, Ap
849	46.2	4.7	1458	4	US-09-902-540-9498	Sequence 9498, Ap	C 922	45.8	4.6	1323	4	US-09-902-540-2671	Sequence 2671, Ap
850	46.2	4.7	1476	4	US-09-902-540-6774	Sequence 6774, Ap	923	45.8	4.6	1401	4	US-09-252-991A-4911	Sequence 4911, Ap
851	46.2	4.7	1509	4	US-09-724-797-89	Sequence 89, Appl	C 924	45.8	4.6	1434	4	US-09-902-540-5292	Sequence 5292, A
852	46.2	4.7	1950	4	US-09-902-540-3116	Sequence 3116, Ap	C 925	45.8	4.6	1569	4	US-09-252-991A-13880	Sequence 13880, A
853	46.2	4.7	2334	4	US-09-902-540-7862	Sequence 7862, Ap	926	45.8	4.6	1628	4	US-09-902-540-9218	Sequence 9218, Ap
854	46.2	4.7	2976	4	US-09-902-540-554	Sequence 554, App	927	45.8	4.6	1651	4	US-09-902-540-6097	Sequence 6097, Ap
855	46.2	4.7	3102	4	US-09-252-991A-4429	Sequence 4429, Ap	928	45.8	4.6	1652	4	US-09-902-540-273	Sequence 273, App
856	46.2	4.7	4050	4	US-09-902-540-604	Sequence 604, App	929	45.8	4.6	1802	4	US-09-949-016-1604	Sequence 1604, Ap
857	46.2	4.7	4320	4	US-09-902-540-577	Sequence 577, App	930	45.8	4.6	2259	4	US-09-252-991A-13556	Sequence 13556, A
858	46.2	4.7	4320	4	US-09-902-540-6854	Sequence 6854, Ap	931	45.8	4.6	2625	4	US-09-902-540-8554	Sequence 8554, Ap
859	46.2	4.7	5132	4	US-09-902-540-597	Sequence 597, App	932	45.8	4.6	2847	4	US-09-902-540-7588	Sequence 7588, Ap
860	46.2	4.7	8614	4	US-09-902-540-787	Sequence 787, App	933	45.8	4.6	4107	4	US-09-902-540-2552	Sequence 2552, Ap
861	46.2	4.7	13256	4	US-09-902-540-1006	Sequence 1006, Ap	934	45.8	4.6	4217	4	US-09-902-540-9677	Sequence 9677, Ap
862	46.2	4.7	14101	4	US-09-902-540-1080	Sequence 1080, Ap	935	45.8	4.6	4835	4	US-09-902-540-627	Sequence 627, App
863	46.2	4.7	18538	4	US-09-902-540-1169	Sequence 1169, Ap	936	45.8	4.6	5661	3	US-08-938-105-2	Sequence 2, Appl
864	46.2	4.7	18809	4	US-09-902-540-1141	Sequence 1141, Ap	937	45.8	4.6	5802	4	US-09-949-016-13346	Sequence 13346, A
865	46.2	4.7	30001	1	US-08-125-468-1	Sequence 1, Appl	938	45.8	4.6	6637	4	US-09-902-540-850	Sequence 850, App
866	46.2	4.7	30001	2	US-08-474-933-1	Sequence 1, Appl	939	45.8	4.6	7404	4	US-09-902-540-3115	Sequence 3115, App
867	46.2	4.7	33500	4	US-09-266-965-76	Sequence 76, Appl	C 940	45.8	4.6	7562	4	US-09-902-540-902	Sequence 902, App
868	46	4.7	528	4	US-09-902-540-9054	Sequence 9054, Ap	941	45.8	4.6	7704	4	US-09-902-540-743	Sequence 743, App
869	46	4.7	606	4	US-09-252-991A-2567	Sequence 2567, Ap	942	45.8	4.6	13637	4	US-09-902-540-1097	Sequence 1097, Ap
870	46	4.7	609	4	US-09-252-991A-9531	Sequence 9531, Ap	943	45.8	4.6	14462	4	US-09-902-540-1090	Sequence 1090, Ap
871	46	4.7	765	4	US-09-902-540-3589	Sequence 3589, Ap	944	45.8	4.6	14462	4	US-09-902-540-9997	Sequence 9997, Ap
872	46	4.7	906	4	US-09-252-991A-1329	Sequence 1329, Ap	C 945	45.8	4.6	15377	4	US-09-902-540-1116	Sequence 1116, Ap
873	46	4.7	936	4	US-09-902-540-7713	Sequence 7713, Ap	C 946	45.8	4.6	16541	4	US-09-902-540-1165	Sequence 1165, Ap
874	46	4.7	942	4	US-09-902-540-6941	Sequence 6941, Ap	C 947	45.8	4.6	17245	4	US-09-902-540-1073	Sequence 1073, Ap
875	46	4.7	1023	4	US-09-252-991A-1283	Sequence 1283, Ap	948	45.8	4.6	17622	4	US-09-902-540-1125	Sequence 1125, Ap
876	46	4.7	1023	4	US-09-902-540-4306	Sequence 4306, Ap	C 949	45.8	4.6	25686	4	US-09-902-540-1246	Sequence 1246, Ap
877	46	4.7	1044	1	US-07-975-526-3	Sequence 3, Appl	C 950	45.8	4.6	34316	4	US-09-902-540-1257	Sequence 1257, Ap
878	46	4.7	1044	3	US-07-974-409C-425	Sequence 425, App	951	45.8	4.6	43280	2	US-08-804-227C-1	Sequence 1, Appl
879	46	4.7	1077	4	US-09-252-991A-7892	Sequence 7892, Ap	952	45.6	4.6	450	4	US-09-902-540-3155	Sequence 3155, Ap
880	46	4.7	1080	4	US-09-252-991A-1187	Sequence 1187, Ap	C 953	45.6	4.6	747	4	US-09-252-991A-14108	Sequence 14108, A
881	46	4.7	1095	4	US-09-902-540-5522	Sequence 5522, Ap	954	45.6	4.6	765	4	US-09-902-540-5240	Sequence 5240, Ap
882	46	4.7	1112	3	US-09-434-288-9	Sequence 9, Appl	955	45.6	4.6	777	4	US-09-902-540-2656	Sequence 2656, Ap
883	46	4.7	1143	4	US-09-902-540-7583	Sequence 7583, Ap	956	45.6	4.6	900	4	US-09-252-991A-1017	Sequence 1017, Ap
884	46	4.7	1167	4	US-09-902-540-9338	Sequence 9338, Ap	C 957	45.6	4.6	924	4	US-09-252-991A-1483	Sequence 1483, Ap
885	46	4.7	1263	4	US-09-902-540-6477	Sequence 6477, Ap	C 958	45.6	4.6	1035	4	US-09-252-991A-14017	Sequence 14017, A
886	46	4.7	1266	4	US-09-252-991A-10804	Sequence 10804, A	959	45.6	4.6	1131	4	US-09-902-540-2616	Sequence 2616, Ap
887	46	4.7	1275	4	US-09-252-991A-2484	Sequence 2484, Ap	960	45.6	4.6	1200	4	US-09-787-292-4	Sequence 4, Appl
888	46	4.7	1317	4	US-09-902-540-9439	Sequence 9439, Ap	961	45.6	4.6	1209	6	5352575-4	Patent No. 5352575
889	46	4.7	1371	4	US-09-252-991A-9717	Sequence 9717, Ap	962	45.6	4.6	1209	6	5352575-4	Patent No. 5352575
890	46	4.7	1383	4	US-09-252-991A-2350	Sequence 2350, Ap	963	45.6	4.6	1213	3	US-09-232-468A-7	Sequence 7, Appl
891	46	4.7	1443	4	US-09-252-991A-10228	Sequence 10228, A	964	45.6	4.6	1213	3	US-09-784-984B-6	Sequence 6, Appl
892	46	4.7	1458	4	US-09-902-540-3540	Sequence 3540, Ap	965	45.6	4.6	1242	4	US-09-902-540-5044	Sequence 5044, Ap
893	46	4.7	1818	4	US-09-252-991A-10345	Sequence 10345, A	966	45.6	4.6	1251	4	US-09-902-540-8793	Sequence 8793, Ap
894	46	4.7	1935	4	US-09-620-312D-236	Sequence 236, App	967	45.6	4.6	1365	4	US-09-252-991A-14122	Sequence 14122, A
895	46	4.7	1987	4	US-09-902-540-3186	Sequence 3186, Ap	C 968	45.6	4.6	1458	4	US-09-252-991A-1112	Sequence 1112, Ap
896	46	4.7	2400	1	US-08-967-513-1	Sequence 1, Appl	969	45.6	4.6	1461	4	US-09-252-991A-972	Sequence 972, App
897	46	4.7	2400	2	US-08-687-645B-1	Sequence 1, Appl	970	45.6	4.6	1485	4	US-09-902-540-8444	Sequence 8444, Ap
898	46	4.7	3597	4	US-09-902-540-5402	Sequence 5402, Ap	971	45.6	4.6	1500	4	US-09-902-540-8297	Sequence 8297, Ap
899	46	4.7	3603	4	US-09-902-540-3266	Sequence 3266, Ap	972	45.6	4.6	1505	1	US-07-915-246-1	Sequence 1, Appl
900	46	4.7	4402	4	US-09-902-540-742	Sequence 742, App	973	45.6	4.6	1545	4	US-09-902-540-2849	Sequence 2849, Ap
901	46	4.7	6083	4	US-09-902-540-763	Sequence 763, App	974	45.6	4.6	1581	4	US-09-902-540-9170	Sequence 9170, Ap
902	46	4.7	10013	4	US-09-949-016-16474	Sequence 16474, A	975	45.6	4.6	1588	4	US-09-490-291-7	Sequence 7, Appl
903	46	4.7	10424	4	US-09-902-540-1015	Sequence 1015, Ap	976	45.6	4.6	1623	4	US-09-902-540-9607	Sequence 9607, Ap



977	45.6	4.6	1663	4	US-09-398-522-108	Sequence 108, App	ci1050	45.4	4.6	28172	4	US-09-902-540-1221	Sequence 1221, Ap
c 978	45.6	4.6	1768	4	US-09-485-529-13	Sequence 13, Appl	1051	45.4	4.6	32278	4	US-09-949-016-14575	Sequence 14575, A
979	45.6	4.6	2124	4	US-09-266-965-44	Sequence 44, Appl	ci1052	45.2	4.6	357	3	US-08-556-9788-83	Sequence 83, Appl
c 980	45.6	4.6	2125	4	US-09-485-529-14	Sequence 14, Appl	ci1053	45.2	4.6	447	4	US-09-252-991A-4677	Sequence 4677, Ap
981	45.6	4.6	2178	4	US-09-302-540-7409	Sequence 7409, Ap	ci1054	45.2	4.6	504	4	US-09-252-991A-4720	Sequence 4720, Ap
982	45.6	4.6	2282	4	US-09-922-445-50	Sequence 50, Appl	ci1055	45.2	4.6	522	4	US-09-252-991A-12264	Sequence 12264, A
c 983	45.6	4.6	3681	4	US-09-581-105-1	Sequence 1, Appl	ci1056	45.2	4.6	702	4	US-09-253-991A-4703	Sequence 4703, Ap
984	45.6	4.6	4095	4	US-09-252-991A-10309	Sequence 10309, A	1057	45.2	4.6	711	4	US-09-902-540-6903	Sequence 6903, Ap
985	45.6	4.6	4164	4	US-09-902-540-4661	Sequence 4661, A	1058	45.2	4.6	807	4	US-09-252-991A-12392	Sequence 12392, A
986	45.6	4.6	4233	4	US-09-551-974A-99	Sequence 99, Appl	1059	45.2	4.6	867	4	US-09-902-540-3225	Sequence 3225, Ap
987	45.6	4.6	4233	4	US-09-565-501A-99	Sequence 99, Appl	1060	45.2	4.6	888	4	US-09-252-991A-7041	Sequence 7041, Ap
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989	45.6	4.6	4233	4	US-09-874-923-99	Sequence 99, Appl	1062	45.2	4.6	1026	4	US-09-252-991A-12295	Sequence 12295, A
990	45.6	4.6	4563	4	US-09-252-991A-930	Sequence 930, App	1063	45.2	4.6	1095	4	US-09-252-991A-6626	Sequence 6626, Ap
991	45.6	4.6	4917	4	US-09-551-974A-100	Sequence 100, App	1064	45.2	4.6	1095	4	US-09-902-540-7052	Sequence 7052, Ap
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994	45.6	4.6	4917	4	US-09-874-923-100	Sequence 100, App	1067	45.2	4.6	1416	4	US-09-902-540-9491	Sequence 9491, Ap
995	45.6	4.6	4929	4	US-09-551-974A-98	Sequence 98, Appl	ci1068	45.2	4.6	1419	4	US-09-253-991A-10421	Sequence 10421, A
996	45.6	4.6	4929	4	US-09-565-501A-98	Sequence 98, Appl	1069	45.2	4.6	1494	4	US-09-902-540-7572	Sequence 7572, Ap
997	45.6	4.6	4929	4	US-09-639-206A-98	Sequence 98, Appl	1070	45.2	4.6	1602	4	US-09-902-540-8469	Sequence 8469, Ap
998	45.6	4.6	4929	4	US-09-874-923-98	Sequence 98, Appl	1071	45.2	4.6	1602	4	US-09-252-991A-9989	Sequence 9989, Ap
c 999	45.6	4.6	6119	4	US-09-902-540-713	Sequence 713, App	ci1072	45.2	4.6	1695	4	US-09-252-991A-10319	Sequence 10319, A
1000	45.6	4.6	6935	4	US-09-902-540-865	Sequence 865, App	1073	45.2	4.6	1697	4	US-09-902-540-2665	Sequence 2665, Ap
c1001	45.6	4.6	7950	4	US-09-902-540-934	Sequence 934, App	1074	45.2	4.6	2028	4	US-09-902-540-7226	Sequence 7226, Ap
1002	45.6	4.6	8241	4	US-09-902-540-798	Sequence 798, App	1075	45.2	4.6	2316	4	US-09-949-016-870	Sequence 870, App
c1003	45.6	4.6	13631	4	US-09-902-540-1092	Sequence 1092, Ap	1076	45.2	4.6	2316	4	US-09-949-016-1945	Sequence 1945, Ap
1004	45.6	4.6	13904	4	US-09-902-540-1076	Sequence 1076, Ap	1077	45.2	4.6	2363	4	US-09-818-780-22	Sequence 22, Appl
1005	45.6	4.6	15132	4	US-09-902-540-1137	Sequence 1137, Ap	1078	45.2	4.6	2376	4	US-09-252-991A-10741	Sequence 10741, A
1006	45.6	4.6	15338	4	US-09-902-540-1121	Sequence 1121, Ap	1079	45.2	4.6	2379	4	US-09-252-991A-9205	Sequence 9205, Ap
1007	45.6	4.6	16350	4	US-09-902-540-1144	Sequence 1144, Ap	1080	45.2	4.6	2844	4	US-09-253-991A-4764	Sequence 4764, Ap
c1008	45.6	4.6	30135	4	US-09-902-540-1249	Sequence 1249, Ap	ci1081	45.2	4.6	3084	4	US-09-252-991A-6639	Sequence 6639, Ap
c1009	45.4	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap	1082	45.2	4.6	3273	4	US-09-252-991A-6578	Sequence 6578, Ap
1010	45.4	4.6	538	1	US-10-095-946-13	Sequence 13, Appl	ci1083	45.2	4.6	3402	4	US-09-902-540-4967	Sequence 4967, Ap
1011	45.4	4.6	538	1	US-09-183-959-13	Sequence 13, Appl	1084	45.2	4.6	4169	4	US-09-902-540-590	Sequence 590, App
1012	45.4	4.6	601	4	US-09-535-315-13	Sequence 13, Appl	ci1085	45.2	4.6	4377	4	US-09-902-540-676	Sequence 676, App
1013	45.4	4.6	601	4	US-09-949-016-55209	Sequence 55209, A	1086	45.2	4.6	4387	4	US-09-902-540-679	Sequence 679, App
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1015	45.4	4.6	897	4	US-09-902-540-7143	Sequence 7143, Ap	1088	45.2	4.6	6201	4	US-09-902-540-740	Sequence 740, App
1016	45.4	4.6	954	3	US-08-911-853-24	Sequence 24, Appl	1089	45.2	4.6	6380	4	US-09-902-540-891	Sequence 891, App
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1021	45.4	4.6	1170	4	US-09-902-540-7350	Sequence 7350, Ap	ci1094	45.2	4.6	17726	4	US-09-902-540-1148	Sequence 1148, Ap
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1024	45.4	4.6	1548	3	US-09-320-774-5	Sequence 5, Appl	ci1097	45.2	4.6	30001	1	US-08-125-468-1	Sequence 1, Appl
1025	45.4	4.6	1572	4	US-09-252-991A-3270	Sequence 3270, Ap	ci1098	45.2	4.6	30001	2	US-08-474-933-1	Sequence 1, Appl
1026	45.4	4.6	1581	2	US-08-762-106-6	Sequence 6, Appl	1099	45	4.6	582	4	US-09-252-991A-6152	Sequence 6152, Ap
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1031	45.4	4.6	2148	4	US-09-902-540-5682	Sequence 5682, Ap	1104	45	4.6	855	4	US-09-902-540-2898	Sequence 2898, Ap
1032	45.4	4.6	2167	2	US-08-461-775-9	Sequence 9, Appl	1105	45	4.6	879	4	US-09-902-540-7823	Sequence 7823, Ap
ci1033	45.4	4.6	2167	3	US-09-031-608-9	Sequence 9, Appl	1106	45	4.6	987	4	US-09-902-540-6321	Sequence 6321, Ap
ci1034	45.4	4.6	2196	4	US-09-252-991A-3536	Sequence 3536, Ap	1107	45	4.6	1161	4	US-09-902-540-3573	Sequence 3573, Ap
1035	45.4	4.6	2286	4	US-09-902-540-2486	Sequence 2486, Ap	1108	45	4.6	1187	1	US-08-440-856A-2	Sequence 2, Appl
ci1036	45.4	4.6	2325	4	US-09-252-991A-3413	Sequence 3413, Ap	1109	45	4.6	1206	4	US-09-902-540-7709	Sequence 7709, Ap
1037	45.4	4.6	2571	4	US-09-984-880-1	Sequence 1, Appl	1110	45	4.6	1377	4	US-09-585-173B-43	Sequence 43, Appl
1038	45.4	4.6	2571	4	US-10-277-032-1	Sequence 1, Appl	1111	45	4.6	1413	4	US-09-252-991A-6071	Sequence 6071, Ap
1039	45.4	4.6	2843	4	US-09-902-540-2841	Sequence 2841, Ap	1112	45	4.6	1455	4	US-09-902-540-3393	Sequence 3393, Ap
ci1040	45.4	4.6	2668	2	US-08-461-775-11	Sequence 11, Appl	1113	45	4.6	1458	4	US-09-902-540-6238	Sequence 6238, Ap
ci1041	45.4	4.6	2668	3	US-09-031-606-11	Sequence 11, Appl	1114	45	4.6	1491	4	US-09-252-991A-6232	Sequence 6232, Ap
1042	45.4	4.6	2973	4	US-09-902-540-4476	Sequence 4476, Ap	1115	45	4.6	1506	4	US-09-252-991A-6228	Sequence 6228, Ap
ci1043	45.4	4.6	3999	4	US-09-902-540-655	Sequence 655, App	1116	45	4.6	1690	4	US-09-620-312D-69	Sequence 69, Appl
1044	45.4	4.6	4180	4	US-09-814-918A-93	Sequence 93, Appl	ci1117	45	4.6	1713	4	US-09-902-540-6981	Sequence 6981, Ap
ci1045	45.4	4.6	5515	4	US-09-902-540-701	Sequence 701, App	ci1118	45	4.6	1743	4	US-09-949-016-945	Sequence 945, App
1046	45.4	4.6	5523	4	US-09-902-540-3952	Sequence 3952, Ap	ci1119	45	4.6	1743	4	US-09-949-016-2709	Sequence 2709, Ap
ci1047	45.4	4.6	16047	4	US-09-902-540-1136	Sequence 1136, Ap	ci1120	45	4.6	1803	4	US-09-902-540-339	Sequence 339, App
1048	45.4	4.6	19979	4	US-09-949-016-12309	Sequence 12309, A	ci1121	45	4.6	1843	4	US-09-902-540-389	Sequence 389, App
1049	45.4	4.6	19980	4	US-09-949-016-13533	Sequence 13533, A	1122	45	4.6	1845	4	US-09-902-540-7160	Sequence 7160, Ap



1123	45	4.6	3192	4	US-09-902-540-4843	Sequence 4843, Ap	1196	44.6	4.5	462	4	US-09-902-540-4652	Sequence 4652, Ap
1124	45	4.6	3651	2	US-08-790-374-1	Sequence 1, Appl1	1197	44.6	4.5	642	4	US-09-902-540-8653	Sequence 8653, Ap
1125	45	4.6	4135	4	US-09-902-540-9587	Sequence 9587, Ap	1198	44.6	4.5	813	4	US-09-252-991A-5455	Sequence 5455, Ap
1126	45	4.6	4494	4	US-09-902-540-659	Sequence 659, App	1199	44.6	4.5	822	4	US-09-902-540-9235	Sequence 9235, Ap
1127	45	4.6	4862	4	US-09-902-540-608	Sequence 608, App	1200	44.6	4.5	837	4	US-09-252-991A-5983	Sequence 5983, Ap
1128	45	4.6	5743	4	US-09-949-016-12687	Sequence 12687, A	1201	44.6	4.5	867	4	US-09-902-540-7100	Sequence 7100, Ap
1129	45	4.6	5743	4	US-09-949-016-12687	Sequence 12687, A	1202	44.6	4.5	897	4	US-09-252-991A-8789	Sequence 8789, Ap
1130	45	4.6	6260	4	US-09-902-540-781	Sequence 781, App	1203	44.6	4.5	1080	4	US-09-902-540-5147	Sequence 5147, Ap
1131	45	4.6	7280	4	US-09-902-540-827	Sequence 827, App	1204	44.6	4.5	1236	4	US-09-252-991A-8061	Sequence 8061, Ap
1132	45	4.6	7812	3	US-09-368-590-1	Sequence 1, Appl1	1205	44.6	4.5	1260	4	US-09-902-540-4016	Sequence 4016, Ap
1133	45	4.6	8604	4	US-09-902-540-916	Sequence 916, App	1206	44.6	4.5	1272	4	US-09-252-991A-14082	Sequence 14082, A
1134	45	4.6	8756	4	US-09-949-016-1438	Sequence 1438, Ap	1207	44.6	4.5	1329	4	US-09-252-991A-14036	Sequence 14036, A
1135	45	4.6	8914	4	US-09-902-540-915	Sequence 915, App	1208	44.6	4.5	1343	4	US-09-902-540-4356	Sequence 4356, Ap
1136	45	4.6	16427	4	US-09-902-540-1160	Sequence 1160, Ap	1209	44.6	4.5	1545	4	US-09-902-540-5060	Sequence 5060, Ap
1137	45	4.6	16924	4	US-09-902-540-1178	Sequence 1178, Ap	1210	44.6	4.5	1578	4	US-09-252-991A-5965	Sequence 5965, Ap
1138	45	4.6	21758	4	US-09-902-540-1238	Sequence 1238, Ap	1211	44.6	4.5	1587	4	US-09-252-991A-16504	Sequence 16504, A
1139	45	4.6	23187	4	US-09-499-522-1	Sequence 1, Appl1	1212	44.6	4.5	1620	4	US-09-252-991A-14186	Sequence 14186, A
1140	45	4.6	35614	4	US-09-902-540-1259	Sequence 1259, Ap	1213	44.6	4.5	1623	4	US-09-252-991A-5431	Sequence 5431, Ap
1141	44.8	4.5	591	4	US-09-902-540-9199	Sequence 9199, Ap	1214	44.6	4.5	1629	4	US-09-902-540-9163	Sequence 9163, Ap
1142	44.8	4.5	660	4	US-09-902-540-3995	Sequence 3995, Ap	1215	44.6	4.5	1938	4	US-09-902-540-3216	Sequence 3216, Ap
1143	44.8	4.5	753	4	US-09-252-991A-6830	Sequence 6830, Ap	1216	44.6	4.5	2005	4	US-09-482-273-15	Sequence 15, Appl1
1144	44.8	4.5	768	4	US-09-902-540-9609	Sequence 9609, Ap	1217	44.6	4.5	2070	4	US-09-252-991A-16098	Sequence 16098, A
1145	44.8	4.5	783	4	US-09-252-991A-8452	Sequence 8452, Ap	1218	44.6	4.5	2154	4	US-09-252-991A-5458	Sequence 5458, Ap
1146	44.8	4.5	858	4	US-09-902-540-8238	Sequence 8238, Ap	1219	44.6	4.5	2163	4	US-09-252-991A-2947	Sequence 2947, Ap
1147	44.8	4.5	948	4	US-09-252-991A-14810	Sequence 14810, A	1220	44.6	4.5	2178	4	US-09-902-540-6462	Sequence 6462, Ap
1148	44.8	4.5	1062	4	US-09-949-016-4732	Sequence 4732, Ap	1221	44.6	4.5	2205	4	US-09-902-540-4101	Sequence 4101, Ap
1149	44.8	4.5	1062	4	US-09-902-540-6043	Sequence 6043, Ap	1222	44.6	4.5	2214	4	US-09-902-540-9189	Sequence 9189, Ap
1150	44.8	4.5	1068	4	US-09-902-540-244	Sequence 244, App	1223	44.6	4.5	2387	4	US-09-902-540-453	Sequence 453, App
1151	44.8	4.5	1095	4	US-09-902-540-4983	Sequence 4983, Ap	1224	44.6	4.5	2556	4	US-09-252-991A-8202	Sequence 8202, Ap
1152	44.8	4.5	1110	4	US-09-252-991A-8388	Sequence 8388, Ap	1225	44.6	4.5	2564	4	US-09-482-273-83	Sequence 83, Appl1
1153	44.8	4.5	1131	4	US-09-252-991A-8486	Sequence 8486, Ap	1226	44.6	4.5	3453	4	US-09-252-991A-8100	Sequence 8100, Ap
1154	44.8	4.5	1162	2	US-08-726-306A-52	Sequence 52, Appl1	1227	44.6	4.5	3546	4	US-09-252-991A-1309	Sequence 1309, Ap
1155	44.8	4.5	1257	4	US-09-902-540-8931	Sequence 8931, Ap	1228	44.6	4.5	3978	4	US-09-266-965-19	Sequence 19, Appl1
1156	44.8	4.5	1275	4	US-09-902-540-3545	Sequence 3545, Ap	1229	44.6	4.5	4591	4	US-09-902-540-3369	Sequence 3369, Ap
1157	44.8	4.5	1320	4	US-09-727-238-1	Sequence 1, Appl1	1230	44.6	4.5	4874	4	US-09-902-540-646	Sequence 646, App
1158	44.8	4.5	1341	4	US-09-902-540-7598	Sequence 7598, Ap	1231	44.6	4.5	5275	4	US-09-902-540-771	Sequence 771, App
1159	44.8	4.5	1365	3	US-09-319-892-1	Sequence 1, Appl1	1232	44.6	4.5	8931	3	US-09-028-934-28	Sequence 28, Appl1
1160	44.8	4.5	1428	4	US-09-252-991A-14802	Sequence 14802, A	1233	44.6	4.5	9039	4	US-09-949-016-16629	Sequence 16629, A
1161	44.8	4.5	1479	4	US-09-902-540-7414	Sequence 7414, Ap	1234	44.6	4.5	9676	4	US-09-949-016-16629	Sequence 16629, A
1162	44.8	4.5	1485	4	US-09-902-540-7202	Sequence 7202, Ap	1235	44.6	4.5	10280	4	US-09-902-540-980	Sequence 980, App
1163	44.8	4.5	1515	4	US-09-902-540-6108	Sequence 6108, Ap	1236	44.6	4.5	12173	4	US-09-902-540-1022	Sequence 1022, Ap
1164	44.8	4.5	1519	4	US-09-902-540-279	Sequence 279, App	1237	44.6	4.5	12249	4	US-09-266-965-74	Sequence 74, Appl1
1165	44.8	4.5	1658	4	US-09-252-991A-14950	Sequence 14950, A	1238	44.6	4.5	17125	4	US-09-902-540-1158	Sequence 1158, Ap
1166	44.8	4.5	1854	4	US-09-902-540-8051	Sequence 8051, Ap	1239	44.6	4.5	17173	4	US-09-902-540-1152	Sequence 1152, Ap
1167	44.8	4.5	1899	4	US-09-252-991A-6781	Sequence 6781, Ap	1240	44.6	4.5	18331	4	US-09-266-965-96	Sequence 96, Appl1
1168	44.8	4.5	1995	4	US-09-902-540-9209	Sequence 9209, Ap	1241	44.6	4.5	23694	4	US-09-902-540-1216	Sequence 1216, Ap
1169	44.8	4.5	2016	4	US-09-902-540-4303	Sequence 4303, Ap	1242	44.6	4.5	23738	4	US-09-902-540-1203	Sequence 1203, Ap
1170	44.8	4.5	2028	4	US-09-252-991A-7091	Sequence 7091, Ap	1243	44.6	4.5	28320	4	US-09-902-540-1254	Sequence 1222, Ap
1171	44.8	4.5	2064	4	US-09-252-991A-9616	Sequence 9616, Ap	1244	44.6	4.5	28559	4	US-09-902-540-1282	Sequence 1254, Ap
1172	44.8	4.5	2136	4	US-09-902-540-5582	Sequence 5582, Ap	1245	44.6	4.5	47818	4	US-09-949-016-12324	Sequence 12324, A
1173	44.8	4.5	2211	4	US-09-902-540-5403	Sequence 5403, Ap	1246	44.6	4.5	48480	4	US-09-949-016-15166	Sequence 15166, A
1174	44.8	4.5	2235	4	US-09-252-991A-7032	Sequence 7032, Ap	1247	44.6	4.5	76164	4	US-09-949-016-12288	Sequence 12288, A
1175	44.8	4.5	2316	4	US-09-902-540-3869	Sequence 3869, Ap	1248	44.6	4.5	76165	4	US-09-949-016-14005	Sequence 14005, A
1176	44.8	4.5	3036	4	US-09-902-540-4040	Sequence 4040, Ap	1249	44.6	4.5	465	4	US-09-252-991A-1459	Sequence 1459, Ap
1177	44.8	4.5	3078	3	US-09-418-817-9	Sequence 9, Appl1	1250	44.4	4.5	546	4	US-09-902-540-5427	Sequence 5427, Ap
1178	44.8	4.5	3162	4	US-09-252-991A-9569	Sequence 9569, Ap	1251	44.4	4.5	720	4	US-09-252-991A-14268	Sequence 14268, A
1179	44.8	4.5	3225	4	US-09-902-540-3099	Sequence 3099, Ap	1252	44.4	4.5	750	4	US-09-902-540-5834	Sequence 5834, Ap
1180	44.8	4.5	3793	4	US-09-902-540-4846	Sequence 4846, Ap	1253	44.4	4.5	756	4	US-09-252-991A-15229	Sequence 15229, A
1181	44.8	4.5	5064	4	US-09-774-528-224	Sequence 224, App	1254	44.4	4.5	819	4	US-09-252-991A-15235	Sequence 15235, A
1182	44.8	4.5	5097	4	US-09-902-540-745	Sequence 745, App	1255	44.4	4.5	1077	4	US-09-902-540-1917	Sequence 1977, Ap
1183	44.8	4.5	5245	4	US-09-902-540-714	Sequence 714, App	1256	44.4	4.5	1089	4	US-09-902-540-9317	Sequence 9317, Ap
1184	44.8	4.5	5883	4	US-09-949-016-5001	Sequence 5001, Ap	1257	44.4	4.5	1116	4	US-09-902-540-9445	Sequence 9445, Ap
1185	44.8	4.5	6217	3	US-09-418-817-1	Sequence 1, Appl1	1258	44.4	4.5	1161	4	US-09-252-991A-10489	Sequence 10489, A
1186	44.8	4.5	6569	4	US-09-949-016-17534	Sequence 17534, A	1259	44.4	4.5	1305	4	US-09-252-991A-11607	Sequence 11607, A
1187	44.8	4.5	8832	4	US-09-902-540-984	Sequence 984, App	1260	44.4	4.5	1305	4	US-09-252-991A-11762	Sequence 11762, A
1188	44.8	4.5	10301	4	US-09-902-540-985	Sequence 985, App	1261	44.4	4.5	1317	4	US-09-252-991A-3556	Sequence 3556, Ap
1189	44.8	4.5	11282	4	US-09-902-540-1039	Sequence 1039, Ap	1262	44.4	4.5	1395	4	US-09-902-540-3185	Sequence 3185, Ap
1190	44.8	4.5	12865	4	US-09-902-540-1048	Sequence 1048, Ap	1263	44.4	4.5	1512	4	US-09-252-991A-1551	Sequence 1551, Ap
1191	44.8	4.5	14330	4	US-09-902-540-1009	Sequence 1009, Ap	1264	44.4	4.5	1600	3	US-09-434-288-10	Sequence 10, Appl1
1192	44.8	4.5	17592	4	US-09-902-540-1138	Sequence 1138, Ap	1265	44.4	4.5	1608	4	US-09-902-540-7945	Sequence 7945, Ap
1193	44.8	4.5	21143	4	US-09-902-540-1151	Sequence 1151, Ap	1266	44.4	4.5	1677	4	US-09-252-991A-1616	Sequence 1616, Ap
1194	44.8	4.5	61158	4	US-09-949-016-15041	Sequence 15041, A	1267	44.4	4.5	1731	2	US-08-466-583-1	Sequence 1, Appl1
1195	44.8	4.5	75431	4	US-09-949-016-15122	Sequence 15122, A	1268	44.4	4.5	1731	4	US-08-265-427-1	Sequence 1, Appl1

1269	44.4	4.5	1731	5	PCT-US95-07820-1	Sequence 1, Appli	1342	44.2	4.5	1629	4	US-09-902-540-8462	Sequence 8462, Ap
1270	44.4	4.5	1878	4	US-09-489-039A-2045	Sequence 2045, Ap	c1343	44.2	4.5	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
c1271	44.4	4.5	2073	4	US-09-252-991A-10279	Sequence 10279, Ap	1344	44.2	4.5	1716	4	US-09-252-991A-15268	Sequence 15268, A
1272	44.4	4.5	2176	6	5320958-1	Patent No. 5320958	1345	44.2	4.5	1740	4	US-09-252-991A-13753	Sequence 13753, A
1273	44.4	4.5	2176	6	5320958-1	Patent No. 5320958	1346	44.2	4.5	1779	4	US-09-902-540-3312	Sequence 3312, Ap
1274	44.4	4.5	2256	4	US-09-902-540-2730	Sequence 2730, Ap	1347	44.2	4.5	1835	3	US-09-417-704-2	Sequence 2, Appli
1275	44.4	4.5	2325	4	US-09-252-991A-218	Sequence 218, Ap	1348	44.2	4.5	1835	3	US-09-252-991A-15408	Sequence 15408, A
1276	44.4	4.5	2325	4	US-09-902-540-4536	Sequence 4536, Ap	c1349	44.2	4.5	1848	4	US-09-252-991A-12316	Sequence 12316, A
1277	44.4	4.5	2330	4	US-09-252-991A-15188	Sequence 15188, A	c1350	44.2	4.5	2040	4	US-09-902-540-3500	Sequence 3500, Ap
1278	44.4	4.5	2772	4	US-09-252-991A-10577	Sequence 10577, A	1351	44.2	4.5	2187	4	US-08-464-340A-3	Sequence 3, Appli
c1279	44.4	4.5	2784	4	US-09-252-991A-194	Sequence 194, App	1352	44.2	4.5	2483	5	PCT-US94-08449A-3	Sequence 3, Appli
1280	44.4	4.5	2946	4	US-09-252-991A-227	Sequence 227, App	c1353	44.2	4.5	2725	4	US-09-902-540-527	Sequence 527, App
1281	44.4	4.5	3186	4	US-09-949-016-1250	Sequence 1250, Ap	1354	44.2	4.5	2751	4	US-09-252-991A-14671	Sequence 14671, A
1282	44.4	4.5	3384	4	US-09-902-540-3780	Sequence 3780, Ap	c1355	44.2	4.5	2872	3	US-09-327-487A-2	Sequence 2, Appli
1283	44.4	4.5	3392	4	US-09-902-540-3089	Sequence 3089, Ap	c1356	44.2	4.5	3201	4	US-09-252-991A-14959	Sequence 14959, A
c1284	44.4	4.5	3603	4	US-09-252-991A-14443	Sequence 14443, A	c1357	44.2	4.5	3255	4	US-09-252-991A-10617	Sequence 10617, A
1285	44.4	4.5	4267	3	US-08-949-155-51	Sequence 51, Appl	1358	44.2	4.5	3375	4	US-09-252-991A-10239	Sequence 10239, A
1286	44.4	4.5	4267	3	US-08-919-964-51	Sequence 51, Appl	1359	44.2	4.5	3402	4	US-09-252-991A-14791	Sequence 14791, A
c1287	44.4	4.5	5663	4	US-09-902-540-839	Sequence 839, App	c1360	44.2	4.5	3783	4	US-09-902-540-4846	Sequence 4846, Ap
c1288	44.4	4.5	6377	4	US-09-902-540-802	Sequence 802, App	1361	44.2	4.5	3841	4	US-09-902-540-607	Sequence 607, App
1289	44.4	4.5	7865	4	US-09-949-016-13537	Sequence 13537, A	c1362	44.2	4.5	4689	3	US-09-105-537-34	Sequence 34, Appl
c1290	44.4	4.5	10835	4	US-09-902-540-1031	Sequence 1031, Ap	c1363	44.2	4.5	5467	4	US-09-902-540-703	Sequence 703, App
c1291	44.4	4.5	11992	4	US-09-902-540-995	Sequence 995, App	c1364	44.2	4.5	6012	4	US-09-902-540-808	Sequence 808, App
1292	44.4	4.5	15689	4	US-09-902-540-1129	Sequence 1129, Ap	1365	44.2	4.5	7012	4	US-09-902-540-890	Sequence 890, App
1293	44.4	4.5	15789	4	US-09-902-540-1139	Sequence 1139, Ap	1366	44.2	4.5	7518	4	US-09-902-540-870	Sequence 870, App
1294	44.4	4.5	18789	4	US-09-949-016-13992	Sequence 12992, A	1367	44.2	4.5	7680	4	US-09-902-540-8948	Sequence 8948, Ap
c1295	44.4	4.5	18917	4	US-09-949-016-13130	Sequence 13129, A	c1368	44.2	4.5	8532	4	US-09-902-540-927	Sequence 927, App
c1296	44.4	4.5	18917	4	US-09-949-016-13130	Sequence 13130, A	c1369	44.2	4.5	8563	4	US-09-902-540-3318	Sequence 3318, Ap
c1297	44.4	4.5	23233	4	US-09-902-540-1184	Sequence 1184, Ap	c1370	44.2	4.5	11476	4	US-09-902-540-955	Sequence 955, App
c1298	44.4	4.5	25497	4	US-09-902-540-1224	Sequence 1224, Ap	c1371	44.2	4.5	11922	4	US-09-902-540-1063	Sequence 1063, Ap
1299	44.4	4.5	34953	4	US-09-902-540-1263	Sequence 1263, Ap	c1372	44.2	4.5	13842	3	US-09-105-537-30	Sequence 30, Appl
c1300	44.4	4.5	670889	4	US-09-949-016-150505	Sequence 12605, A	1373	44.2	4.5	15351	4	US-09-902-540-1154	Sequence 1154, Ap
c1301	44.4	4.5	670889	4	US-09-949-016-150505	Sequence 12605, A	c1374	44.2	4.5	18471	4	US-09-902-540-1167	Sequence 1167, Ap
c1302	44.4	4.5	670890	4	US-09-949-016-14207	Sequence 14207, A	1375	44.2	4.5	20235	1	US-07-642-734C-3	Sequence 3, Appli
1303	44.2	4.5	483	4	US-09-252-991A-15272	Sequence 15272, A	1376	44.2	4.5	20235	3	US-08-439-009A-3	Sequence 3, Appli
1304	44.2	4.5	594	4	US-09-252-991A-3950	Sequence 3950, Ap	c1377	44.2	4.5	21010	4	US-09-902-540-1188	Sequence 1188, Ap
1305	44.2	4.5	627	4	US-09-902-540-3827	Sequence 3827, Ap	c1378	44.2	4.5	21758	4	US-09-902-540-1238	Sequence 1238, Ap
c1306	44.2	4.5	720	4	US-09-902-540-4895	Sequence 4895, Ap	c1379	44.2	4.5	28493	4	US-09-902-540-1241	Sequence 1241, Ap
1307	44.2	4.5	765	4	US-09-252-991A-3922	Sequence 3922, Ap	1380	44.2	4.5	31713	4	US-09-949-016-15960	Sequence 16960, A
c1308	44.2	4.5	798	4	US-09-252-991A-9181	Sequence 9181, Ap	1381	44.2	4.5	34552	4	US-09-902-540-1262	Sequence 1262, Ap
1309	44.2	4.5	810	4	US-09-252-991A-3647	Sequence 3647, Ap	c1382	44.2	4.5	36778	3	US-09-105-537-5	Sequence 5, Appli
1310	44.2	4.5	837	4	US-09-252-991A-15324	Sequence 15324, A	c1383	44.2	4.5	38506	3	US-09-320-878-19	Sequence 19, Appl
1311	44.2	4.5	879	4	US-09-252-991A-3602	Sequence 3602, Ap	c1384	44.2	4.5	38506	4	US-09-141-908-1	Sequence 1, Appli
1312	44.2	4.5	888	4	US-09-902-540-8741	Sequence 8741, Ap	c1385	44.2	4.5	38506	4	US-09-657-440-19	Sequence 19, Appl
1313	44.2	4.5	903	4	US-09-252-991A-8894	Sequence 8894, Ap	c1386	44.2	4.4	426	4	US-09-252-991A-16285	Sequence 16285, A
1314	44.2	4.5	930	4	US-09-902-540-8794	Sequence 8794, Ap	c1387	44.2	4.4	426	4	US-09-252-991A-2270	Sequence 2270, Ap
1315	44.2	4.5	942	4	US-09-902-540-8794	Sequence 8794, Ap	c1388	44.2	4.4	492	4	US-09-252-991A-4051	Sequence 4051, Ap
1316	44.2	4.5	975	4	US-09-252-991A-12244	Sequence 12244, A	1389	44.2	4.4	537	4	US-09-902-540-3308	Sequence 3308, Ap
c1317	44.2	4.5	999	4	US-09-252-991A-14326	Sequence 14326, A	1390	44.2	4.4	765	4	US-09-902-540-8591	Sequence 8591, Ap
1318	44.2	4.5	1005	4	US-09-902-540-6685	Sequence 6685, Ap	1391	44.2	4.4	897	3	US-09-434-288-6	Sequence 6, Appli
1319	44.2	4.5	1018	1	US-08-444-083-6	Sequence 6, Appli	1392	44.2	4.4	948	4	US-09-252-991A-2569	Sequence 2569, Ap
1320	44.2	4.5	1018	1	US-08-286-304-6	Sequence 6, Appli	c1393	44.2	4.4	957	4	US-09-252-991A-5476	Sequence 5476, Ap
1321	44.2	4.5	1018	1	US-08-442-745-6	Sequence 6, Appli	1394	44.2	4.4	981	4	US-09-252-991A-5453	Sequence 5453, Ap
1322	44.2	4.5	1018	1	US-08-443-129-6	Sequence 6, Appli	c1395	44.2	4.4	1026	4	US-09-252-991A-2349	Sequence 2349, Ap
1323	44.2	4.5	1018	1	US-08-443-952-6	Sequence 6, Appli	1396	44.2	4.4	1062	4	US-09-252-991A-16067	Sequence 16067, A
1324	44.2	4.5	1018	1	US-08-443-130-6	Sequence 6, Appli	c1397	44.2	4.4	1110	4	US-09-252-991A-1858	Sequence 1858, Ap
1325	44.2	4.5	1018	3	US-08-898-911-6	Sequence 6, Appli	c1398	44.2	4.4	1110	4	US-09-252-991A-8823	Sequence 8823, Ap
1326	44.2	4.5	1018	5	PCT-US95-04467-6	Sequence 6, Appli	1399	44.2	4.4	1116	4	US-09-252-991A-2104	Sequence 2104, Ap
1327	44.2	4.5	1080	4	US-09-902-540-9563	Sequence 9563, Ap	c1400	44.2	4.4	1126	3	US-08-949-155-5	Sequence 5, Appli
c1328	44.2	4.5	1116	4	US-09-252-991A-13384	Sequence 13384, A	c1401	44.2	4.4	1126	3	US-09-819-964-5	Sequence 5, Appli
c1329	44.2	4.5	1194	4	US-09-252-991A-4021	Sequence 4021, Ap	c1402	44.2	4.4	1152	4	US-09-252-991A-1791	Sequence 1791, Ap
1330	44.2	4.5	1233	4	US-09-252-991A-15366	Sequence 15366, A	1403	44.2	4.4	1281	4	US-09-902-540-2838	Sequence 2838, Ap
c1331	44.2	4.5	1257	4	US-09-252-991A-15464	Sequence 15464, A	1404	44.2	4.4	1332	4	US-09-902-540-8694	Sequence 8694, Ap
1332	44.2	4.5	1290	4	US-09-902-540-5641	Sequence 5641, Ap	1405	44.2	4.4	1333	3	US-09-372-422A-9	Sequence 9, Appli
c1333	44.2	4.5	1292	4	US-09-902-540-137	Sequence 127, App	1406	44.2	4.4	1338	4	US-09-902-540-7158	Sequence 7158, Ap
1334	44.2	4.5	1377	4	US-09-252-991A-13964	Sequence 13964, A	1407	44.2	4.4	1611	4	US-09-902-540-5836	Sequence 5836, Ap
1335	44.2	4.5	1392	4	US-09-902-540-6975	Sequence 6975, Ap	1408	44.2	4.4	1612	4	US-09-902-540-128	Sequence 128, App
1336	44.2	4.5	1518	4	US-09-252-991A-12104	Sequence 12104, A	1409	44.2	4.4	1683	4	US-09-252-991A-11226	Sequence 11226, A
1337	44.2	4.5	1530	4	US-09-902-540-8329	Sequence 8329, Ap	1410	44.2	4.4	1716	4	US-09-902-540-9034	Sequence 9034, Ap
c1338	44.2	4.5	1539	4	US-09-648-183-1	Sequence 1, Appli	1411	44.2	4.4	1734	4	US-09-252-991A-9061	Sequence 9061, Ap
c1339	44.2	4.5	1539	4	US-09-648-183-2	Sequence 2, Appli	1412	44.2	4.4	1755	4	US-09-949-016-2716	Sequence 2716, Ap
1340	44.2	4.5	1593	4	US-09-252-991A-14376	Sequence 14376, A	1413	44.2	4.4	1902	4	US-09-902-540-2344	Sequence 2344, Ap
1341	44.2	4.5	1614	4	US-09-252-991A-10453	Sequence 10453, A	c1414	44.2	4.4	1908	4	US-09-252-991A-16529	Sequence 16529, A



Db 628 TACCCGGAATACCTGAGGCGCGCTGGCGTGTGGCCACCGTGGGCTGTGCTTTTC 687  
Qy 714 CTCAGAGTCTGTGGCGCGGAAAGTGTGCAACCTCCGAAAGGAGACGTGGCGCCGAG 773  
Db 688 GACAACTGCTGTGGAGCGCGCGGGTGTGCGAAGCGCAGCCGGAAGTGTGCGATACCCGC 747  
Qy 774 TGTGTGCGAAACCTAAACGAACATCCGCGGCGAGTCAAGGTCTTACATCAGCTTCCTG 833  
Db 748 GGCATCCAGAGCTCAACTTGGCGCTGAAGACGACGCGGGTGTGACTCTGCTGTCTG 807  
Qy 834 CCCTGGCGGATGAGTCACTTGGCCCTTCAAGATCT 870  
Db 808 CCGATCGCGCGCGGTGAGCGTCTGTGCGAAGCGCT 844

## RESULT 2

US-09-452-239-45

; Sequence 45, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 45

; LENGTH: 953

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-452-239-45

Query Match 16.4%; Score 161.8; DB 3; Length 953;

Best Local Similarity 55.1%; Pred. No. 1.2e-22;

Matches 338; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

Qy 273 CGGGAGCACCCGGCGCTGCGAAGCCCTGAGGCTGTGACCTGGAGCAGCGCGAGGGGAT 332  
Db 186 CCGAGCAGAGTGATGCGGACCTGCGCTCATCACCGACAGACCCATGGGGTTAC 245  
Qy 333 TCTATGATGACCTGGAGCAGGCCCAAGCTCTTGGCCAACTTGGCGGGCTCATCCAGGCC 392  
Db 246 ATGCAGTCTCTCGGACGAGCGCAGCTGTGGGATGCTGATCAAGATGGCGGCGCC 305

Qy 393 AAGAGGCGCTGGACCTGGGACCTTCAGGGCTACTCGCCCTGGCCCTGGCCCTGGCG 452  
Db 306 AAGAAGACATCGAGTGGGCGGTGTTCAGGGGCTACTCGCTGTGGCCACCGCTGGCG 365

Qy 453 CTGCCCGCGAGCGGGCGTGTGTGACTCGAGGTGAGCGCGAGCCCGCGAGCTGGGA 512  
Db 366 CTCGCCGAGAGCGGACAGTGTGTGGCCATCGACCGACCGGAGTGTCTACAGGTGGT 425

Qy 513 CGGGCCCTGTGGAGGCGAGCGGAGCGAGCACAAGATCGACTCTCGGCTGAAGCCCGCC 572  
Db 426 CGCCCTTTCATCGAAGGCGCGCATGGCGCACAGGTGGACTTCGCGAGGGCACCGGC 485

Qy 573 TTGGAGACCTTGACGAGTGTGGCGGGGGGCGA---GGCGGCACCTTCACGTGGCC 629  
Db 486 CTGGGCGCGCTGGACGAGTCTCTCGTTCGAGGACGACGCGCGCGAGCTACACTTCGG 545

Qy 630 GTGGTGGATGCGGACAAGAGAACTGTCTCGCTACTACGAGCGCTGCTCGAGCTGTG 689  
Db 546 TTCGTGGAGCGCGACAGGCCAACTACGTGCGGTACCAAGAGAGCTGTGAAGTGTGTC 605

Qy 690 CGACCCGAGGATCTCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGTGCAACT 749  
Db 606 CGCGTGGCGGCACTATCATCTACGACAAACAGCTCTGGGGGCGGACGCTGGCGTGGCG 665

Qy 750 CCGAAGGGGAGCCTGGCGGCGGAGTGTGTGCGAAACCTTAAACGCAACGCAATCGGGCGGAC 809  
Db 666 GGGGCGACCCCATGTCCGACCTCGACACCCCGCTTCTCCGCGCCCTCAGGAGCCTCAAC 725  
Qy 810 GTCAGGGTCTACATCAGGCTCTGCCCCCTGGCGGATGGACTCACCTTGGCCCTTCAAGATC 869  
Db 726 GCCAAGCTCGCGCGCGACCCGCGGCATCGAGGTCTGCCAGCTGCCATCGCCGACGAGTCT 785  
Qy 870 TAGGGCTGGCCCC 882  
Db 786 ACCATCTGCCGCC 798

## RESULT 3

US-09-452-239-43

; Sequence 43, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 43

; LENGTH: 1049

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (352)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (948)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (992)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (994)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (999)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1003)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1038)

US-09-452-239-43

Query Match 16.1%; Score 159.2; DB 3; Length 1049;

Best Local Similarity 54.8%; Pred. No. 4e-22;

Matches 336; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

Qy 273 CGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGTGACCTGGAGCAGCGCGAGGGGAT 332  
Db 186 CCGAGCAGAGTGATGATGCGGACCTGCGCTCATCACGACAGACCCATGGGGTTAC 245  
Qy 333 TCTATGATGACCTGGAGCAGGCCCAAGCTCTTGGCCAACTTGGCGGGCTCATCCAGGCC 392  
Db 246 ATGCAGTCTCTCGGACGAGGCGCAGCTGTGGGATGCTGATCAAGATGGCGGCGCC 305

Qy 393 AAGAGGCGCTGGACCTGGGACACCTTCAGGGCTACTCGCCCTGGCCCTGGCCCTGGCG 452  
Db 306 AAGAAGACGATCGAGGTGGGCGGTGTTTCAGGGGCTACTCGCTGTGNCACCGCGCTGGCG 365

QY 453 CTGCCCCGCGAGCGGGCGCTGTGACCTCGGAGGTGGAACGCGAGCCCCCGGAGCTGGGA 512  
DB 366 CTCCCGAGGAGCGGAAGGTGTGGGATCGACACCGACCGGAGGTGCTACGAGGTGGGT 425  
QY 513 CGGCCCTGTGAGGCGAGCGGAGCGGAGCAAGATCGACCTCCGGCTGAAGCCCGGC 572  
DB 426 CGCCCTTTCATTGAGAAAGCGGCATGGCGCACAGGTGACTTCCGAGGGCACCGGC 485  
QY 573 TTGGAGACCTTGACGAGCTGTGCGCGGGCGA-----GGCCGGCACCTTTCGAGTGGCC 629  
DB 486 CTGGCGCGCTTGACGAGCTCTCGTGGAGGACGAGCGCGCGGAGCTACGACTTCGCG 545  
QY 630 GTGGTGTGTCGAGCAAGAGAACTGCTCGGCTACTACGAGCGCTGCTGAGCTGCTG 689  
DB 546 TTGCTGGAGCGGACAAAGCCCACTACGTGCGGTACACAGCAGCTGTGCTGAAGCTGGTC 605  
QY 690 CGACCCGAGGACATCTCGCGCTCTCAGAGTCTGTGGCGGGGAAGTGTGCAACCT 749  
DB 606 CGGCTCGGCGGCACTATCATCTAGCAACACCGCTCTGGGCGGCGACGGTGGCGCTGCCG 665  
QY 750 CCGAAAGGGGACGTGGCGGCGGAGTGTGTCGAAACCTTAAACGAAACGATCCGCGCGGAC 809  
DB 666 GCGGACACCCCATGTCCGACCTCGACACCGCTTCTCCGCGCCCTCAGGACCTCAAC 725  
QY 810 GTGAGGCTTACATGAGCTCTGCGGCTGCGGCGAGTGAATCACTTGGCTTCAAGATC 869  
DB 726 GCGAAGCTCGCGCGGACCGCGCATCGAGTCTGCGAGTCTGCCATCGCCATCGCGACGCGTC 785  
QY 870 TAGGCTGGCCCC 882  
DB 786 ACCATCTGCGGCC 798

## RESULT 4

US-09-452-239-13

; Sequence 13, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Caboon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; EARLIER FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 997

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (483)

US-09-452-239-13

Query Match 16.0%; Score 158.6; DB 3; Length 997;  
Best Local Similarity 54.2%; Pred. No. 5.1e-22;  
Matches 373; Conservative 0; Mismatches 300; Indels 15; Gaps 2;

QY 273 CGGAGCACCGCGCTGCGAAGCCTGAGCTGCTGACCTGAGAGAGCGCGAGGGGAT 332  
DB 187 CGGAGCGGAGTGATGCGGATCTGCGCTCATCAGGACCAAGCACCATGCGGGGTTTC 246  
QY 333 TCTATGATGACCTGCGAGAGGCGCCAGCTTCTTGGCCAACTGCGCGGCTCATCCAGGCC 392  
DB 247 ATGCACTGCTGCGCGATGAGGCGAGCTGCTGGGATGCTGTAAGATGGCGGAGCG 306  
QY 393 AGAAGGCGGTGACCTGGGACCTTTCAGGGGTACTCGCCCTGCGCCCTGGCCCTGGCG 452  
DB 307 AAGAGGACAAATCGAGGTGGGTGTCTTTCACGGGTACTCGCTGCTGCGAGCGGCTGGCG 366

QY 453 CTGCCCCGCGAGCGGGCGCTGTGACCTCGGAGGTGGAACGCGAGCCCCCGGAGCTGGGA 512  
DB 367 CTCCCGAGGAGCGGAAGGTGTGGGATCGACACCGACCGGAGGTGCTACGAGATCGGG 426  
QY 513 CGGCCCTGTGAGGCGAGCGGAGCGGAGCAAGATCGACCTCCGGCTGAAGCCCGGC 572  
DB 427 CGCGCGCTTCTTGAGAAAGCGGGGTGGCGCAAGGTGACTTCCAAAGGGGAAANGGG 486  
QY 573 TTGGAGACCTTGACGAGCTGTCT-----GGCGCGGGCGAGGCGCGCACCTTC 620  
DB 487 CTGGAGAACTTGACGAGCTGTCTCGCCGAGGAGGCGCGCGGGCGCGAGGCGGCTTC 546  
QY 621 GACGTGGCGGTGTGATCGGACAAAGAGAACTGCTCCGCTACTACGAGCGCTGCTG 680  
DB 547 GACTTCGCTTCTGTGAGCGCGGACAAAGCCCACTACGTCAAGTACCCAGCAGAGTCTG 606  
QY 681 CAGCTGCTCGGACCGGAGGATCTCGCGCTCTCAGAGTCTGTGGCGCGGGAAGGTG 740  
DB 607 CAGCTGCTGCGGTCGCGCGGCGACATCTGTGTACGAAACACGCTGTGGCGCGGACGGTG 666  
QY 741 CTGCAACCTCCGAAAGGGGACGTGGCGCGGAGTGTGCGAAACCTTAAACGAAACGCATC 800  
DB 667 GCGCTCGCGCGGACACGCGCTGTCTGAGCTTGGACCGGAGGTCTCTCGTGGCATCAGG 726  
QY 801 CGGCGGAGCTCAGGCTTACATCAGCTCTCTGCCCTCGGCGAGTGAATCACTTGGCC 860  
DB 727 GACCTCAACTCAGGCTCGCGCGGACCGCGCATCGAGCTCTGCGCAACTCGGCATCGCC 786  
QY 861 TTCAGAT---CTAGGGCTGGCCCTAGTGTGAGTGGGCTCGAGGAGGGTGTGCTGGGAAC 917  
DB 787 GACGGGATCACCATCTGCGCGCGCTCTGTGTGAGGTGAGACCGAGACCTTACCGGCCGA 846  
QY 918 CCAGGAATTGACCTGAGTGTATAATT 945  
DB 847 TCATCCATCGCTCTCGGTGATTAATT 874

## RESULT 5

US-09-452-239-41

; Sequence 41, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Caboon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 41

; LENGTH: 1078

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-452-239-41

Query Match 15.9%; Score 157.2; DB 3; Length 1078;  
Best Local Similarity 57.1%; Pred. No. 9.7e-22;  
Matches 307; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

QY 214 AGTGCTGCTTCCCCCGAGGACAGCGCTGTGGAGTATCTTCTGAGCGGCTCCATGC 273  
DB 200 AGAGCTGTCTCCAGAGCGACGCTCTACCACTATCTCTGAGAGAGCGGTGTACCCGC 259  
QY 274 GCGAGCACCGCGCTGCGAAGCCTGAGGCTGTGTGACCTCTGAGCAGCGCGAGGGGAT 333  
DB 260 GCGAGCACAGTGTGATGAAGGAGCTCCGCGAGATCACCGCCCAACCACTGAACTGA 319  
QY 334 CTATGATGACCTGCGAGAGGCGCCAGCTCTTGGCCAACTTGGCGCGGCTCATCCAGGCCA 393

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Db 320 TGACGACGTCGGCGGACGAGGGCCAGTTCCTCAACATGCTGTCTCAAGCTCATCGGCGCCA 379
Qy 394 AGAAGCGCTGACCTGGGACACCTTACCGGGCTACTCCGGCCCTGGGCCCTGGCCCTGGCGC 453
Db 380 AGAAGACCATGGAGATCGGCGTCTACACCGGCTACTCCCTCTCGCCACCGCGCTCGCCA 439
Qy 454 TGCCCGCGACGCGCGCTGGTGTGACCTGCGAGGTGGACGGCGGACGCCCGGAGCTGGGAC 513
Db 440 TCCCCGACGAGCGCACATCTTGGCCATGATGATCAACCGCGAGAACTAGAGCTGGGGC 499
Qy 514 GGCCCTCTGGAGGCGGCGGAGCGGAGGACCAAGATCGACCTCCGGCTGAAGCCCGCCT 573
Db 500 TGCCGTGTCATCGAAGAGCGCGGCTGGCGCACAAAGATGACTTCCTCGGAGGGCCCGGCGC 559
Qy 574 TGGAGACCTTGACGAGCTGTCTGGCGC---GGGCGAGGCGGCGACCTTCGAGCTGGCGC 630
Db 560 TGCCGTGTGGACGCGCTGCTGGAGGACGAGGCGCAACACCGCACCTTTGCACTTCGTCT 619
Qy 631 TGGTGTATGCGGACAGGAGAACTGCTCGCCCTACTACGAGCGCTGCCTGCACTGCTGC 690
Db 620 TCGTGAGCGCGNACAGGAACTACTCAACTACCGAGCGCCTCATGAAGCTGCTCA 679
Qy 691 GACCCGAGGCGCATCTCGCGCTCCTCAGAGTCTGTGGCGCGGAAAGGTGCTGCAACC 748
Db 680 AGCTCGGCGGCTCCTCGGCTACGACAAACAGCTCTGTGGAACGGCTCCGTGCTGCC 737

RESULT 6
US-09-452-239-35
; Sequence 35, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 1018
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (817)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (826)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (874)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (891)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (924)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (934)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (961)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (970)..(971)
; FEATURE:
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; NAME/KEY: unsure
; LOCATION: (1012)
US-09-452-239-35

Query Match 15.7%; Score 155.6; DB 3; Length 1018;
Best Local Similarity 56.6%; Pred. No. 2e-21;
Matches 309; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

Qy 214 AGTGTCTGTTCCCTCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGCGCTCCATGC 273
Db 177 AGAGCCTGTCTAAGAGCGACGACCTGTACCACTAGTACATCTCTGGACACGAGCGGTGTACCCGC 236
Qy 274 GGGAGCACCCGCGCTGCGAAGCCTGAGGCTGTGACCTCTGGAGCAGCCGCGAGGGGAT 333
Db 237 GGGAGCGGAGAGCATGAGGAGCTGCGGAGATCACCGCCAAAGCACCCATGGAACCTGA 296
Qy 334 CTATGATGACCTGCGAGGAGCGCCAGCTTTGGCCAACTTGGCGGGGCTCATTCAGGCCA 393
Db 297 TGACCACCTTCCGCCGACGAGGGCCAGTTCTCTCAACATGCTCATCAAGCTCATCGGGCGCA 356
Qy 394 AGAAGCGCTGACCTGGGACCTTTCACGGGCTACTTCGGCCCTGGGCCCTGGGCCCTGGCGC 453
Db 357 AGAAGACCATGAGATCGGCGTCTACACCGGCTACTCTCTGCTCGCCACCGCGCTCGCCA 416
Qy 454 TGCCCGCGGACGCGCGCTGTGTGACCTGCGAGGTGGACGCGCAGCGCCCGGAGCTGGGAC 513
Db 417 TCCCGGACGAGCGCACCATCTTTGGCCATGGACATCAACCGCGAGAACTACGAGCTGGGGC 476
Qy 514 GGGCCCTGTGGAGGAGCGCGGAGGCGGAGGACAAAGATCGACCTTCGGCTGGAAGCCGCT 573
Db 477 TGCCGTGTCATCGAAGAGCGCGCGCTGGCGCAAAAGATCGACTTCGCGGAGGGCCCGCGC 536
Qy 574 TGGAGACCTTGACGAGCTGTCTGGCGC---GGGCGAGGCGCGCACCTTCGACGTGGCGC 630
Db 537 TGCCGTCTTGACGCGCTGCTGGAGGAGCGAGGCCAAACACCGGAGCTTCGACTTCGTCT 596
Qy 631 TGGTGTATGCGGACAAAGGAGAACTGCTCGCCCTACTACGAGCGCTGCCTGCACTGCTGC 690
Db 597 TCGTGGAGCGCGACAAAGGACAACTACCTACACGAGCGCTCATGAAGCTGCTCA 656
Qy 691 GACCCGAGGCGATCTCGCGCTCTCAGAGTCTGTGGCGCGGAAAGGTGCTGCAACCTC 750
Db 657 AGTGTGGCGGCGCTCTCGGCTACGACAAACACCTCTGGAACGGCTCCGTGCTGCCCGC 716
Qy 751 CGAAG 756
Db 717 CGGAG 722

RESULT 7
US-09-452-239-1
; Sequence 1, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (806)
; FEATURE:
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NAME/KEY: unsure  
LOCATION: (810)  
US-09-452-239-1

Query Match 15.6%; Score 154; DB 3; Length 891;  
Best Local Similarity 56.7%; Pred. No. 4e-21;  
Matches 305; Conservative 0; Mismatches 230; Indels 3; Gaps 1;

QY 214 ATGTCCTGTTCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGCCGCTCCATGC 273  
DB |||||  
QY 181 AGAGCCTGTCTAAGAGCGAGCAGCTCTACAGTACATCTCTGGACAGCGGTGTACCCGC 240  
DB |||||  
QY 274 GGGAGCACCGCGCTGCGAAGCCTGAGCTGTGACCTCTGGAGAGCGCGAGGGGATT 333  
DB |||||  
QY 241 GGGAGCGGAGAGCATGAAGAGCTCCGCGAGATCACCCCAAGACCCATGGAACCTGA 300  
DB |||||  
QY 334 CTATGATGACCTGCGAGAGGCCAGCTCTTGGCCAACTTGGCGCGCTCATCCAGGCCA 393  
DB |||||  
QY 301 TGACGACCTCCGCCGAGAGGGGAGTTCTTGNACATGTCTCAAGCTCATCGGGGCCA 360  
DB |||||  
QY 394 AGAAGCGCTGACCTGGGACCTTCAAGGCTTACTCCGCCCTTGGCCCTTGGCCCTGGCGC 453  
DB |||||  
QY 361 AGAAGACCATGAGATCGCGCTTACACCGGCTACTCGCTCTCGCCACCGCGCTCGCAC 420  
DB |||||  
QY 454 TGCCCGCGAGCGCGCTGTGACCTGCGAGGTGAGCGGAGCGGAGCGGAGCTGGGAC 513  
DB |||||  
QY 421 TCCCGAGAGCGGACGACGATCTTGGCCATGGACATCAACCGCGAGAACTACGAGCTAGGCC 480  
DB |||||  
QY 514 GGCCCTGTGGAGGAGCGGCGGAGCACAAGATCGACCTCCGGCTGGAAGCCGCT 573  
DB |||||  
QY 481 TTCCCTGTGATCAAGAGCGCGGTGGGCCACAGATCGACTTCCGAGGGGCCCGCGC 540  
DB |||||  
QY 574 TGGAGACCTTGGAGAGCTGTGGCGC---GGGCGAGGCGCGACCTTTCAGCTGGCCG 630  
DB |||||  
QY 541 TCCCGCTCTGGAGAGCTCGTGGCGGACAGGAGCAGCAGCGGTGTTCGACTTGGCCT 600  
DB |||||  
QY 631 TGGTGTGCGGACAGAGGAACTGTCTCGCCTACTACAGAGCGCTGCTGAGCTGCTGC 690  
DB |||||  
QY 601 TGTGAGCGCCGACAGGACAACTACTCAGCTTACCAGCGGCTCTTGAAGCTGGTGA 660  
DB |||||  
QY 691 GACCGGAGCATCTCCGCTCTCAGAGTCTGTGGCGCGGAGGTGCTGCAACC 748  
DB |||||  
QY 661 GGCCCGCGGCTCTATCGGCTACGACACACGCTGTGGAAAGCGCTCCGCTGCTCCC 718  
DB |||||

## RESULT 8

US-09-410-551B-1  
Sequence 1, Application US/09410551B  
Patent No. 6503737  
GENERAL INFORMATION:  
APPLICANT: KOSAN BIOSCIENCES, Inc.  
APPLICANT: REEVES, CHRISTOPHER  
APPLICANT: CHU, DANIEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: SANTI, DANIEL  
APPLICANT: WU, KAI  
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA  
FILE REFERENCE: 30062-20026.00  
CURRENT APPLICATION NUMBER: US/09/410,551B  
CURRENT FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: US 60/139,650  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: US 60/123,810  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/102,748  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: Streptomyces hygroscopicus

NAME/KEY: CDS  
LOCATION: (52275) ... (71465)  
US-09-410-551B-1

Query Match 15.5%; Score 153; DB 4; Length 77536;  
Best Local Similarity 55.4%; Pred. No. 1.1e-20;  
Matches 341; Conservative 0; Mismatches 265; Indels 9; Gaps 2;

QY 252 TATCTTCTGAGCGCTCCATGCGGGAGCACCCGGGCTCGGAAGCCTGAGGCTGTGAC 311  
DB |||||  
QY 8195 TACGTACGGAAGGTGTCCCTGCGCATGACGAGGTGCTGAGCGGCTGCGCGCAGACG 8254  
DB |||||  
QY 312 CTGGAGAGCCGACAGGGGATTCTAT---GATGACCTGCGAGAGCCGAGCTCTTGGCC 368  
DB |||||  
QY 8255 GCCGAGCTGCCGGGCGGTGCGCTACTGCCGCTGTCAGGCGCGAGGAGGACAGTTCTCGAG 8314  
DB |||||  
QY 369 AACCTTGGCGGCTCATCCAGGCCAAGAGGCGCTGGACCTCGGCACTTTCACGGGCTAC 428  
DB |||||  
QY 8315 TTCTCTGTGCGTTTACCGGCGCGGTGAGTGTGAGATCGGAGCTACACCGGCTAC 8374  
DB |||||  
QY 429 TCCGCCCTTGGCCCTTGGCGCTGCCCGCGGACGGCGCTGTGTGACCTTCGAGGTG 488  
DB |||||  
QY 8375 AGCACGCTCTGCTGGCGCGGATTGGCGCGCGGCGGCTGTGTGACGTGCGATGTC 8434  
DB |||||  
QY 489 GACGCGACGCCCGGAGCTGGGACCGCCCTGTGAGGAGCGGCGGAGCGGAGCACAAG 548  
DB |||||  
QY 8435 ATGCCGAAGTGGCCGAGGTGGCGGAGCGGTACTTGGGAGGAGCGGGGTTGCCGACCG 8494  
DB |||||  
QY 549 ATCGACCTCCGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTGCT---GGCGGCG 602  
DB |||||  
QY 8495 ATCGACGCTCCGATCGGAGACGCCCGGACCGCTCTACCGGCTGCTGACGAGGCGGCG 8554  
DB |||||  
QY 603 GCGGAGCGCGCACCTTCGACGTGGCGCGTGTGGATGCGGACAAAGAGAACTGCTCCGCC 662  
DB |||||  
QY 8555 GCGGCGCGGAGTCTTGCACATGTGTTCATCGACGCGGACAAAGCGCGCTACCCGCGC 8614  
DB |||||  
QY 663 TACTACGAGCGTGTGCTGAGCTGTGAGCCCGGAGGATCTTCCGCTCTCTAGAGTTC 722  
DB |||||  
QY 8615 TACTACGAGCGCGCTGCCGTGTGTAAGCGCGCGGCTGATCTCTCTGCAACACG 8674  
DB |||||  
QY 723 CTGTGGCGGGAAGGTGCTGCAACTCCGAAGGGGAGCTGGCGGCGAGGTGTGCGCA 782  
DB |||||  
QY 8675 CTGTCTTTCGCGGCTGGCGGACGAGCGGTGCGAGGACCCGAGACACGCTCGCGGTAC 8734  
DB |||||  
QY 783 AACCTAAACGAACGATCCGCGGAGCGTCAAGGCTCTACATCAGCTCTGCTGCCCTGGCG 842  
DB |||||  
QY 8735 GAACCTAACGCGGCTGCGGACGAGCAGCGGCTGGACCTGGCGATGCTGACGCGGCG 8794  
DB |||||  
QY 843 GATGACTCACCTTG 857  
DB |||||  
QY 8795 GACGCGCTCACCTG 8809  
DB |||||

## RESULT 9

US-09-940-316B-1  
Sequence 1, Application US/09940316B  
Patent No. 6759536  
GENERAL INFORMATION:  
APPLICANT: KOSAN BIOSCIENCES, Inc.  
APPLICANT: REEVES, CHRISTOPHER  
APPLICANT: CHU, DANIEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: SANTI, DANIEL  
APPLICANT: WU, KAI  
TITLE OF INVENTION: POLYKETIDES ENCODING THE fbaA GENE OF THE PK-520 POLYKETIDE SYNTHASE  
FILE REFERENCE: 30062-20026.11  
CURRENT APPLICATION NUMBER: US/09/940,316B  
CURRENT FILING DATE: 2001-08-27  
PRIOR APPLICATION NUMBER: 09/410,551  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: US 60/139,650









APPLICANT: Akira ARISAWA et al.  
TITLE OF INVENTION: Genes Encoding A 3-Acylation  
TITLE OF INVENTION: Enzyme For Macrolide Antibodies  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/708,866A  
FILING DATE: 19910531  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1810 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptomyces thermotolerans  
STRAIN: ATCC 11416  
FEATURE:  
NAME/KEY: -35 signal  
LOCATION: 120..125  
IDENTIFICATION METHOD: S  
FEATURE:  
NAME/KEY: -10 signal  
LOCATION: 143..148  
IDENTIFICATION METHOD: S  
FEATURE:  
NAME/KEY: RBS  
LOCATION: 194..198 AND 201..205  
IDENTIFICATION METHOD: S  
US-07-708-866A-1

Query Match 12.4%; Score 122.8; DB 1; Length 1810;  
Best Local Similarity 58.5%; Pred. No. 5e-15;  
Matches 233; Conservative 0; Mismatches 162; Indels 3; Gaps 1;  
QY 243 CTGTGGCAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCGCGCGCTGCGAAGCCCTGAGG 302  
DB 1412 CTGCTGGATACGCCAGAGAGCGTCTCGTGGCGAGCAGCGCGTGTGCGGAGCTGCGG 1471  
QY 303 CTGCTGACCTGGAGCAGCGCAGGGGGATTCTPAT---GATGACCTGCGAGCAGGCCCAG 359  
DB 1472 GAGTTGACGGCGGCCCTGCGGGCGGACGCGCCATGCAGATCATGCGGAGGAGGCCCAG 1531  
QY 360 CTCTTGGCAACCTGGCGGGCTCATCCAGGCCAAGACGCTGCACCTGGGCACCTTC 419  
DB 1532 CTCCTCGCGCTGCTCATCCGGGTCAAGGGGCGGCCCCAGGTCTTGAGATCGGCACGTTTC 1591  
QY 420 ACGGGGTACTTCGCGCCTGGCCCTGGCGCTGCGCGGACCGGCGCGTGGTGACC 479  
DB 1592 ACCGGGTACAGCAGCTGTGATGGCCCGGGGACACTGCCCGCGCGCGGATCGTCACC 1651

QY 480 TCGGAGGTGGACGCGCAGCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCGAGGCCCGAGGCG 539  
DB 1652 TCGGACATCACCGAGCGGTGGCCCCCGCGCTCGGCGGCCCTTCTGGCGGCGAGCGGGGTC 1711  
QY 540 GAGCAACAAGATCGACCTCCGGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGGCG 599  
DB 1712 GCGGACCGCATCGACCTTCGCATCGGCGAGCGCGCCCGGACCTGTCCGAGCTGCGTGCA 1771  
QY 600 GCGGGCGAGGCCGCGCACCTTCGACCTGGCCCTGGGTGGA 637  
DB 1772 CACGAAGCGCAGCGCATCTTCGACCTGGTGTTCGTGCA 1809

Search completed: April 19, 2005, 20:55:24  
Job time : 255 secs

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Run on: April 19, 2005, 17:29:29 ; Search time 1403 Seconds
        (without alignments)
        4172.932 Million cell updates/sec

Title: US-10-017-407A-305
Perfect score: 989
Sequence: 1 GCGGGCCGCGAGTCCGAGA.....caaaaaaaaaaaaaaaaaaa 989
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
               4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                  Maximum Match 10%

Database : N_Geneseq_16Dec04.*
Listing first 1500 summaries
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.   Score Match Length DB ID Description
RESULT 1
ID AAA37107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 3; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 2
ID AAF34419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 4; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 3
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 6; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 4
ID ACD58458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 5
ID ACH04560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;

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Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 6
ID ACD68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 7
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 8
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 9
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 10
ID ADD70343 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 11
ID ADD38464 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 12
ID ADD39420 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 13
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 14
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;

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Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 15  
ID ADE50595 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 16  
ID ADE20207 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 17  
ID ADE50118 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 18  
ID ADE21676 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 19  
ID ADF30101 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 20  
ID ADF5994 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 21  
ID ADH99498 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 22  
ID ADJ37302 standard; cDNA; 989 BP.  
DE Human tumour therapy associated PRO1558 cDNA.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 23  
ID ADE96678 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;

RESULT 24  
ID ADF25989 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 25  
ID ADF24888 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 26  
ID ADF29624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 27  
ID ADE97155 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 28  
ID ADH03193 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 29  
ID ADH04147 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 30  
ID ADH03670 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 31  
ID ADG68226 standard; cDNA; 989 BP.  
DE Human PRO polypeptide cDNA #11.  
PN US2003170228-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 32  
ID ADH04624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 33  
ID ADH03193 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;

ID ADH61625 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 34  
ID ADL94824 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 35  
ID ADO42276 standard; cDNA; 989 BP.  
DE Human NOVX polynucleotide #63.  
PN US2004058338-A1.  
PD 25-MAR-2004.  
PA (AGEE/) AGEE M L.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BERG/) BERGHS C.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CATT/) CATTERTON E.  
PA (DIPI/) DIPIPO V A.  
PA (EDIN/) EDINGER S R.  
PA (EISE/) EISEN A.  
PA (ELLE/) ELLERMAN K.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (ROTH/) ROTHBERG B G.  
PA (GUOX/) GUO X S.  
PA (HERR/) HERRMANN J L.  
PA (HALV/) HALVORSEN Y.  
PA (JIWV/) JI W.  
PA (KEKU/) KEKUDA R.  
PA (KHRA/) KHRAMTSOV N V.  
PA (LARO/) LAROCHELLE W J.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MILL/) MILLER C E.  
PA (ORTT/) ORT T.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (PEYM/) PEYMAN J A.  
PA (RIEG/) RIEGER D K.  
PA (ROTH/) ROTHENBERG M E.  
PA (SHEN/) SHENOY S G.  
PA (SMIT/) SMITHSON G.  
PA (SPAD/) SPADERNA S K.  
PA (SPYT/) SPYTEK K A.  
PA (STON/) STONE D J.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZHON/) ZHONG M.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 36  
ID ABA05419 standard; cDNA; 1037 BP.  
DE Human O-methyltransferase family member 25692 encoding cDNA.  
PN WO200183719-A2.  
PD 08-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.7%; Score 985.8; DB 6; Length 1037;  
Best Local Similarity 99.8%; Pred. No. 1.7e-155;  
RESULT 37

ID AAZ98166 standard; cDNA; 985 BP.  
DE Human signal peptide containing protein HSPP-58 cDNA SEQ ID NO:192.  
PN WO200000610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 99.3%; Score 981.8; DB 3; Length 985;  
Best Local Similarity 99.8%; Pred. No. 8.1e-155;  
RESULT 38  
ID ABQ61039 standard; cDNA; 1100 BP.  
DE Human PRO1558 protein encoding sequence.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 99.3%; Score 981.8; DB 6; Length 1100;  
Best Local Similarity 99.8%; Pred. No. 8e-155;  
RESULT 39  
ID ADO42272 standard; cDNA; 988 BP.  
DE Human NOVX polynucleotide #61.  
PN US2004058338-A1.  
PD 25-MAR-2004.  
PA (AGEE/) AGEE M L.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BERG/) BERGHS C.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CATT/) CATTERTON E.  
PA (DIPI/) DIPIPO V A.  
PA (EDIN/) EDINGER S R.  
PA (EISE/) EISEN A.  
PA (ELLE/) ELLERMAN K.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (ROTH/) ROTHBERG B G.  
PA (GUOX/) GUO X S.  
PA (HERR/) HERRMANN J L.  
PA (HALV/) HALVORSEN Y.  
PA (JIWV/) JI W.  
PA (KEKU/) KEKUDA R.  
PA (KHRA/) KHRAMTSOV N V.  
PA (LARO/) LAROCHELLE W J.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MILL/) MILLER C E.  
PA (ORTT/) ORT T.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (PEYM/) PEYMAN J A.  
PA (RIEG/) RIEGER D K.  
PA (ROTH/) ROTHENBERG M E.  
PA (SHEN/) SHENOY S G.  
PA (SMIT/) SMITHSON G.  
PA (SPAD/) SPADERNA S K.  
PA (SPYT/) SPYTEK K A.  
PA (STON/) STONE D J.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZHON/) ZHONG M.  
Query Match 98.8%; Score 977; DB 12; Length 988;  
Best Local Similarity 99.9%; Pred. No. 5.1e-154;  
RESULT 40  
ID AAH34455 standard; cDNA; 967 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 94.9%; Score 938.2; DB 4; Length 967;  
Best Local Similarity 99.4%; Pred. No. 1.5e-147;  
RESULT 41

ID ADQ87466 standard; cDNA; 927 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4343.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD) WU T D.  
 PA (ZHOU) ZHOU Y.  
 Query Match 93.5%; Score 925; DB 13; Length 927;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-145;  
 RESULT 42  
 ID AAC76634 standard; cDNA; 812 BP.  
 DE Human ORFX ORF2189 polynucleotide sequence SEQ ID NO:4377.  
 PN WO200508473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 80.9%; Score 799.8; DB 3; Length 812;  
 Best Local Similarity 99.1%; Pred. No. 1.8e-124;  
 RESULT 43  
 ID ABA05420 standard; cDNA; 789 BP.  
 DE Human O-methyltransferase family member 25692 coding sequence.  
 PN WO2001083719-A2.  
 PD 08-NOV-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 79.8%; Score 789; DB 6; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-122;  
 RESULT 44  
 ID AAD56372 standard; DNA; 876 BP.  
 DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.  
 PN WO2003038038-A2.  
 PD 08-MAY-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 71.0%; Score 701.8; DB 9; Length 876;  
 Best Local Similarity 86.5%; Pred. No. 3.9e-108;  
 RESULT 45  
 ID AAD56361 standard; DNA; 885 BP.  
 DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.  
 PN WO2003038038-A2.  
 PD 08-MAY-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 70.9%; Score 701; DB 9; Length 885;  
 Best Local Similarity 86.2%; Pred. No. 5.3e-108;  
 RESULT 46  
 ID ADO42274 standard; cDNA; 787 BP.  
 DE Human NOVX polynucleotide #62.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 PA (AGEE) AGEE M L.  
 PA (ALSO) ALSOBOOK J P.  
 PA (ANDE) ANDERSON D W.  
 PA (BERG) BERGHS C.  
 PA (BOLD) BOLDOG F L.  
 PA (BURG) BURGESS C E.  
 PA (CATT) CATTERTON E.  
 PA (DIPI) DIPIPO V A.  
 PA (EDIN) EDINGER S R.  
 PA (EISE) EISEN A.  
 PA (ELLE) ELLERMAN K.  
 PA (GANG) GANGOLLI E A.  
 PA (GERL) GERLACH V.  
 PA (GORM) GORMAN L.  
 PA (ROTH) ROTHBERG B G.  
 PA (GUOX) GUO X S.  
 PA (HERR) HERRMANN J L.  
 PA (HALV) HALVORSEN Y.  
 PA (JIWW) JI W.  
 PA (KEKU) KEKUDA R.  
 PA (KHRA) KHRAMTSOV N V.  
 PA (LARO) LAROCHELLE W J.  
 PA (LEPL) LEFLEY D M.  
 PA (LILL) LI L.  
 PA (MACD) MACDOUGALL J R.  
 PA (MILL) MILLER C E.  
 PA (ORTT) ORT T.

PA (PADI) PADIGARU M.  
 PA (PATT) PATTURAJAN M.  
 PA (PENA) PENA C E A.  
 PA (PEYN) PEYMAN J A.  
 PA (RIEG) RIEGER D K.  
 PA (ROTH) ROTHENBERG M E.  
 PA (SHEN) SHENOY S G.  
 PA (SMIT) SMITHSON G G.  
 PA (SPAD) SPADERNA S K.  
 PA (SPYT) SPYTEK K A.  
 PA (STON) STONE D J.  
 PA (TAUP) TAUPIER R J.  
 PA (VERN) VERNET C A M.  
 PA (VOSS) VOSS E Z.  
 PA (ZHON) ZHONG M.  
 Query Match 59.0%; Score 583.6; DB 12; Length 787;  
 Best Local Similarity 90.1%; Pred. No. 2e-88;  
 RESULT 47  
 ID ACH35195 standard; cDNA; 474 BP.  
 DE Human endothelial cell cDNA #3328.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA) DRMANAC R T.  
 PA (LABA) LABAT I.  
 PA (STAC) STACHE-CRAIN B.  
 PA (DICK) DICKSON M C.  
 PA (JONE) JONES L W.  
 Query Match 42.7%; Score 422; DB 9; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-61;  
 RESULT 48  
 ID ACH35890 standard; cDNA; 458 BP.  
 DE Human endothelial cell cDNA #4023.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA) DRMANAC R T.  
 PA (LABA) LABAT I.  
 PA (STAC) STACHE-CRAIN B.  
 PA (DICK) DICKSON M C.  
 PA (JONE) JONES L W.  
 Query Match 41.8%; Score 413; DB 9; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-60;  
 RESULT 49  
 ID ADD34178 standard; DNA; 770 BP.  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.  
 PN WO2003020220-A2.  
 PD 13-MAR-2003.  
 PA (UYEM) UNIV EMORY.  
 Query Match 40.9%; Score 404.4; DB 10; Length 770;  
 Best Local Similarity 80.4%; Pred. No. 1.5e-58;  
 RESULT 50  
 ID ABN94134 standard; DNA; 326 BP.  
 DE Gene #632 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE) GENE LOGIC INC.  
 Query Match 31.5%; Score 312; DB 6; Length 326;  
 Best Local Similarity 99.7%; Pred. No. 3.9e-43;  
 RESULT 51  
 ID ADS72763 standard; cDNA; 257 BP.  
 DE Human kidney tumour specific cDNA, SEQ ID 1360.  
 PN US2003109434-A1.  
 PD 12-JUN-2003.  
 PA (CORI) CORIXA CORP.  
 Query Match 26.0%; Score 257; DB 7; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-34;  
 RESULT 52  
 ID ADS72855 standard; cDNA; 257 BP.  
 DE Human kidney tumour specific cDNA, SEQ ID 1452.  
 PN US2003109434-A1.  
 PD 12-JUN-2003.  
 PA (CORI) CORIXA CORP.  
 Query Match 25.7%; Score 254.4; DB 7; Length 257;  
 Best Local Similarity 99.2%; Pred. No. 1.6e-33;



RESULT 53  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 19.7%; Score 194.8; DB 12; Length 11171;  
Best Local Similarity 55.1%; Pred. No. 1.2e-23;  
RESULT 54  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 19.7%; Score 194.8; DB 12; Length 11171;  
Best Local Similarity 55.1%; Pred. No. 1.2e-23;  
RESULT 55  
ID ADM80044 standard; DNA; 675 BP.  
DE Spiramycin biosynthesis orf5\*, SEQ ID 11.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 19.6%; Score 193.8; DB 12; Length 675;  
Best Local Similarity 58.1%; Pred. No. 1.9e-23;  
RESULT 56  
ID ADN97560 standard; DNA; 675 BP.  
DE S ambofaciens spiramycin biosynthetic gene ORF5\*.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 19.6%; Score 193.8; DB 12; Length 675;  
Best Local Similarity 58.1%; Pred. No. 1.9e-23;  
RESULT 57  
ID ABD04592 standard; DNA; 846 BP.  
DE Pseudomonas aeruginosa polynucleotide #3196.  
PN US651795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 19.1%; Score 189; DB 11; Length 846;  
Best Local Similarity 56.0%; Pred. No. 1.2e-22;  
RESULT 58  
ID AAQ44449 standard; DNA; 2381 BP.  
DE 3-acylating enzyme coding sequence.  
PN JP06038750-A.  
PD 15-FEB-1994.  
PA (MEIJ ) MEIJI SEIKA KAISHA.  
Query Match 18.8%; Score 185.8; DB 2; Length 2381;  
Best Local Similarity 57.3%; Pred. No. 4e-22;  
RESULT 59  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midecamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 18.8%; Score 185.8; DB 12; Length 84428;  
Best Local Similarity 57.3%; Pred. No. 3.6e-22;  
RESULT 60  
ID ADI39159 standard; DNA; 85692 BP.  
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.4%; Score 182.4; DB 12; Length 85692;  
Best Local Similarity 57.4%; Pred. No. 1.3e-21;  
RESULT 61  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.  
PN WO2003106653-A2.

PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.1%; Score 179.2; DB 12; Length 86941;  
Best Local Similarity 57.9%; Pred. No. 4.6e-21;  
RESULT 62  
ID AAC89765 standard; cDNA; 178 BP.  
DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
PN WO200073324-A2.  
PD 07-DEC-2000.  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
Query Match 17.7%; Score 174.8; DB 4; Length 178;  
Best Local Similarity 98.9%; Pred. No. 2.9e-20;  
RESULT 63  
ID ABS63429 standard; cDNA; 953 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.4%; Score 161.8; DB 6; Length 953;  
Best Local Similarity 55.1%; Pred. No. 4.1e-18;  
RESULT 64  
ID ABS63428 standard; cDNA; 1049 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.1%; Score 159.2; DB 6; Length 1049;  
Best Local Similarity 54.8%; Pred. No. 1.1e-17;  
RESULT 65  
ID ABS63413 standard; cDNA; 997 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.0%; Score 158.6; DB 6; Length 997;  
Best Local Similarity 54.2%; Pred. No. 1.4e-17;  
RESULT 66  
ID ADA71076 standard; DNA; 1338 BP.  
DE Rice gene, SEQ ID 4399.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 16.0%; Score 158.6; DB 8; Length 1338;  
Best Local Similarity 55.2%; Pred. No. 1.4e-17;  
RESULT 67  
ID ABS63427 standard; cDNA; 1078 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 15.9%; Score 157.2; DB 6; Length 1078;  
Best Local Similarity 57.1%; Pred. No. 2.4e-17;  
RESULT 68  
ID ABS63424 standard; cDNA; 1018 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 15.7%; Score 155.6; DB 6; Length 1018;  
Best Local Similarity 56.6%; Pred. No. 4.5e-17;  
RESULT 69  
ID ABS63407 standard; cDNA; 891 BP.

DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.6%; Score 154; DB 6; Length 891;  
 Best Local Similarity 56.7%; Pred. No. 8.3e-17;  
 RESULT 70  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 Query Match 15.5%; Score 153; DB 3; Length 77536;  
 Best Local Similarity 55.4%; Pred. No. 1.1e-16;  
 RESULT 71  
 ID ADA49019 standard; DNA; 1112 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 15.4%; Score 152.8; DB 9; Length 1112;  
 Best Local Similarity 58.3%; Pred. No. 1.3e-16;  
 RESULT 72  
 ID AAX25215 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.4%; Score 152.4; DB 2; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.5e-16;  
 RESULT 73  
 ID AAD05742 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase (CCOA-OMT) cDNA.  
 PN WO200134817-A2.  
 PD 17-MAY-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.4%; Score 152.4; DB 5; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.5e-16;  
 RESULT 74  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 15.3%; Score 151.4; DB 8; Length 82746;  
 Best Local Similarity 57.3%; Pred. No. 2e-16;  
 RESULT 75  
 ID ABZ40101 standard; DNA; 666 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 15.1%; Score 149.2; DB 10; Length 666;  
 Best Local Similarity 53.5%; Pred. No. 5.3e-16;  
 RESULT 76  
 ID AAX25210 standard; cDNA; 1003 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.1%; Score 149.2; DB 2; Length 1003;  
 Best Local Similarity 58.0%; Pred. No. 5.2e-16;  
 RESULT 77  
 ID ADA49212 standard; DNA; 798 BP.  
 DE Maize gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 15.0%; Score 148; DB 9; Length 798;  
 Best Local Similarity 53.7%; Pred. No. 8.3e-16;  
 RESULT 78  
 ID ABS63425 standard; cDNA; 1118 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.

PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1118;  
 Best Local Similarity 53.7%; Pred. No. 8.2e-16;  
 RESULT 79  
 ID ABS63408 standard; cDNA; 1146 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1146;  
 Best Local Similarity 53.7%; Pred. No. 8.2e-16;  
 RESULT 80  
 ID ADR73686 standard; DNA; 1252 BP.  
 DE Rice promoter putative caffeoyl CoA3O methyltransferase CDS.  
 PN WO2004070039-A2.  
 PD 19-AUG-2004.  
 PA (CROP-) CROPDESIGN NV.  
 Query Match 14.9%; Score 147.6; DB 13; Length 1252;  
 Best Local Similarity 54.2%; Pred. No. 9.5e-16;  
 RESULT 81  
 ID ADD34177 standard; DNA; 407 BP.  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
 PN WO2003020220-A2.  
 PD 13-MAR-2003.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 14.9%; Score 147.4; DB 10; Length 407;  
 Best Local Similarity 73.3%; Pred. No. 1.1e-15;  
 RESULT 82  
 ID AAA81501 standard; DNA; 48275 BP.  
 DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 48275;  
 Best Local Similarity 53.1%; Pred. No. 1.2e-15;  
 RESULT 83  
 ID AAA81489 standard; DNA; 837096 BP.  
 DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 110000;  
 Best Local Similarity 53.1%; Pred. No. 1.1e-15;  
 RESULT 84  
 ID AAF21610 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 349980;  
 Best Local Similarity 53.1%; Pred. No. 1.1e-15;  
 RESULT 85  
 ID AAL61190 standard; DNA; 504 BP.  
 DE Actinosynnema pretiosum O-methyltransferase gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 14.8%; Score 146.6; DB 8; Length 504;  
 Best Local Similarity 57.7%; Pred. No. 1.4e-15;  
 RESULT 86  
 ID AAX25208 standard; cDNA; 1160 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 14.8%; Score 146.4; DB 2; Length 1160;  
 Best Local Similarity 53.5%; Pred. No. 1.5e-15;

RESULT 87  
 ID ABS63409 standard; cDNA; 1057 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.6%; Score 144.4; DB 6; Length 1057;  
 Best Local Similarity 57.3%; Pred. No. 3.3e-15;  
 RESULT 88  
 ID ADA71075 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4398.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.3%; Score 141.8; DB 8; Length 783;  
 Best Local Similarity 57.4%; Pred. No. 9e-15;  
 RESULT 89  
 ID ACL3248 standard; DNA; 509 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13239.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Query Match 14.2%; Score 140.8; DB 9; Length 509;  
 Best Local Similarity 60.3%; Pred. No. 1.3e-14;  
 RESULT 90  
 ID ABS63412 standard; cDNA; 1058 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.2%; Score 140.6; DB 6; Length 1058;  
 Best Local Similarity 50.6%; Pred. No. 1.4e-14;  
 RESULT 91  
 ID ADA70823 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4146.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.2%; Score 140; DB 8; Length 783;  
 Best Local Similarity 52.9%; Pred. No. 1.8e-14;  
 RESULT 92  
 ID ABN87118 standard; cDNA; 1103 BP.  
 DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:12.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135.6; DB 6; Length 1103;  
 Best Local Similarity 57.0%; Pred. No. 9.6e-14;  
 RESULT 93  
 ID ABN87121 standard; cDNA; 773 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:16.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 773;  
 Best Local Similarity 56.9%; Pred. No. 1.2e-13;  
 RESULT 94  
 ID ABN87122 standard; cDNA; 789 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:17.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 789;  
 Best Local Similarity 56.9%; Pred. No. 1.2e-13;  
 RESULT 95  
 ID ABN87120 standard; cDNA; 693 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:15.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.3%; Score 131.6; DB 6; Length 693;  
 Best Local Similarity 56.9%; Pred. No. 4.5e-13;  
 RESULT 96  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.9%; Score 127.4; DB 5; Length 109519;  
 Best Local Similarity 55.8%; Pred. No. 2e-12;  
 RESULT 97  
 ID ABN87126 standard; cDNA; 689 BP.  
 DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:21.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.8%; Score 126.8; DB 6; Length 689;  
 Best Local Similarity 57.1%; Pred. No. 2.8e-12;  
 RESULT 98  
 ID ABS63410 standard; cDNA; 923 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 12.7%; Score 126; DB 6; Length 923;  
 Best Local Similarity 56.6%; Pred. No. 3.8e-12;  
 RESULT 99  
 ID AAX25209 standard; cDNA; 944 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 12.7%; Score 126; DB 2; Length 944;  
 Best Local Similarity 56.6%; Pred. No. 3.8e-12;  
 RESULT 100  
 ID ADA8371 standard; DNA; 835 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 12.7%; Score 125.4; DB 9; Length 835;  
 Best Local Similarity 55.0%; Pred. No. 4.9e-12;  
 RESULT 101  
 ID ADC68436 standard; cDNA; 1051 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.6%; Score 125; DB 10; Length 1051;  
 Best Local Similarity 54.0%; Pred. No. 5.6e-12;  
 RESULT 102  
 ID ADC68544 standard; cDNA; 1059 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.5%; Score 123.4; DB 10; Length 1059;  
 Best Local Similarity 53.9%; Pred. No. 1e-11;  
 RESULT 103  
 ID ADC68545 standard; cDNA; 1063 BP.  
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.4%; Score 122.6; DB 10; Length 1063;

Best Local Similarity 54.2%; Pred. No. 1.4e-11;  
RESULT 104  
ID ABN87112 standard; cDNA; 765 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:6.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 12.0%; Score 118.4; DB 6; Length 765;  
Best Local Similarity 53.7%; Pred. No. 7.1e-11;  
RESULT 105  
ID AAQ14978 standard; DNA; 1810 BP.  
DE Acya gene.  
PN BP459525-A.  
PD 04-DEC-1991.  
PA (SAOC) MERCIAN CORP.  
Query Match 11.9%; Score 118; DB 2; Length 1810;  
Best Local Similarity 57.8%; Pred. No. 8.1e-11;  
RESULT 106  
ID ABN87245 standard; cDNA; 1161 BP.  
DE Lolium perenne CCoAMT1 cDNA sequence SEQ ID NO:168.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.9%; Score 117.8; DB 6; Length 1161;  
Best Local Similarity 53.7%; Pred. No. 8.9e-11;  
RESULT 107  
ID ABN87110 standard; cDNA; 758 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:4.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.7%; Score 115.6; DB 6; Length 758;  
Best Local Similarity 52.8%; Pred. No. 2.1e-10;  
RESULT 108  
ID ABN87115 standard; cDNA; 793 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:9.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.7%; Score 115.6; DB 6; Length 793;  
Best Local Similarity 52.8%; Pred. No. 2.1e-10;  
RESULT 109  
ID ABN87108 standard; cDNA; 1113 BP.  
DE Lolium perenne LpCCoAMTA nucleotide sequence SEQ ID NO:1.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.6%; Score 115; DB 6; Length 1113;  
Best Local Similarity 52.8%; Pred. No. 2.6e-10;  
RESULT 110  
ID ABN87246 standard; cDNA; 1199 BP.  
DE Lolium perenne CCoAMT2 cDNA sequence SEQ ID NO:170.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.6%; Score 115; DB 6; Length 1199;  
Best Local Similarity 52.8%; Pred. No. 2.6e-10;  
RESULT 111  
ID ABN87111 standard; cDNA; 774 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:5.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.5%; Score 113.8; DB 6; Length 774;  
Best Local Similarity 53.0%; Pred. No. 4.2e-10;  
RESULT 112

ID ABN87113 standard; cDNA; 777 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:7.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.4%; Score 113.2; DB 6; Length 777;  
Best Local Similarity 52.2%; Pred. No. 5.3e-10;  
RESULT 113  
ID ABN87114 standard; cDNA; 792 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:8.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.1%; Score 110; DB 6; Length 792;  
Best Local Similarity 51.9%; Pred. No. 1.8e-09;  
RESULT 114  
ID AAT24153 standard; cDNA to mRNA; 111 BP.  
DE Human gene signature HUMGS06156.  
PN WO9514772-A1.  
PD 01-JUN-1995.  
PA (MATS) MATSUBARA K.  
PA (OKUB) OKUBO K.  
Query Match 10.8%; Score 106.8; DB 2; Length 111;  
Best Local Similarity 97.3%; Pred. No. 6.5e-09;  
RESULT 115  
ID ABK2368 standard; cDNA; 343 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #275.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 6; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 116  
ID ADB5562 standard; DNA; 343 BP.  
DE Toxicity-related gene, SEQ ID 688.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 10; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 117  
ID ABT40596 standard; DNA; 343 BP.  
DE Toxicity modelling related rat gene SEQ ID No 298.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 10; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 118  
ID AAA68001 standard; DNA; 1012 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 9.8%; Score 96.8; DB 3; Length 1012;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 119  
ID ADD41751 standard; DNA; 1012 BP.  
DE O-methyl transferase DNA #9.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 9.8%; Score 96.8; DB 10; Length 1012;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 120  
ID AAV23912 standard; DNA; 1026 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.

PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
 RESULT 121  
 ID AAZ06875 standard; cDNA; 1026 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 1.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
 RESULT 122  
 ID AAA67913 standard; DNA; 1026 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 3; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
 RESULT 123  
 ID ADD41663 standard; DNA; 1026 BP.  
 DE O-methyl transferase DNA #1.  
 PN US200311373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 9.8%; Score 96.8; DB 10; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
 RESULT 124  
 ID ABN87119 standard; cDNA; 628 BP.  
 DE Lollium perenne LpCCoAMTb partial nucleotide sequence SEQ ID NO:14.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 9.6%; Score 95.4; DB 6; Length 628;  
 Best Local Similarity 53.7%; Pred. No. 4.9e-07;  
 RESULT 125  
 ID ACL23249 standard; DNA; 542 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13240.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Query Match 9.6%; Score 95.2; DB 9; Length 542;  
 Best Local Similarity 50.9%; Pred. No. 5.3e-07;  
 RESULT 126  
 ID ADK69906 standard; DNA; 1180 BP.  
 DE Maize W64A CCoAMT2 gene, seq id 3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 127  
 ID ADK69926 standard; DNA; 1199 BP.  
 DE Maize W64A CCoAMT2 gene insertion mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.6%; Score 95.2; DB 10; Length 1180;  
 Best Local Similarity 58.5%; Pred. No. 5.2e-07;  
 RESULT 128  
 ID ABD00975 standard; DNA; 675 BP.  
 DE Klebsiella pneumoniae polynucleotide seqid 6750.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 9.4%; Score 93.4; DB 11; Length 675;  
 Best Local Similarity 52.3%; Pred. No. 1.1e-06;  
 RESULT 129  
 ID ADK69918 standard; DNA; 1172 BP.  
 DE Maize W64A CCoAMT2 gene deletion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1172;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 130  
 ID ADK69927 standard; DNA; 1178 BP.  
 DE Maize W64A CCoAMT2 gene deletion mutant #2.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1178;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 131  
 ID ADK69919 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 132  
 ID ADK69920 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #2.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 133  
 ID ADK69928 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #7.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 134  
 ID ADK69923 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #5.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 135  
 ID ADK69904 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene, seq id 1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 136  
 ID ADK69922 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 137  
 ID ADK69924 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAMT2 gene substitution mutant #6.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 138  
 ID ADK69929 standard; DNA; 1181 BP.

DE Maize W64A CCOAOMT2 gene substitution mutant #8.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 139  
 ID ADK69931 standard; DNA; 1181 BP.  
 DE Maize W64A CCOAOMT2 gene substitution mutant #10.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 140  
 ID ADK69921 standard; DNA; 1181 BP.  
 DE Maize W64A CCOAOMT2 gene substitution mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 141  
 ID ADK69930 standard; DNA; 1181 BP.  
 DE Maize W64A CCOAOMT2 gene substitution mutant #9.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1181;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 142  
 ID ADK69917 standard; DNA; 1186 BP.  
 DE Maize W64A CCOAOMT2 gene insertion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1186;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 143  
 ID ADK69925 standard; DNA; 1196 BP.  
 DE Maize W64A CCOAOMT2 gene insertion mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1196;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 144  
 ID ADK69932 standard; DNA; 1199 BP.  
 DE Maize W64A CCOAOMT2 gene insertion mutant #5.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Query Match 9.4%; Score 93; DB 10; Length 1199;  
 Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
 RESULT 145  
 ID ABS63415 standard; cDNA; 931 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 8.9%; Score 88; DB 6; Length 931;  
 Best Local Similarity 50.7%; Pred. No. 8.3e-06;  
 RESULT 146  
 ID ABS63430 standard; cDNA; 534 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 8.9%; Score 87.8; DB 6; Length 534;

Best Local Similarity 54.1%; Pred. No. 9.1e-06;  
 RESULT 147  
 ID ADR62522 standard; cDNA; 995 BP.  
 DE Cotton cDNA sequence, SEQ ID 3303.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Query Match 8.8%; Score 86.8; DB 13; Length 995;  
 Best Local Similarity 50.6%; Pred. No. 1.3e-05;  
 RESULT 148  
 ID ACN60610 standard; cDNA; 617 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-F5, SEQ:15391.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 8.7%; Score 85.6; DB 13; Length 617;  
 Best Local Similarity 47.9%; Pred. No. 2.1e-05;  
 RESULT 149  
 ID ABS63418 standard; cDNA; 962 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 8.7%; Score 85.6; DB 6; Length 962;  
 Best Local Similarity 52.2%; Pred. No. 2.1e-05;  
 RESULT 150  
 ID ABS63419 standard; cDNA; 1023 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 8.7%; Score 85.6; DB 6; Length 1023;  
 Best Local Similarity 52.2%; Pred. No. 2.1e-05;  
 RESULT 151  
 ID AAQ32259 standard; cDNA; 1258 BP.  
 DE Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).  
 PN DE4117747-A.  
 PD 03-DEC-1992.  
 PA (FARB) BAYER AG.  
 Query Match 8.5%; Score 84.4; DB 2; Length 1258;  
 Best Local Similarity 49.8%; Pred. No. 3.3e-05;  
 RESULT 152  
 ID ADN74200 standard; cDNA; 780 BP.  
 DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.  
 PN WO2004035798-A2.  
 PD 29-APR-2004.  
 PA (CROP-) CROPDESIGN NV.  
 Query Match 8.5%; Score 84; DB 12; Length 780;  
 Best Local Similarity 51.9%; Pred. No. 3.9e-05;  
 RESULT 153  
 ID ADN73162 standard; cDNA; 780 BP.  
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.  
 PN WO2004035798-A2.  
 PD 29-APR-2004.  
 PA (CROP-) CROPDESIGN NV.  
 Query Match 8.5%; Score 84; DB 12; Length 780;  
 Best Local Similarity 51.9%; Pred. No. 3.9e-05;  
 RESULT 154  
 ID AAC4547 standard; DNA; 1032 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 8.5%; Score 84; DB 3; Length 1032;  
 Best Local Similarity 51.9%; Pred. No. 3.8e-05;

RESULT 155  
ID AAC2559 standard; DNA; 1033 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1033;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 156  
ID ABN98364 standard; DNA; 1072 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYV/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURE/) HURBAN P.  
Query Match 8.5%; Score 84; DB 6; Length 1072;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 157  
ID AAC44172 standard; DNA; 1180 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1180;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 158  
ID ADR5554 standard; cDNA; 1233 BP.  
DE Cotton cDNA sequence, SEQ ID 6335.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 8.0%; Score 79.6; DB 13; Length 1233;  
Best Local Similarity 49.2%; Pred. No. 0.00021;  
RESULT 159  
ID ABS63417 standard; cDNA; 980 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.0%; Score 79.2; DB 6; Length 980;  
Best Local Similarity 51.2%; Pred. No. 0.00024;  
RESULT 160  
ID AAV23845 standard; DNA; 760 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 161  
ID AAZ06846 standard; cDNA; 760 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
PN US5952486-A.

PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 162  
ID AAA69584 standard; cDNA; 760 BP.  
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
PN WO2000036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 163  
ID AAA67932 standard; DNA; 760 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 164  
ID ADD41682 standard; DNA; 760 BP.  
DE O-methyl transferase DNA #5.  
PN US200313173-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 7.7%; Score 76.2; DB 10; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 165  
ID ABS63416 standard; cDNA; 929 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 7.5%; Score 74.4; DB 6; Length 929;  
Best Local Similarity 50.5%; Pred. No. 0.0015;  
RESULT 166  
ID ABS54112 standard; DNA; 870 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 7.4%; Score 73.2; DB 6; Length 870;  
Best Local Similarity 48.4%; Pred. No. 0.0024;  
RESULT 167  
ID ACN55288 standard; cDNA; 546 BP.  
DE Cotton androecium tissue EST Clone ID: LJB3828-032-Q6-K6-D4, SEQ:10069.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.4%; Score 72.8; DB 13; Length 546;  
Best Local Similarity 50.2%; Pred. No. 0.0029;  
RESULT 168  
ID ACN40884 standard; cDNA; 1067 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326926, SEQ ID NO:5958.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 71; DB 13; Length 1067;  
Best Local Similarity 50.7%; Pred. No. 0.0057;  
RESULT 169  
ID AAQ13306 standard; DNA; 1107 BP.  
DE Human catechol-O-methyltransferase gene.  
PN WO9111513-A.

PD 08-AUG-1991.  
PA (ORIN ) ORION YHTYMAE OY.  
Query Match 7.2%; Score 71; DB 2; Length 1107;  
Best Local Similarity 50.7%; Pred. No. 0.0056;  
RESULT 170  
ID ACN40883 standard; cDNA; 1289 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA226561, SEQ ID NO:5956.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 71; DB 13; Length 1289;  
Best Local Similarity 50.7%; Pred. No. 0.0056;  
RESULT 171  
ID AAC77872 standard; cDNA; 1350 BP.  
DE Human cancer associated gene sequence SEQ ID NO:266.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 70.6; DB 3; Length 1350;  
Best Local Similarity 50.4%; Pred. No. 0.0065;  
RESULT 172  
ID ABS54113 standard; DNA; 811 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCoAOMT-2) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 7.1%; Score 70; DB 6; Length 811;  
Best Local Similarity 47.9%; Pred. No. 0.0084;  
RESULT 173  
ID ADH02845 standard; cDNA; 888 BP.  
DE Petunia E2O cDNA #SEQ ID 4.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.6; DB 10; Length 888;  
Best Local Similarity 50.3%; Pred. No. 0.0097;  
RESULT 174  
ID ADH02842 standard; cDNA; 969 BP.  
DE Petunia difE cDNA #SEQ ID 1.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.6; DB 10; Length 969;  
Best Local Similarity 50.3%; Pred. No. 0.0097;  
RESULT 175  
ID ABZ83278 standard; cDNA; 1024 BP.  
DE Toxicologically relevant human nucleotide sequence #437.  
PN WO2003016500-A2.  
PD 27-FEB-2003.  
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
Query Match 7.0%; Score 69.4; DB 10; Length 1024;  
Best Local Similarity 50.4%; Pred. No. 0.01;  
RESULT 176  
ID ADE84973 standard; DNA; 1206 BP.  
DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
PN WO2003038129-A2.  
PD 08-MAY-2003.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 7.0%; Score 69.4; DB 10; Length 1206;  
Best Local Similarity 50.4%; Pred. No. 0.01;  
RESULT 177  
ID ADQ85986 standard; cDNA; 1291 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2858.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 7.0%; Score 69.4; DB 12; Length 1291;  
Best Local Similarity 50.4%; Pred. No. 0.01;  
RESULT 178  
ID ACN44731 standard; cDNA; 1311 BP.  
DE Human mRNA sequence hCT1955643.

PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 7.0%; Score 69.4; DB 11; Length 1311;  
Best Local Similarity 50.4%; Pred. No. 0.01;  
RESULT 179  
ID ABX63642 standard; cDNA; 1327 BP.  
DE Human cDNA #642 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Query Match 7.0%; Score 69.4; DB 8; Length 1327;  
Best Local Similarity 50.4%; Pred. No. 0.01;  
RESULT 180  
ID ADH02882 standard; cDNA; 841 BP.  
DE Fuchsia FMT (3282) cDNA #SEQ ID 41.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.2; DB 10; Length 841;  
Best Local Similarity 49.5%; Pred. No. 0.011;  
RESULT 181  
ID ADH02884 standard; cDNA; 943 BP.  
DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.2; DB 10; Length 943;  
Best Local Similarity 49.5%; Pred. No. 0.011;  
RESULT 182  
ID AAC42096 standard; DNA; 1186 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.9%; Score 68.6; DB 3; Length 1186;  
Best Local Similarity 46.7%; Pred. No. 0.014;  
RESULT 183  
ID ADR65555 standard; cDNA; 749 BP.  
DE Cotton cDNA sequence, SEQ ID 6336.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 6.9%; Score 68; DB 13; Length 749;  
Best Local Similarity 49.5%; Pred. No. 0.018;  
RESULT 184  
ID ADH02852 standard; cDNA; 1006 BP.  
DE Torenia TMT5.nt cDNA #SEQ ID 11.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 6.8%; Score 67.4; DB 10; Length 1006;  
Best Local Similarity 50.1%; Pred. No. 0.023;  
RESULT 185  
ID ABA90338 standard; cDNA; 1149 BP.  
DE Human polynucleotide #13.  
PN WO200181363-A1.  
PD 01-NOV-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 6.8%; Score 67; DB 6; Length 1149;  
Best Local Similarity 51.5%; Pred. No. 0.026;  
RESULT 186  
ID AAV23874 standard; DNA; 1074 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
Best Local Similarity 49.3%; Pred. No. 0.028;  
RESULT 187



ID AAZ06877 standard; cDNA; 1074 BP.  
 DE Fine O-methyl transferase (OMT) partial cDNA 3.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 188  
 ID AAA67961 standard; DNA; 1074 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 189  
 ID ADD41711 standard; DNA; 1074 BP.  
 DE O-methyl transferase DNA #7.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 190  
 ID AAV23875 standard; DNA; 1075 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 191  
 ID AAZ06878 standard; cDNA; 1075 BP.  
 DE Fine O-methyl transferase (OMT) partial cDNA 4.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 192  
 ID AAA67962 standard; DNA; 1075 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 193  
 ID ADD41712 standard; DNA; 1075 BP.  
 DE O-methyl transferase DNA #8.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 194  
 ID AAX53491 standard; DNA; 114955 BP.  
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
 PN WO9913886-A1.  
 PD 25-MAR-1999.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 6.7%; Score 66.6; DB 2; Length 114955;  
 Best Local Similarity 33.8%; Pred. No. 0.027;  
 RESULT 195  
 ID AAD19545 standard; cDNA; 744 BP.  
 DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.

PN WO200173090-A2.  
 PD 04-OCT-2001.  
 PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.  
 Query Match 6.7%; Score 66.4; DB 4; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 196  
 ID ADI30327 standard; cDNA; 744 BP.  
 DE Alfalfa harvest inducible cDNA sequence H12.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 197  
 ID ADI30333 standard; DNA; 1906 BP.  
 DE Alfalfa harvest inducible H12 gene genomic DNA sequence.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 1906;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 198  
 ID ABS63420 standard; cDNA; 912 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 6.7%; Score 66.2; DB 6; Length 912;  
 Best Local Similarity 47.9%; Pred. No. 0.036;  
 RESULT 199  
 ID ABS54115 standard; DNA; 967 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Query Match 6.6%; Score 64.8; DB 6; Length 967;  
 Best Local Similarity 49.0%; Pred. No. 0.061;  
 RESULT 200  
 ID ABO55289 standard; cDNA; 553 BP.  
 DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.5%; Score 64.6; DB 6; Length 553;  
 Best Local Similarity 49.5%; Pred. No. 0.067;  
 RESULT 201  
 ID AAC11287 standard; cDNA; 143 BP.  
 DE Human secreted protein 5' EST, SEQ ID NO: 15362.  
 PN EP1033401-A2.  
 PD 06-SEP-2000.  
 PA (GEST) GENSET.  
 Query Match 6.5%; Score 64.4; DB 3; Length 143;  
 Best Local Similarity 98.5%; Pred. No. 0.075;  
 RESULT 202  
 ID ABS63426 standard; cDNA; 600 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 6.5%; Score 64.2; DB 6; Length 600;  
 Best Local Similarity 53.4%; Pred. No. 0.078;  
 RESULT 203  
 ID ABS63411 standard; cDNA; 510 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.

Query Match 6.4%; Score 63.6; DB 6; Length 510;  
Best Local Similarity 45.9%; Pred. No. 0.099;  
RESULT 204  
ID ADQ19501 standard; DNA; 135005 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.4%; Score 63; DB 12; Length 135005;  
Best Local Similarity 47.8%; Pred. No. 0.11;  
RESULT 205  
ID ABX09141 standard; DNA; 75216 BP.  
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv230.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP) INST PASTEUR.  
Query Match 6.3%; Score 62.8; DB 6; Length 75216;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 206  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 207  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 208  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.13;  
RESULT 209  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.13;  
RESULT 210  
ID ABS54114 standard; DNA; 845 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCoAOMT-3) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 6.2%; Score 61.6; DB 6; Length 845;  
Best Local Similarity 48.5%; Pred. No. 0.21;  
RESULT 211  
ID AAX53491 standard; DNA; 114955 BP.  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
PN WO9913886-A1.  
PD 25-MAR-1999.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 6.2%; Score 61.2; DB 2; Length 114955;  
Best Local Similarity 31.2%; Pred. No. 0.21;  
RESULT 212  
ID AAQ61817 standard; DNA; 1578 BP.  
DE Open reading frame of pseudorabies virus.  
PN WO9408000-A1.  
PD 14-APR-1994.  
PA (ALKU) AKZO NV.  
Query Match 6.1%; Score 60.8; DB 2; Length 1578;  
Best Local Similarity 45.3%; Pred. No. 0.28;  
RESULT 213  
ID ABQ61846 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Query Match 6.1%; Score 60.4; DB 6; Length 349980;  
Best Local Similarity 49.0%; Pred. No. 0.28;  
RESULT 214  
ID ABZ14595 standard; DNA; 729 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCR1) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.1%; Score 60; DB 6; Length 729;  
Best Local Similarity 48.5%; Pred. No. 0.39;  
RESULT 215  
ID AAC45004 standard; DNA; 917 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.  
PN BP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 60; DB 3; Length 917;  
Best Local Similarity 48.5%; Pred. No. 0.39;  
RESULT 216  
ID ABS63422 standard; cDNA; 982 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 6.1%; Score 60; DB 6; Length 982;  
Best Local Similarity 48.7%; Pred. No. 0.39;  
RESULT 217  
ID ADH02867 standard; cDNA; 1079 BP.  
DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 6.1%; Score 60; DB 10; Length 1079;  
Best Local Similarity 48.7%; Pred. No. 0.39;  
RESULT 218  
ID ACA38007 standard; DNA; 1143 BP.  
DE Prokaryotic essential gene #19664.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 60; DB 8; Length 1143;  
Best Local Similarity 45.4%; Pred. No. 0.38;  
RESULT 219  
ID AAA68101 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.  
PN WO20002099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 6.0%; Score 59.6; DB 3; Length 399;  
Best Local Similarity 55.2%; Pred. No. 0.46;  
RESULT 220  
ID ADD41851 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #2.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 6.0%; Score 59.6; DB 10; Length 399;  
Best Local Similarity 55.2%; Pred. No. 0.46;  
RESULT 221  
ID ADI23934 standard; DNA; 7185 BP.  
DE Streptomyces refuineus 024A locus ORF7.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 7185;  
Best Local Similarity 46.9%; Pred. No. 0.43;  
RESULT 222  
ID ADI23920 standard; DNA; 61944 BP.  
DE Streptomyces refuineus 024A locus (NRRL 3143).  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 61944;  
Best Local Similarity 46.9%; Pred. No. 0.4;  
RESULT 223  
ID ADQ22939 standard; DNA; 4667 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.0%; Score 59.2; DB 12; Length 4667;  
Best Local Similarity 44.6%; Pred. No. 0.5;

RESULT 224  
 ID ADQ22939 standard; DNA; 4667 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.0%; Score 59; DB 12; Length 4667;  
 Best Local Similarity 44.8%; Pred. No. 0.54;  
 RESULT 225  
 ID ABQ93881 standard; DNA; 10800 BP.  
 DE Human laminin alpha-5-like NOVIC DNA, SEQ ID NO:5.  
 PN WO200253742-A2.  
 PD 11-JUL-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.0%; Score 59; DB 6; Length 10800;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 226  
 ID ADO10046 standard; cDNA; 10800 BP.  
 DE Novel human protein Novic cDNA.  
 PN US2004052806-A1.  
 PD 18-MAR-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (TCH/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (GROS/) GROSSE W M.  
 PA (LEPL/) LEPLEY D M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (STON/) STONE D J.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (ANDE/) ANDERSON D W.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (EISE/) EISEN A.  
 Query Match 6.0%; Score 59; DB 12; Length 10800;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 227  
 ID ABQ93879 standard; DNA; 10809 BP.  
 DE Human laminin alpha-5-like NOVIA DNA, SEQ ID NO:1.  
 PN WO200253742-A2.  
 PD 11-JUL-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.0%; Score 59; DB 6; Length 10809;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 228  
 ID ADO10042 standard; cDNA; 10809 BP.  
 DE Novel human protein Novia cDNA.  
 PN US2004052806-A1.  
 PD 18-MAR-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (TCH/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (GROS/) GROSSE W M.  
 PA (LEPL/) LEPLEY D M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (STON/) STONE D J.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (ANDE/) ANDERSON D W.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (EISE/) EISEN A.  
 Query Match 6.0%; Score 59; DB 12; Length 10800;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 229  
 ID ADH02847 standard; cDNA; 1077 BP.  
 DE Petunia E33 cDNA #SEQ ID 5.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITEL-) INT FLOWER DEV PTY LTD.  
 Query Match 5.9%; Score 58.8; DB 10; Length 1077;  
 Best Local Similarity 48.5%; Pred. No. 0.61;  
 RESULT 230  
 ID AAF25795 standard; DNA; 3849 BP.  
 DE S. chrysomallus acm-C DNA.  
 PN DE19928313-A1.  
 PD 21-DEC-2000.  
 PA (KELL/) KELLER U.  
 Query Match 5.9%; Score 58.8; DB 4; Length 3849;  
 Best Local Similarity 45.9%; Pred. No. 0.59;  
 RESULT 231  
 ID RAD55726 standard; DNA; 5858 BP.  
 DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.9%; Score 58.8; DB 8; Length 5858;  
 Best Local Similarity 48.3%; Pred. No. 0.58;  
 RESULT 232  
 ID ADA71279 standard; DNA; 897 BP.  
 DE Rice gene, SEQ ID 4602.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.9%; Score 58; DB 8; Length 897;  
 Best Local Similarity 44.9%; Pred. No. 0.84;  
 RESULT 233  
 ID AAL40781 standard; DNA; 88421 BP.  
 DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.  
 PN WO200231155-A2.  
 PD 18-APR-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.9%; Score 58; DB 6; Length 88421;  
 Best Local Similarity 44.5%; Pred. No. 0.74;  
 RESULT 234  
 ID ABN87109 standard; cDNA; 557 BP.  
 DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:3.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 5.8%; Score 57.8; DB 6; Length 557;  
 Best Local Similarity 49.7%; Pred. No. 0.91;  
 RESULT 235  
 ID ABZ22145 standard; DNA; 1029 BP.  
 DE Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.  
 PN JP2002247985-A.  
 PD 03-SEP-2002.  
 PA (RIKA) RIKAGAKU KENKYUSHO.  
 Query Match 5.8%; Score 57.4; DB 8; Length 1029;

PA (GORM/) GORMAN L.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (STON/) STONE D J.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (ANDE/) ANDERSON D W.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (EISE/) EISEN A.  
 Query Match 6.0%; Score 59; DB 12; Length 10809;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 229  
 ID ADH02847 standard; cDNA; 1077 BP.  
 DE Petunia E33 cDNA #SEQ ID 5.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITEL-) INT FLOWER DEV PTY LTD.  
 Query Match 5.9%; Score 58.8; DB 10; Length 1077;  
 Best Local Similarity 48.5%; Pred. No. 0.61;  
 RESULT 230  
 ID AAF25795 standard; DNA; 3849 BP.  
 DE S. chrysomallus acm-C DNA.  
 PN DE19928313-A1.  
 PD 21-DEC-2000.  
 PA (KELL/) KELLER U.  
 Query Match 5.9%; Score 58.8; DB 4; Length 3849;  
 Best Local Similarity 45.9%; Pred. No. 0.59;  
 RESULT 231  
 ID RAD55726 standard; DNA; 5858 BP.  
 DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.9%; Score 58.8; DB 8; Length 5858;  
 Best Local Similarity 48.3%; Pred. No. 0.58;  
 RESULT 232  
 ID ADA71279 standard; DNA; 897 BP.  
 DE Rice gene, SEQ ID 4602.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.9%; Score 58; DB 8; Length 897;  
 Best Local Similarity 44.9%; Pred. No. 0.84;  
 RESULT 233  
 ID AAL40781 standard; DNA; 88421 BP.  
 DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.  
 PN WO200231155-A2.  
 PD 18-APR-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.9%; Score 58; DB 6; Length 88421;  
 Best Local Similarity 44.5%; Pred. No. 0.74;  
 RESULT 234  
 ID ABN87109 standard; cDNA; 557 BP.  
 DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:3.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 5.8%; Score 57.8; DB 6; Length 557;  
 Best Local Similarity 49.7%; Pred. No. 0.91;  
 RESULT 235  
 ID ABZ22145 standard; DNA; 1029 BP.  
 DE Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.  
 PN JP2002247985-A.  
 PD 03-SEP-2002.  
 PA (RIKA) RIKAGAKU KENKYUSHO.  
 Query Match 5.8%; Score 57.4; DB 8; Length 1029;

Best Local Similarity 48.6%; Pred. No. 1;  
RESULT 236  
ID ADO42841 standard; DNA; 1275 BP.  
DE Pseudomonas aurantiaca S-4380 levansucrase encoding sequence.  
PN KR2003005996-A.  
PD 23-JAN-2003.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
PA (REAL-) REAL BIOTECH CO LTD.  
Query Match 5.8%; Score 57.4; DB 11; Length 1275;  
Best Local Similarity 45.6%; Pred. No. 1;  
RESULT 237  
ID ADA4866 standard; DNA; 584 BP.  
DE Banana gene conferring disease resistance in plants.  
PN WO200300906-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.8%; Score 57.2; DB 9; Length 584;  
Best Local Similarity 60.1%; Pred. No. 1.1;  
RESULT 238  
ID ADS73531 standard; cDNA; 73882 BP.  
DE tcp gene cluster.  
Query Match 5.8%; Score 57.2; DB 13; Length 73882;  
Best Local Similarity 44.6%; Pred. No. 1;  
RESULT 239  
ID ADRO1234 standard; DNA; 1113 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF12 protein SPKG DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.8%; Score 57; DB 13; Length 1113;  
Best Local Similarity 43.2%; Pred. No. 1.2;  
RESULT 240  
ID ADRO1210 standard; DNA; 36602 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 1, SEQ ID 1.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.8%; Score 57; DB 13; Length 36602;  
Best Local Similarity 43.2%; Pred. No. 1.1;  
RESULT 241  
ID ADB74275 standard; DNA; 38494 BP.  
DE Mycobacterium leprae DNA #2.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38494;  
Best Local Similarity 50.9%; Pred. No. 1.1;  
RESULT 242  
ID ADB74386 standard; DNA; 38675 BP.  
DE Mycobacterium leprae DNA #20.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38675;  
Best Local Similarity 50.9%; Pred. No. 1.1;  
RESULT 243  
ID AAD14507 standard; DNA; 1182 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme DNA #3.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 244  
ID ADD26448 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus ORF6 DNA.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 245  
ID ADG47793 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus 15 kb gene ORF6 DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 246  
ID ACA62930 standard; DNA; 1182 BP.  
DE DNA encoding clavulanic acid synthesis associated protein #6.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 247  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.7%; Score 56.8; DB 8; Length 2000;  
Best Local Similarity 10.5%; Pred. No. 1.3;  
RESULT 248  
ID AAD14501 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 249  
ID ADD26442 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 11.6 kb genomic fragment.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 250  
ID ADG47787 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 15 kb gene fragment DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 251  
ID ACA62924 standard; DNA; 11604 BP.  
DE Clavulanic acid synthesis associated DNA.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 252  
ID AAO91580 standard; DNA; 15079 BP.  
DE S. clavuligerus cla gene region.  
PN CA2108113-A.  
PD 09-APR-1995.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 2; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 253  
ID AAD14499 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15 Kb genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 254  
ID ACA62922 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15kb genomic DNA sequence.

PN US6514735-B1.  
 PD 04-FEB-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15079;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 255  
 ID ADD26455 standard; DNA; 15120 BP.  
 DE Streptomyces clavuligerus 15 kb genomic fragment.  
 PN US6589775-B1.  
 PD 08-JUL-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 256  
 ID ADG47775 standard; DNA; 15120 BP.  
 DE Streptomyces clavuligerus 15 kb gene.  
 PN US2003207411-A1.  
 PD 06-NOV-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 257  
 ID AAX83426 standard; DNA; 22976 BP.  
 DE Genomic region containing human lipolysis stimulated receptor gene.  
 PN WO9907737-A2.  
 PD 18-FEB-1999.  
 PA (GEST ) GENSET.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 Query Match 5.7%; Score 56.8; DB 2; Length 22976;  
 Best Local Similarity 45.8%; Pred. No. 1.2;  
 RESULT 258  
 ID AAD36874 standard; DNA; 29870 BP.  
 DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
 PN WO2003040372-A2.  
 PD 15-MAY-2003.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 8; Length 29870;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 259  
 ID ABL67924 standard; DNA; 41936 BP.  
 DE Ovary cancer related gene sequence SEQ ID NO:6261.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 5.7%; Score 56.8; DB 6; Length 41936;  
 Best Local Similarity 45.6%; Pred. No. 1.2;  
 RESULT 260  
 ID ADA71360 standard; DNA; 2450 BP.  
 DE Rice gene, SEQ ID 4683.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.7%; Score 56.6; DB 8; Length 2450;  
 Best Local Similarity 43.1%; Pred. No. 1.4;  
 RESULT 261  
 ID ADJ11693 standard; DNA; 3414 BP.  
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 329.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 Query Match 5.7%; Score 56.6; DB 11; Length 3414;

Best Local Similarity 43.1%; Pred. No. 1.4;  
 RESULT 262  
 ID RAD54235 standard; DNA; 25085 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF5 DNA.  
 PN WO200286176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.6; DB 10; Length 25085;  
 Best Local Similarity 45.1%; Pred. No. 1.3;  
 RESULT 263  
 ID RAD54230 standard; DNA; 50543 BP.  
 DE Streptomyces amphibiosporus lactimidomycin DNA.  
 PN WO200286176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.6; DB 10; Length 50543;  
 Best Local Similarity 45.1%; Pred. No. 1.3;  
 RESULT 264  
 ID AAA09696 standard; DNA; 3957 BP.  
 DE HSV-2 immediate early protein ICP4 DNA sequence.  
 PN WO9516779-A1.  
 PD 22-JUN-1995.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 Query Match 5.7%; Score 56.4; DB 5; Length 3957;  
 Best Local Similarity 49.8%; Pred. No. 1.5;  
 RESULT 265  
 ID ADG75121 standard; DNA; 3957 BP.  
 DE Human herpesvirus 2 ICP4 ORF DNA - SEQ ID 193.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.7%; Score 56.4; DB 10; Length 3957;  
 Best Local Similarity 49.8%; Pred. No. 1.5;  
 RESULT 266  
 ID ADI23932 standard; DNA; 15738 BP.  
 DE Streptomyces refuineus 024A locus ORF6.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.4; DB 10; Length 15738;  
 Best Local Similarity 51.7%; Pred. No. 1.4;  
 RESULT 267  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
 Best Local Similarity 49.8%; Pred. No. 1.3;  
 RESULT 268  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
 Best Local Similarity 49.8%; Pred. No. 1.3;  
 RESULT 269  
 ID ABZ66780 standard; DNA; 1143 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 222.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.2; DB 10; Length 1143;  
 Best Local Similarity 45.6%; Pred. No. 1.7;  
 RESULT 270  
 ID AAQ98470 standard; cDNA; 2744 BP.  
 DE MiSP1-containing plasmid pMiss1.  
 PN WO9525165-A1.  
 PD 21-SEP-1995.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.7%; Score 56.2; DB 2; Length 2744;  
 Best Local Similarity 48.0%; Pred. No. 1.6;

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RESULT 271
ID ABL50559 standard; DNA; 14186 BP.
DE Micromonospora carbonacea everminomicin locus nucleotide contig 5.
PN WO200115180-A2.
PD 02-AUG-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match
Best Local Similarity 5.7%; Score 56.2; DB 4; Length 14186;
Pred. No. 1.5;
RESULT 272
ID ABZ66811 standard; DNA; 48221 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 280.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 5.7%; Score 56.2; DB 10; Length 48221;
Pred. No. 1.5;
RESULT 273
ID ACH44935 standard; cDNA; 494 BP.
DE Human foetal brain cDNA #5660.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 5.7%; Score 56; DB 9; Length 494;
Pred. No. 1.8;
RESULT 274
ID ABD15803 standard; DNA; 1098 BP.
DE Pseudomonas aeruginosa polynucleotide #14407.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1098;
Pred. No. 1.8;
RESULT 275
ID ACA42208 standard; DNA; 1473 BP.
DE Prokaryotic essential gene #23865.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 56; DB 8; Length 1473;
Pred. No. 1.8;
RESULT 276
ID ABD15660 standard; DNA; 1566 BP.
DE Pseudomonas aeruginosa polynucleotide #14264.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1566;
Pred. No. 1.8;
RESULT 277
ID ABD15749 standard; DNA; 1908 BP.
DE Pseudomonas aeruginosa polynucleotide #14353.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1908;
Pred. No. 1.8;
RESULT 278
ID AAZ07194 standard; cDNA; 2109 BP.
DE Human lung tumour protein SAL-50 5' cDNA sequence.
PN WO9338973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 56; DB 2; Length 2109;
Pred. No. 1.8;
RESULT 279
ID AAC79147 standard; cDNA; 2109 BP.
DE Human lung tumour-specific cDNA #100.
PN WO200060077-A2.
PD 05-FEB-1998.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 56; DB 3; Length 2109;
Pred. No. 1.8;
RESULT 280
ID AAD33222 standard; cDNA; 2109 BP.
DE Human lung tumour-specific protein SAL-50 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 4; Length 2109;
Pred. No. 1.8;
RESULT 281
ID ADD66461 standard; cDNA; 2109 BP.
DE Human lung tumour-specific related cDNA, SEQ ID NO 153.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 10; Length 2109;
Pred. No. 1.8;
RESULT 282
ID ADE87715 standard; cDNA; 2109 BP.
DE Human lung tumour antigen cDNA #100.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 10; Length 2109;
Pred. No. 1.8;
RESULT 283
ID AAH15254 standard; cDNA; 2142 BP.
DE Human cDNA sequence SEQ ID NO:13376.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 5.7%; Score 56; DB 4; Length 2142;
Pred. No. 1.8;
RESULT 284
ID AAH14344 standard; cDNA; 2198 BP.
DE Human cDNA sequence SEQ ID NO:11730.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 5.7%; Score 56; DB 4; Length 2198;
Pred. No. 1.8;
RESULT 285
ID AAX61221 standard; DNA; 2392 BP.
DE Mouse DNA demethylase, dMTase2, coding sequence.
PN WO9324583-A1.
PD 20-MAY-1999.
PA (UYMC-) UNIV MCGILL.
Query Match
Best Local Similarity 5.7%; Score 56; DB 2; Length 2392;
Pred. No. 1.8;
RESULT 286
ID ADD14651 standard; cDNA; 2392 BP.
DE Human src biomarker polynucleotide SEQ ID NO:45.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 5.7%; Score 56; DB 10; Length 2392;
Pred. No. 1.8;
RESULT 287
ID AAV68520 standard; DNA; 4257 BP.
DE The nucleotide sequence of the Herpes simplex virus ICP4.
PN WO9846637-A2.
PD 22-OCT-1998.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 45.6%; Score 56; DB 2; Length 4257;
Pred. No. 1.7;
RESULT 288
ID AAV10362 standard; cDNA; 4257 BP.
DE Infected cell protein number 4 alpha-4 gene.
PN WO9804709-A2.
PD 05-FEB-1998.
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PA (ARCH-) ARCH DEV CORP.  
Query Match 5.7%; Score 56; DB 2; Length 4257;  
Best Local Similarity 45.6%; Pred. No. 1.7;  
RESULT 289  
ID ADC59464 standard; DNA; 4943 BP.  
DE DNA sequence encoding novel human tyrosine kinase protein.  
PN JF2003024075-A.  
PD 28-JAN-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 5.7%; Score 56; DB 10; Length 4943;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 290  
ID ADQ83709 standard; cDNA; 4943 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #523.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.7%; Score 56; DB 12; Length 4943;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 291  
ID AAD34321 standard; cDNA; 4988 BP.  
DE Human PKIN-24 cDNA.  
PN WO200218557-A2.  
PD 07-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.7%; Score 56; DB 6; Length 4988;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 292  
ID AAG76213 standard; DNA; 12001 BP.  
DE HSV L/ST region.  
PN WO9428156-A1.  
PD 08-DEC-1994.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 5.7%; Score 56; DB 2; Length 12001;  
Best Local Similarity 45.6%; Pred. No. 1.7;  
RESULT 293  
ID AAL02789 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5477.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 294  
ID AAL07516 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 10204.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 295  
ID ABA08208 standard; DNA; 13862 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 296  
ID ABL64982 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3319.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 297  
ID ABL65219 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3556.  
PN WO200194629-A2.

PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 298  
ID ABL97455 standard; DNA; 43058 BP.  
DE Gene #3953 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 299  
ID ADH08262 standard; cDNA; 780 BP.  
DE Fuchsia FMT cDNA #SEQ ID 21.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT. FLOWER DEV PTY LTD.  
Query Match 5.6%; Score 55.8; DB 10; Length 780;  
Best Local Similarity 49.1%; Pred. No. 2;  
RESULT 300  
ID ADA70053 standard; DNA; 1152 BP.  
DE Rice gene. SEQ ID 3376.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.6%; Score 55.8; DB 8; Length 1152;  
Best Local Similarity 45.5%; Pred. No. 1.9;  
RESULT 301  
ID ADJ11565 standard; DNA; 1152 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 201.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
Query Match 5.6%; Score 55.8; DB 11; Length 1152;  
Best Local Similarity 45.5%; Pred. No. 1.9;  
RESULT 302  
ID AAA50254 standard; DNA; 1926 BP.  
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.  
PN WO200047778-A1.  
PD 17-AUG-2000.  
PA (PHAR-) PHARMACOPEDIA INC.  
Query Match 5.6%; Score 55.8; DB 3; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 303  
ID AAF82902 standard; DNA; 1926 BP.  
DE EBV tethering protein EBNA1 encoding DNA.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.6%; Score 55.8; DB 4; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 304  
ID ADK65580 standard; DNA; 1926 BP.  
DE Human herpesvirus 4 nuclear antigen-1 coding sequence.  
PN DE10207135-A1.  
PD 11-SEP-2003.  
PA (EURO-) EUROIMMUN GMBH.  
Query Match 5.6%; Score 55.8; DB 10; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 305  
ID AAA75454 standard; DNA; 2580 BP.

DE Nucleotide sequence of the Epstein Barr nuclear antigen.  
PN US6114111-A.  
PD 05-SEP-2000.  
PA (RIGB-) RIGEL PHARM INC.  
Query Match 5.6%; Score 55.8; DB 3; Length 2580;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 306  
ID AAI64275 standard; DNA; 2580 BP.  
DE Epstein-Barr virus nuclear antigen coding sequence.  
PN US6316223-B1.  
PD 13-NOV-2001.  
PA (RIGB-) RIGEL PHARM INC.  
Query Match 5.6%; Score 55.8; DB 6; Length 2580;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 307  
ID AAX90923 standard; DNA; 5452 BP.  
DE Anti-sense strand of pCMVEBNA plasmid.  
PN WO9947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 5452;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 308  
ID AAZ33778 standard; DNA; 8705 BP.  
DE Vector pShuttle DNA.  
PN WO9950457-A1.  
PD 07-OCT-1999.  
PA (UTAH) UNIV UTAH RES FOUND.  
Query Match 5.6%; Score 55.8; DB 2; Length 8705;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 309  
ID ADM10659 standard; DNA; 8705 BP.  
DE Expression vector pShuttle.  
PN US2004077082-A1.  
PD 22-APR-2004.  
PA (KOEH/) KOEHN R K.  
PA (RUFF/) RUFFNER D E.  
PA (PRAK/) PRAKASH R K.  
Query Match 5.6%; Score 55.8; DB 12; Length 8705;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 310  
ID ADP64415 standard; DNA; 9482 BP.  
DE Vector pCEPpu nucleotide sequence SEQ ID NO:1.  
PN WO2004053137-A2.  
PD 24-JUN-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 9482;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 311  
ID AAZ22301 standard; cDNA; 9551 BP.  
DE cDNA encoding a human trichohyalin (TRHY) protein.  
PN US958752-A.  
PD 28-SEP-1999.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.6%; Score 55.8; DB 2; Length 9551;  
Best Local Similarity 49.9%; Pred. No. 1.8;  
RESULT 312  
ID AAV21683 standard; DNA; 9600 BP.  
DE Vector plasmid pCMVKnitr-EPI.  
PN WO9806437-A2.  
PD 19-FEB-1998.  
PA (CHIR) CHIRON CORP.  
Query Match 5.6%; Score 55.8; DB 2; Length 9600;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 313  
ID ABS71027 standard; DNA; 10285 BP.  
DE pCEP-Xa-FC construct DNA sequence.  
PN WO200256905-A2.  
PD 25-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 314  
ID AAT40348 standard; DNA; 10596 BP.  
DE Plasmid pcisEBON for expression of hepatocyte growth factor.

DE ABS66453 standard; DNA; 10285 BP.  
DE Plasmid pCEP-Xa-FC\* expressing human IgG/protease cleavage site.  
PN WO200256907-A2.  
PD 23-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
PA (MAUR/) MAURER P.  
PA (LECH/) LECHNER F.  
PA (ORTM/) ORTMANN R.  
PA (LUEO/) LUEOEND R.  
PA (STAU/) STAUFENBIEL M.  
PA (FREY/) FREY P.  
Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 315  
ID ADL67154 standard; DNA; 10330 BP.  
DE Plasmid pCEP-mb7-H6(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:24.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10330;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 316  
ID AAZ22248 standard; DNA; 10380 BP.  
DE Nucleotide sequence of pCEP4 vector.  
PN WO9947921-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10380;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 317  
ID ADL67152 standard; DNA; 10477 BP.  
DE Plasmid pCEP-mb7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:22.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10477;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 318  
ID ADL67150 standard; DNA; 10516 BP.  
DE Plasmid pCEP-hsb7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:20.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10516;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 319  
ID ADL67148 standard; DNA; 10561 BP.  
DE Plasmid pCEP-hsb7-H4(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:18.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10561;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 320  
ID AAQ51731 standard; DNA; 10596 BP.  
DE Plasmid pcisEBON for subcloning huHGF variants.  
PN WO9323541-A1.  
PD 25-NOV-1993.  
PA (GETH) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 321  
ID AAX15650 standard; DNA; 10596 BP.  
DE Nucleotide sequence of plasmid pcis.EBON.  
PN US5879910-A.  
PD 09-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 322  
ID AAT40348 standard; DNA; 10596 BP.  
DE Plasmid pcisEBON for expression of hepatocyte growth factor.



PN US5547856-A.  
 PD 20-AUG-1996.  
 PA (GETH ) GENENTECH INC.  
 Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 323  
 ID ADL67175 standard; DNA; 10615 BP.  
 DE Plasmid pCEP-hbB7-H6-COMP-FLAG nucleotide sequence SEQ ID NO:45.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10615;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 324  
 ID ADL67153 standard; DNA; 10774 BP.  
 DE Plasmid pCEP-mB7-H6 (ECD) -FC nucleotide sequence SEQ ID NO:23.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10774;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 325  
 ID ADL67151 standard; DNA; 10921 BP.  
 DE Plasmid pCEP-mB7-H5 (ECD) -FC nucleotide sequence SEQ ID NO:21.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10921;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 326  
 ID ADL67149 standard; DNA; 10961 BP.  
 DE Plasmid pCEP-hbB7-H5 (ECD) -FC nucleotide sequence SEQ ID NO:19.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10961;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 327  
 ID ADL67147 standard; DNA; 11006 BP.  
 DE Plasmid pCEP-hbB7-H4 (ECD) -FC nucleotide sequence SEQ ID NO:17.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11006;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 328  
 ID ADL67176 standard; DNA; 11059 BP.  
 DE Plasmid pCEP-hbB7-H6-Xal-FC\* nucleotide sequence SEQ ID NO:46.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11059;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 329  
 ID ADL2379 standard; DNA; 11693 BP.  
 DE Vector pCMR2.  
 PN WO2004065561-A2.  
 PD 05-AUG-2004.  
 PA (PTCT-) PTC THERAPEUTICS INC.  
 Query Match 5.6%; Score 55.8; DB 13; Length 11693;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 330  
 ID ADO07395 standard; DNA; 11924 BP.  
 DE Modified human hepsin plasmid pCEP4W/hep36.  
 PN WO2004033630-A2.  
 PD 22-APR-2004.  
 PA (SCHD ) SCHERING AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11924;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 331  
 ID ADO07394 standard; DNA; 12242 BP.  
 DE Modified human hepsin plasmid pCEP4W/hepEK.  
 PN WO2004033630-A2.  
 PD 19-FEB-2004.

PD 22-APR-2004.  
 PA (SCHD ) SCHERING AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 12242;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 332  
 ID AAA59553 standard; DNA; 16080 BP.  
 DE DNA clone pCEK Cl.27 encoding a human beta-secretase enzyme.  
 PN WO200047618-A2.  
 PD 17-AUG-2000.  
 PA (ELAN-) ELAN PHARM INC.  
 Query Match 5.6%; Score 55.8; DB 3; Length 16080;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 333  
 ID ADL71910 standard; cDNA; 17753 BP.  
 DE Expression vector pCytTs-OPE.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 17753;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 334  
 ID ADN12161 standard; DNA; 172281 BP.  
 DE Epstein-Barr virus genome B95-8.  
 PN WO2004027036-A2.  
 PD 01-APR-2004.  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 Query Match 5.6%; Score 55.8; DB 12; Length 172281;  
 Best Local Similarity 46.7%; Pred. No. 1.7;  
 RESULT 335  
 ID AAH03407 standard; cDNA; 726 BP.  
 DE Human cDNA clone (5'-primer) SEQ ID NO:242.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.6%; Score 55.6; DB 4; Length 726;  
 Best Local Similarity 53.5%; Pred. No. 2.1;  
 RESULT 336  
 ID AAL61200 standard; DNA; 1026 BP.  
 DE Actinosynnema pretiosum glucose 1-dehydrogenase gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 5.6%; Score 55.6; DB 8; Length 1026;  
 Best Local Similarity 46.2%; Pred. No. 2.1;  
 RESULT 337  
 ID ABD11061 standard; DNA; 774 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9665.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.6%; Score 55.4; DB 11; Length 774;  
 Best Local Similarity 45.2%; Pred. No. 2.3;  
 RESULT 338  
 ID ABX56066 standard; DNA; 3033 BP.  
 DE M. echinospora calicheamicin biosynthesis gene orfVI.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.6%; Score 55.4; DB 8; Length 3033;  
 Best Local Similarity 44.4%; Pred. No. 2.2;  
 RESULT 339  
 ID AAQ46806 standard; DNA; 29879 BP.  
 DE eryA region of S. erythraea chromosome.  
 PN WO9313663-A1.  
 PD 22-JUL-1993.  
 PA (ABBO ) ABBOTT LAB.  
 Query Match 5.6%; Score 55.4; DB 2; Length 29879;  
 Best Local Similarity 49.3%; Pred. No. 2.1;  
 RESULT 340  
 ID ADM45913 standard; DNA; 84428 BP.  
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
 PN JP2004049100-A.  
 PD 19-FEB-2004.

PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.6%; Score 55.4; DB 12; Length 84428;  
Best Local Similarity 48.3%; Pred. No. 2;  
RESULT 341  
ID AB278139 standard; cDNA; 1679 BP.  
DE Human cancer-related coding sequence, 187P3F2.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1679;  
Best Local Similarity 46.9%; Pred. No. 2.4;  
RESULT 342  
ID ACC00700 standard; cDNA; 1885 BP.  
DE Orvza sativa oil trait related cDNA sequence SEQ ID NO:149.  
PN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1885;  
Best Local Similarity 47.8%; Pred. No. 2.4;  
RESULT 343  
ID ACA38134 standard; DNA; 1887 BP.  
DE Prokaryotic essential gene #19791.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1887;  
Best Local Similarity 45.0%; Pred. No. 2.4;  
RESULT 344  
ID AAA63350 standard; DNA; 21185 BP.  
DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.6%; Score 55.2; DB 3; Length 21185;  
Best Local Similarity 50.3%; Pred. No. 2.2;  
RESULT 345  
ID AAA63348 standard; DNA; 63164 BP.  
DE Streptomyces globisporus C-1027 gene cluster.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.6%; Score 55.2; DB 3; Length 63164;  
Best Local Similarity 50.3%; Pred. No. 2.2;  
RESULT 346  
ID ADK13938 standard; DNA; 2559 BP.  
DE Human methyl-CpG-binding protein DNA #11.  
PN US6709817-B1.  
PD 23-MAR-2004.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 347  
ID ADQ19517 standard; DNA; 2559 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2336.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 348  
ID ADQ84224 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1038.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 349  
ID ADQ83456 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #270.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 350  
ID ADQ86702 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3577.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 351  
ID ADQ84685 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1499.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 352  
ID ADQ85601 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2415.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 353  
ID ACN40385 standard; cDNA; 2559 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326502, SEQ ID NO:5131.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 354  
ID ADM80034 standard; DNA; 30943 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 1.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.6%; Score 55; DB 12; Length 30943;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 355  
ID ADN97550 standard; DNA; 30943 BP.  
DE S anobofaciens spiramycin biosynthetic enzyme genomic region.  
PN WO2004033889-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 5.6%; Score 55; DB 12; Length 30943;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 356  
ID AAV21187 standard; DNA; 53789 BP.  
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS ) NOVARTIS AG.  
Query Match 5.6%; Score 55; DB 2; Length 53789;  
Best Local Similarity 47.9%; Pred. No. 2.4;  
RESULT 357  
ID AAA68012 standard; DNA; 594 BP.

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DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.
PN WO200022099-A1.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 358
ID ADD41762 standard; DNA; 594 BP.
DE O-methyl transferase DNA #11.
PN US2003131373-A1.
PA (BLOK-) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 359
ID AAV23843 standard; DNA; 607 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 360
ID AAZ06844 standard; cDNA; 607 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.
PN US952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 361
ID AAA69594 standard; cDNA; 607 BP.
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.9%; Pred. No. 2.9;
RESULT 362
ID AAA67930 standard; DNA; 607 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 363
ID ADD41680 standard; DNA; 607 BP.
DE O-methyl transferase DNA #3.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK-) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 607;
Best Local Similarity 57.8%; Pred. No. 2.9;
RESULT 364
ID ABZ77318 standard; cDNA; 2684 BP.
DE Nucleotide sequence of a murine ACDK3 polypeptide.
PN WO2003008557-A2.
PD 30-JAN-2003.
PA (OYFL) UNIV FLORIDA.
Query Match 5.5%; Score 54.8; DB 8; Length 2684;
Best Local Similarity 50.6%; Pred. No. 2.8;
RESULT 365
ID ADA69536 standard; DNA; 980 BP.
DE Rice gene, SEQ ID 2859.
PN WO2003000898-A1.

PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 54.6; DB 8; Length 980;
Best Local Similarity 48.5%; Pred. No. 3.1;
RESULT 366
ID ADT43292 standard; cDNA; 1221 BP.
DE Bacterial polynucleotide #18043.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 54.6; DB 13; Length 1221;
Best Local Similarity 49.1%; Pred. No. 3.1;
RESULT 367
ID RAV19115 standard; DNA; 1308 BP.
DE Human secreted apoptosis-related protein hSARP2 DNA.
PN WO9813493-A2.
PD 02-APR-1998.
PA (LXRE-) LXR BIOTECHNOLOGY INC.
Query Match 5.5%; Score 54.6; DB 2; Length 1308;
Best Local Similarity 45.5%; Pred. No. 3;
RESULT 368
ID ADT44641 standard; cDNA; 789 BP.
DE Bacterial polynucleotide #19392.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 54.4; DB 13; Length 789;
Best Local Similarity 50.4%; Pred. No. 3.3;
RESULT 369
ID ADF31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 39949;
Best Local Similarity 45.6%; Pred. No. 3.2;
RESULT 370
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 48200;
Best Local Similarity 45.6%; Pred. No. 3.2;
RESULT 371
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 65140;
Best Local Similarity 51.9%; Pred. No. 3.2;
RESULT 372
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
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PN WO200159126-A2.  
PD 16-APR-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTP) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAEVRIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 5.5%; Score 54.2; DB 4; Length 125401;  
Best Local Similarity 51.9%; Pred. No. 3.1;  
RESULT 373  
ID ACA23654 standard; DNA; 897 BP.  
DE Prokaryotic essential gene #5311.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.5%; Score 54; DB 8; Length 897;  
Best Local Similarity 44.4%; Pred. No. 3.9;  
RESULT 374  
ID ACC00684 standard; cDNA; 1118 BP.  
DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:117.  
PN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.5%; Score 54; DB 8; Length 1118;  
Best Local Similarity 46.2%; Pred. No. 3.9;  
RESULT 375  
ID ADC33596 standard; cDNA; 1118 BP.  
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 101).  
PN WO2003001902-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.5%; Score 54; DB 10; Length 1118;  
Best Local Similarity 46.2%; Pred. No. 3.9;  
RESULT 376  
ID ABK12029 standard; DNA; 1217 BP.  
DE DNA encoding aminoglycoside multidrug resistance protein.  
PN KE99074514-A.  
PD 05-OCT-1999.  
PA (DONG-) DONGWHA PHARM IND CO LTD.  
PA (SUHJ/) SUH J W.  
Query Match 5.5%; Score 54; DB 3; Length 1217;  
Best Local Similarity 46.3%; Pred. No. 3.8;  
RESULT 377  
ID AAV67187 standard; DNA; 1380 BP.  
DE M. luteus salt-resistant glutaminase encoding DNA.  
PN JP10243787-A.  
PD 14-SEP-1998.  
PA (FUND-) FUNDOKIN SHOYU KK.  
Query Match 5.5%; Score 54; DB 2; Length 1380;  
Best Local Similarity 47.1%; Pred. No. 3.8;  
RESULT 378  
ID AAS85408 standard; cDNA; 4056 BP.  
DE DNA encoding novel human diagnostic protein #21212.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 54; DB 5; Length 4056;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 379  
ID ADQ85821 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2689.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 12; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 380  
ID ADQ86986 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3861.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 12; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 381  
ID ADQ83667 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #481.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 13; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 382  
ID ACN40643 standard; cDNA; 4378 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326729, SEQ ID NO:5544.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 5.5%; Score 54; DB 13; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 383  
ID ABZ11999 standard; cDNA; 4530 BP.  
DE Human polynucleotide SEQ ID NO 881.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 54; DB 6; Length 4530;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 384  
ID ADM44517 standard; cDNA; 4530 BP.  
DE Novel human arginine-rich protein cDNA #881.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Query Match 5.5%; Score 54; DB 12; Length 4530;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 385  
ID AAA31496 standard; DNA; 451 BP.  
DE Plant microsatellite marker #457.  
PN WO9967421-A1.  
PD 29-DEC-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
Query Match 5.4%; Score 53.8; DB 3; Length 451;  
Best Local Similarity 57.1%; Pred. No. 4.3;  
RESULT 386  
ID ADM80038 standard; DNA; 1272 BP.  
DE Spiramycin biosynthesis orf2\*c, SEQ ID 5.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
Best Local Similarity 48.0%; Pred. No. 4.1;  
RESULT 387  
ID ADN97554 standard; DNA; 1272 BP.  
DE S ambiofaciens spiramycin biosynthetic gene ORF2\*c.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.

PA (CNRS ) CNRS.  
Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
Best Local Similarity 48.0%; Pred. No. 4.1;  
RESULT 388  
ID ABA95453 standard; DNA; 2082 BP.  
DE Thermus thermophilus uvrd coding sequence.  
PN WO200173052-A2.  
PD 04-OCT-2001.  
PA (MCHE/) MCHENRY C S.  
Query Match 5.4%; Score 53.8; DB 4; Length 2082;  
Best Local Similarity 48.1%; Pred. No. 4.1;  
RESULT 389  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
Best Local Similarity 48.0%; Pred. No. 3.9;  
RESULT 390  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
Best Local Similarity 48.0%; Pred. No. 3.9;  
RESULT 391  
ID AAT80414 standard; DNA; 44377 BP.  
DE Platenolide synthase gene cluster.  
PN EP791655-A2.  
PD 27-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
Best Local Similarity 48.0%; Pred. No. 3.8;  
RESULT 392  
ID AAT78508 standard; DNA; 44377 BP.  
DE Platenolide synthase gene cluster.  
PN EP791656-A2.  
PD 27-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
Best Local Similarity 48.0%; Pred. No. 3.8;  
RESULT 393  
ID ADK16023 standard; DNA; 64492 BP.  
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
PN US2004053274-A1.  
PD 18-MAR-2004.  
PA (TOKD ) TOKYO INST TECHNOLOGY.  
Query Match 5.4%; Score 53.8; DB 12; Length 64492;  
Best Local Similarity 50.6%; Pred. No. 3.7;  
RESULT 394  
ID AAD08215 standard; DNA; 114793 BP.  
DE Human genome from BAC clone, hbm168.  
PN WO200142434-A1.  
PD 14-JUN-2001.  
PA (MERI ) MERCK & CO INC.  
Query Match 5.4%; Score 53.8; DB 4; Length 114793;  
Best Local Similarity 47.2%; Pred. No. 3.7;  
RESULT 395  
ID AAZ32020 standard; DNA; 38734 BP.  
DE Human METH1 related EST AL021529.  
PN WO9937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
Query Match 5.4%; Score 53.6; DB 2; Length 38734;  
Best Local Similarity 44.9%; Pred. No. 4.1;  
RESULT 396  
ID AAC90077 standard; DNA; 38734 BP.

DE AL021529 cDNA clone.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Query Match 5.4%; Score 53.6; DB 5; Length 38734;  
Best Local Similarity 44.9%; Pred. No. 4.1;  
RESULT 397  
ID AAL61221 standard; DNA; 1554 BP.  
DE Actinosynnema pretiosum transcriptional activator gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 5.4%; Score 53.4; DB 8; Length 1554;  
Best Local Similarity 48.5%; Pred. No. 4.8;  
RESULT 398  
ID AAZ50651 standard; cDNA; 2248 BP.  
DE Corn starch synthase SSB DNA fragment inserted in pSPB47.  
PN WO200006755-A2.  
PD 10-FEB-2000.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 5.4%; Score 53.4; DB 3; Length 2248;  
Best Local Similarity 50.2%; Pred. No. 4.8;  
RESULT 399  
ID AAQ14183 standard; cDNA; 2338 BP.  
DE N.clavipes dragline silk protein coding sequence.  
PN EP452925-A.  
PD 23-OCT-1991.  
PA (UYWY-) UNIV OF WYOMING.  
Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.8;  
RESULT 400  
ID AAV23249 standard; cDNA; 2338 BP.  
DE Nephila clavipes spider silk protein encoding cDNA.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.8;  
RESULT 401  
ID AAZ36195 standard; cDNA; 2338 BP.  
DE N. clavipes spider silk protein 1 encoding cDNA.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.4%; Score 53.4; DB 3; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.8;  
RESULT 402  
ID AAI57831 standard; cDNA; 4176 BP.  
DE Human polynucleotide SEQ ID NO 34.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSE INC.  
Query Match 5.4%; Score 53.4; DB 4; Length 4176;  
Best Local Similarity 48.9%; Pred. No. 4.7;  
RESULT 403  
ID AAL61225 standard; DNA; 11905 BP.  
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster II.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 5.4%; Score 53.4; DB 8; Length 11905;  
Best Local Similarity 48.5%; Pred. No. 4.5;  
RESULT 404  
ID ADL15447 standard; DNA; 85915 BP.

DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.  
PN WO2004018703-A2.  
PD 04-MAR-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.4%; Score 53.4; DB 13; Length 85915;  
Best Local Similarity 46.2%; Pred. No. 4.3;  
RESULT 405  
Query Match 5.4%; Score 53.4; DB 11; Length 110000;  
Best Local Similarity 45.7%; Pred. No. 4.3;  
RESULT 406  
ID ACA26842 standard; DNA; 900 BP.  
DE Prokaryotic essential gene #8499.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.4%; Score 53.2; DB 8; Length 900;  
Best Local Similarity 49.6%; Pred. No. 5.3;  
RESULT 407  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PN WO200277179-A2.  
PD 03-OCT-2002.  
PA (REGC) UNIV CALIFORNIA.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 5.4%; Score 53.2; DB 10; Length 135638;  
Best Local Similarity 47.9%; Pred. No. 4.6;  
RESULT 408  
ID ADT42272 standard; cDNA; 1695 BP.  
DE Bacterial polynucleotide #17023.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.4%; Score 53; DB 13; Length 1695;  
Best Local Similarity 46.2%; Pred. No. 5.6;  
RESULT 409  
ID ADJ27274 standard; cDNA; 1929 BP.  
DE Mouse HSP70.1 coding sequence.  
PN WO2003061684-A2.  
PD 31-JUL-2003.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 5.4%; Score 53; DB 11; Length 1929;  
Best Local Similarity 44.3%; Pred. No. 5.6;  
RESULT 410  
ID ADT42037 standard; cDNA; 3444 BP.  
DE Bacterial polynucleotide #16788.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.4%; Score 53; DB 13; Length 3444;  
Best Local Similarity 48.5%; Pred. No. 5.5;  
RESULT 411  
ID AAT45060 standard; cDNA; 1236 BP.  
DE Maize Tst2 cDNA nucleotide sequence.  
PN WO9505732-A1.  
PD 02-MAR-1995.  
PA (UYIA) UNIV YALE.  
Query Match 5.3%; Score 52.8; DB 2; Length 1236;  
Best Local Similarity 47.3%; Pred. No. 6.1;  
RESULT 412  
ID ACA38386 standard; DNA; 2712 BP.  
DE Prokaryotic essential gene #20043.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.8; DB 8; Length 2712;  
Best Local Similarity 46.8%; Pred. No. 6;  
RESULT 413  
ID ACA40526 standard; DNA; 2715 BP.  
DE Prokaryotic essential gene #22183.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.8; DB 8; Length 2715;  
Best Local Similarity 46.8%; Pred. No. 6;  
RESULT 414  
ID ADP30617 standard; DNA; 34719 BP.  
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.  
PN JP2004180638-A.  
PD 02-JUL-2004.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.3%; Score 52.8; DB 12; Length 34719;  
Best Local Similarity 50.4%; Pred. No. 5.6;  
RESULT 415  
Query Match 5.3%; Score 52.8; DB 4; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 5.4;  
RESULT 416  
Query Match 5.3%; Score 52.8; DB 4; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 5.4;  
RESULT 417  
ID ADJ39074 standard; cDNA; 447 BP.  
DE Plant cDNA #74.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZERBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
Query Match 5.3%; Score 52.6; DB 12; Length 447;  
Best Local Similarity 47.4%; Pred. No. 6.8;  
RESULT 418  
ID ACA03588 standard; DNA; 1275 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #71.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
Query Match 5.3%; Score 52.6; DB 8; Length 1275;  
Best Local Similarity 43.1%; Pred. No. 6.6;  
RESULT 419  
ID ADC13276 standard; DNA; 1275 BP.  
DE DNA of HIV construct TatRevNef-opt-native\_ZA SEQ ID NO 55.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 5.3%; Score 52.6; DB 10; Length 1275;  
Best Local Similarity 43.1%; Pred. No. 6.6;  
RESULT 420  
ID ACA38006 standard; DNA; 1368 BP.  
DE Prokaryotic essential gene #19663.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.6; DB 8; Length 1368;  
Best Local Similarity 43.9%; Pred. No. 6.6;  
RESULT 421  
ID ADG73813 standard; cDNA; 2466 BP.  
DE Human variant subtilase-like serine protease polynucleotide.  
PN WO2003106667-A2.  
PD 24-DEC-2003.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 5.3%; Score 52.6; DB 12; Length 2466;

Best Local Similarity 45.8%; Pred. No. 6.5;  
RESULT 422  
ID AAH26500 standard; cDNA; 2561 BP.  
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.3%; Score 52.6; DB 5; Length 2561;  
Best Local Similarity 47.3%; Pred. No. 6.4;  
RESULT 423  
ID ADR07733 standard; cDNA; 2778 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1239.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.3%; Score 52.6; DB 13; Length 2778;  
Best Local Similarity 45.8%; Pred. No. 6.4;  
RESULT 424  
ID ACA03550 standard; DNA; 3624 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #33.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
Query Match 5.3%; Score 52.6; DB 8; Length 3624;  
Best Local Similarity 43.1%; Pred. No. 6.4;  
RESULT 425  
ID ADC13268 standard; DNA; 3624 BP.  
DE DNA of HIV construct p2PolTatRevNef-opt-native\_C SEQ ID NO 47.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
PA (OYST-) UNIV STELLENBOSCH.  
Query Match 5.3%; Score 52.6; DB 10; Length 3624;  
Best Local Similarity 43.1%; Pred. No. 6.4;  
RESULT 426  
ID ADG73810 standard; cDNA; 3705 BP.  
DE Human subtilase-like serine protease polynucleotide.  
PN WO2003106667-A2.  
PD 24-DEC-2003.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 5.3%; Score 52.6; DB 12; Length 3705;  
Best Local Similarity 45.8%; Pred. No. 6.4;  
RESULT 427  
ID ADO56090 standard; DNA; 4199 BP.  
DE Thermus thermophilus VI ATPase gene operon.  
PN WO2004046350-A1.  
PD 03-JUN-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
Query Match 5.3%; Score 52.6; DB 12; Length 4199;  
Best Local Similarity 55.1%; Pred. No. 6.4;  
RESULT 428  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.8;  
RESULT 429  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.8;  
RESULT 430  
ID ABL61294 standard; DNA; 1227 BP.  
DE N. uniformis p-hydroxymandelate oxidase DNA.  
PN WO200234921-A2.  
PD 02-MAY-2002.  
PA (STAM) DSM NV.  
PA (STAM) DSM BIOTECH GMBH.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Query Match 5.3%; Score 52.4; DB 6; Length 1227;  
Best Local Similarity 45.0%; Pred. No. 7.1;  
RESULT 431  
ID ABL69280 standard; DNA; 1891 BP.  
DE Prostate cancer related gene sequence SEQ ID NO:7617.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;

Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 432  
ID ABV94243 standard; cDNA; 1891 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:234.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 433  
ID ABK84580 standard; cDNA; 1891 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1151.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 434  
ID ADS88586 standard; cDNA; 1891 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:129.  
PN WO2004035785-A1.  
PD 29-APR-2004.  
PA (NIGA) NGK INSULATORS LTD.  
Query Match 5.3%; Score 52.4; DB 13; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 435  
ID AA53918 standard; cDNA; 3978 BP.  
DE Adenyl cyclase type I-C1 C1 alpha domain coding sequence.  
PN US6107076-A.  
PD 22-AUG-2000.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 5.3%; Score 52.4; DB 3; Length 3978;  
Best Local Similarity 47.8%; Pred. No. 6.9;  
RESULT 436  
ID ADL15099 standard; DNA; 5117 BP.  
DE Human male brain KIA0533 protein DNA for cancer treatment.  
PN WO2003088268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 5.3%; Score 52.4; DB 10; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 437  
ID ADN95659 standard; DNA; 5117 BP.  
DE Human BRC/LEC-related gene sequence SeqID583.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 5.3%; Score 52.4; DB 11; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 438  
ID ADR24163 standard; DNA; 5117 BP.  
DE Breast cancer prognosis marker #24.  
PN WO2004055545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 5.3%; Score 52.4; DB 13; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 439  
ID ABQ93882 standard; DNA; 5204 BP.  
DE Human laminin alpha-5-like NOVID DNA, SEQ ID NO:7.  
PN WO200253742-A2.  
PD 11-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.3%; Score 52.4; DB 6; Length 5204;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 440  
ID ADM87490 standard; cDNA; 5403 BP.  
DE Human EST derived nucleotide sequence SEQ ID NO:583.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.

Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 5403;  
RESULT 441  
ID AAI58165 standard; cDNA; 5640 BP.  
DE Human polynucleotide SEQ ID NO 368.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 4; Length 5640;  
RESULT 442  
ID ADQ98371 standard; cDNA; 5640 BP.  
DE DNA encoding human GPCR-like protein seqid 41.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 5; Length 5640;  
RESULT 443  
ID ADB48131 standard; cDNA; 5640 BP.  
DE Novel human cDNA SEQ ID NO 41.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRNA/) DRWANAC R T.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 9; Length 5640;  
RESULT 444  
ID ABO72930 standard; cDNA; 8296 BP.  
DE Human laminin alpha 5 2743 N-terminal amino acids cDNA SEQ ID NO:35.  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PA (BIOS-) BIOSTRATUM INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 8296;  
RESULT 445  
ID AAD27805 standard; DNA; 11091 BP.  
DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #2.  
PN WO200198342-A1.  
PD 27-DEC-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11091;  
RESULT 446  
ID AAD27804 standard; DNA; 11118 BP.  
DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #1.  
PN WO200198342-A1.  
PD 27-DEC-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11118;  
RESULT 447  
ID AAD55817 standard; DNA; 11238 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #7.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 10; Length 11238;  
RESULT 448  
ID ACN40816 standard; cDNA; 11344 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326869, SEQ ID NO:5846.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 13; Length 11344;

Best Local Similarity 50.0%; Pred. No. 6.7;  
RESULT 449  
ID ABO72906 standard; cDNA; 11350 BP.  
DE Human laminin alpha 5 encoding cDNA SEQ ID NO:1.  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PA (BIOS-) BIOSTRATUM INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11350;  
RESULT 450  
ID ADI28066 standard; cDNA; 11367 BP.  
DE ECMCAD gene clone 6382722CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11367;  
RESULT 451  
ID ADN04477 standard; cDNA; 11426 BP.  
DE Antipsoriatic cDNA sequence #440.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 11426;  
RESULT 452  
ID ADM87010 standard; cDNA; 11640 BP.  
DE Human protein encoding cDNA SEQ ID NO:103.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 11640;  
RESULT 453  
ID AAD55810 standard; DNA; 60196 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 10; Length 60196;  
RESULT 454  
ID AAC47161 standard; DNA; 738 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 52.2; DB 3; Length 738;  
RESULT 455  
ID AAC47930 standard; DNA; 833 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 52.2; DB 3; Length 833;  
RESULT 456  
ID AAT95356 standard; DNA; 2004 BP.  
DE Nephila clavipes spider silk protein 2 Kb DNA sequence.  
PN WO9708315-A1.  
PD 06-MAR-1997.  
PA (BASE/) BASEL R M.  
PA (ELIO/) ELION G R.  
Query Match  
Best Local Similarity 47.8%; Pred. No. 7.6;  
RESULT 457  
ID ADSS6080 standard; cDNA; 2505 BP.  
DE Bacterial polynucleotide #8067.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.



PA (GOLD/) GOLDMAN B S.  
Query Match 5.3%; Score 52.2; DB 13; Length 2505;  
Best Local Similarity 48.3%; Pred. No. 7.5;  
RESULT 458  
ID ACA38157 standard; DNA; 2757 BP.  
DE Prokaryotic essential gene #19814.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.2; DB 8; Length 2757;  
Best Local Similarity 46.7%; Pred. No. 7.5;  
RESULT 459  
ID ADC30607 standard; cDNA; 4542 BP.  
DE Human novel cDNA sequence, SEQ ID NO:689.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.3%; Score 52.2; DB 10; Length 4542;  
Best Local Similarity 47.8%; Pred. No. 7.4;  
RESULT 460  
ID AAD54236 standard; DNA; 6297 BP.  
DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.  
PN WO20028176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.3%; Score 52.2; DB 10; Length 6297;  
Best Local Similarity 47.2%; Pred. No. 7.3;  
RESULT 461  
ID ABQ77491 standard; DNA; 67459 BP.  
DE S. aurantiaca DNA containing sti gene cluster.  
PN DE10128661-A1.  
PD 19-DEC-2002.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Query Match 5.3%; Score 52.2; DB 8; Length 67459;  
Best Local Similarity 43.5%; Pred. No. 6.9;  
RESULT 462  
ID ADO59147 standard; DNA; 70782 BP.  
DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.  
PN DE10241152-A1.  
PD 18-MAR-2004.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Query Match 5.3%; Score 52.2; DB 12; Length 70782;  
Best Local Similarity 44.2%; Pred. No. 6.9;  
RESULT 463  
ID ACF06127 standard; DNA; 1218 BP.  
DE Bacterial P450 enzyme encoding DNA SEQ ID NO:37.  
PN WO2003052050-A2.  
PD 26-JUN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 5.3%; Score 52; DB 9; Length 1218;  
Best Local Similarity 50.6%; Pred. No. 8.3;  
RESULT 464  
ID ABD03077 standard; DNA; 1248 BP.  
DE Pseudomonas aeruginosa polynucleotide #1691.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.3%; Score 52; DB 11; Length 1248;  
Best Local Similarity 50.4%; Pred. No. 8.3;  
RESULT 465  
ID ABD02833 standard; DNA; 1302 BP.  
DE Pseudomonas aeruginosa polynucleotide #1437.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.3%; Score 52; DB 11; Length 1302;  
Best Local Similarity 50.4%; Pred. No. 8.3;  
RESULT 466  
ID ABL40020 standard; DNA; 1491 BP.  
DE Synthetic gag polynucleotide sequence SEQ ID NO:99.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR ) CHIRON CORP.

PA (UYST-) UNIV STELLENBOSCH.  
Query Match 5.3%; Score 52; DB 6; Length 1491;  
Best Local Similarity 46.4%; Pred. No. 8.2;  
RESULT 467  
ID ADM73833 standard; DNA; 1491 BP.  
DE HIV-1 polynucleotide #68.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBURG E J V.  
Query Match 5.3%; Score 52; DB 12; Length 1491;  
Best Local Similarity 46.4%; Pred. No. 8.2;  
RESULT 468  
ID ABD02890 standard; DNA; 1956 BP.  
DE Pseudomonas aeruginosa polynucleotide #1494.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.3%; Score 52; DB 11; Length 1956;  
Best Local Similarity 50.4%; Pred. No. 8.2;  
RESULT 469  
ID ADP69917 standard; DNA; 3078 BP.  
DE Mammalian codon optimised E. coli LacZ gene.  
PN WO2004050872-A1.  
PD 17-JUN-2004.  
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
Query Match 5.3%; Score 52; DB 12; Length 3078;  
Best Local Similarity 45.4%; Pred. No. 8.1;  
RESULT 470  
ID ABD11785 standard; DNA; 498 BP.  
DE Pseudomonas aeruginosa polynucleotide #10389.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 498;  
Best Local Similarity 46.5%; Pred. No. 9.2;  
RESULT 471  
ID ABD11976 standard; DNA; 561 BP.  
DE Pseudomonas aeruginosa polynucleotide #10580.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 561;  
Best Local Similarity 46.5%; Pred. No. 9.1;  
RESULT 472  
ID ABD12080 standard; DNA; 1053 BP.  
DE Pseudomonas aeruginosa polynucleotide #10684.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 1053;  
Best Local Similarity 46.5%; Pred. No. 9;  
RESULT 473  
ID ACA27206 standard; DNA; 1227 BP.  
DE Prokaryotic essential gene #8863.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.8; DB 8; Length 1227;  
Best Local Similarity 46.9%; Pred. No. 8.9;  
RESULT 474  
ID ABD04500 standard; DNA; 1233 BP.  
DE Pseudomonas aeruginosa polynucleotide #3104.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 1233;  
Best Local Similarity 48.2%; Pred. No. 8.9;  
RESULT 475  
ID ACN44729 standard; cDNA; 1253 BP.  
DE Mouse mRNA sequence mCT7005.

PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGE-) SAGRES DISCOVERY.  
Query Match 5.2%; Score 51.8; DB 11; Length 1253;  
Best Local Similarity 47.6%; Pred. No. 8.9;  
RESULT 476  
ID ADT44764 standard; cDNA; 1347 BP.  
DE Bacterial polynucleotide #19515.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1347;  
Best Local Similarity 46.3%; Pred. No. 8.9;  
RESULT 477  
ID ABD04263 standard; DNA; 1386 BP.  
DE Pseudomonas aeruginosa polynucleotide #2867.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 1386;  
Best Local Similarity 48.2%; Pred. No. 8.9;  
RESULT 478  
ID ADS64227 standard; cDNA; 1659 BP.  
DE Bacterial polynucleotide #16214.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1659;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 479  
ID ADS63845 standard; cDNA; 1677 BP.  
DE Bacterial polynucleotide #15832.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1677;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 480  
ID ADS63476 standard; cDNA; 1677 BP.  
DE Bacterial polynucleotide #15463.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1677;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 481  
ID ABZ81830 standard; DNA; 2072 BP.  
DE Receptor FZD10 nucleic acid sequence.  
PN WO2003012082-A2.  
PD 13-FEB-2003.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2072;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 482  
ID AAD17401 standard; DNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP) gene.  
PN WO200164717-A1.

PD 07-SEP-2001.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 5.2%; Score 51.8; DB 4; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 483  
ID ABV73022 standard; cDNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP)-1 encoding cDNA.  
PN WO200255547-A2.  
PD 18-JUL-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (SVIN-) ST VINCENTS INST MEDICAL RES.  
Query Match 5.2%; Score 51.8; DB 6; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 484  
ID ABX75330 standard; cDNA; 2075 BP.  
DE Human cDNA encoding Frizzled-8.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 485  
ID AAD52558 standard; DNA; 2075 BP.  
DE FRP DNA.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 486  
ID ADC71197 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein (sFRP) cDNA.  
PN US6600018-B1.  
PD 29-JUL-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.2%; Score 51.8; DB 10; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 487  
ID ADH43319 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein 1 (sFRP-1) cDNA.  
PN US2003187223-A1.  
PD 02-OCT-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (UYMA-) UNIV MASSACHUSETTS.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.2%; Score 51.8; DB 12; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 488  
ID ACA43985 standard; DNA; 2145 BP.  
DE Prokaryotic essential gene #25642.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.8; DB 8; Length 2145;  
Best Local Similarity 44.4%; Pred. No. 8.8;  
RESULT 489  
ID AAK94307 standard; cDNA; 2525 BP.  
DE Human full-length cDNA, SEQ ID NO: 2971.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.2%; Score 51.8; DB 4; Length 2525;  
Best Local Similarity 43.0%; Pred. No. 8.8;  
RESULT 490  
ID ADL30938 standard; cDNA; 2525 BP.  
DE Full length human cDNA clone SeqID 2971.  
PN EPI396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.2%; Score 51.8; DB 12; Length 2525;  
Best Local Similarity 43.0%; Pred. No. 8.8;  
RESULT 491  
ID ABS78645 standard; cDNA; 2597 BP.

DE Human cDNA encoding CGDD3, INCYTE 3089944CB1.  
 PN WO200272830-A2.  
 PD 19-SEP-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 2597;  
 Best Local Similarity 43.0%; Pred. No. 8.8;  
 RESULT 492  
 ID ABX77526 standard; cDNA; 4462 BP.  
 DE Differentially expressed breast cancer associated cDNA #21.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4462;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 493  
 ID AAS12954 standard; cDNA; 4469 BP.  
 DE Human Frizzled Related Protein (FRP-1) cDNA.  
 PN WO200164949-A2.  
 PD 07-SEP-2003.  
 PA (ALCO-) ALCON LAB INC.  
 Query Match 5.2%; Score 51.8; DB 4; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 494  
 ID ABT10165 standard; cDNA; 4469 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 299.  
 PN WO200259271-A2.  
 PD 01-AUG-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 495  
 ID ABZ34845 standard; cDNA; 4469 BP.  
 DE Coding sequence SEQ ID 203, differentially expressed in osteogenesis.  
 PN WO200281745-A2.  
 PD 17-OCT-2002.  
 PA (AVET-) AVENTIS PHARMA SA.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 496  
 ID ADP21417 standard; DNA; 4469 BP.  
 DE Gene SFRP1 for screening for cardiac therapeutic preparation.  
 PN WO2004050894-A2.  
 PD 17-JUN-2004.  
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
 Query Match 5.2%; Score 51.8; DB 12; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 497  
 ID ADR24996 standard; DNA; 4469 BP.  
 DE Breast cancer prognosis marker #857.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 5.2%; Score 51.8; DB 13; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 498  
 ID ADR99015 standard; DNA; 4469 BP.  
 DE Secreted frizzled-related protein 1, SFRP1, coding sequence, SEQ ID 21.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB-) BAYER PHARM CORP.  
 Query Match 5.2%; Score 51.8; DB 13; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 499  
 ID AAA10594 standard; DNA; 10732 BP.  
 DE Gene encoding a subunit of cellulose synthase.  
 PN JP2000060568-A.  
 PD 29-FEB-2000.  
 PA (MIZU/) MIZUNO K.  
 PA (OJIP-) OJI PAPER CO.  
 Query Match 5.2%; Score 51.8; DB 3; Length 10732;  
 Best Local Similarity 13.2%; Pred. No. 8.4;  
 RESULT 500

ID AAL61170 standard; DNA; 14055 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #1.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW-) UNIV WASHINGTON.  
 Query Match 5.2%; Score 51.8; DB 8; Length 14055;  
 Best Local Similarity 44.1%; Pred. No. 8.4;  
 RESULT 501  
 ID AAD54645 standard; DNA; 113193 BP.  
 DE Streptomyces nodosus amphoterin (amph) biosynthetic gene cluster.  
 PN WO200297082-A2.  
 PD 05-DEC-2002.  
 PA (OYDU-) UNIV COLLEGE DUBLIN.  
 Query Match 5.2%; Score 51.8; DB 8; Length 113193;  
 Best Local Similarity 46.9%; Pred. No. 7.9;  
 RESULT 502  
 ID ACC00687 standard; cDNA; 893 BP.  
 DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:123.  
 PN WO2003002751-A2.  
 PD 09-JAN-2003.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 9.7;  
 RESULT 503  
 ID ADC23602 standard; cDNA; 893 BP.  
 DE cDNA encodes protein used to alter plant oil phenotype (SeqID 107).  
 PN WO2003001902-A2.  
 PD 09-JAN-2003.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 10; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 9.7;  
 RESULT 504  
 ID ACA38013 standard; DNA; 1242 BP.  
 DE Prokaryotic essential gene #19670.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 1242;  
 Best Local Similarity 44.5%; Pred. No. 9.7;  
 RESULT 505  
 ID ABD15461 standard; DNA; 1311 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14065.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 1311;  
 Best Local Similarity 43.9%; Pred. No. 9.6;  
 RESULT 506  
 ID ADS60055 standard; cDNA; 2055 BP.  
 DE Bacterial polynucleotide #12042.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.2%; Score 51.6; DB 13; Length 2055;  
 Best Local Similarity 48.3%; Pred. No. 9.5;  
 RESULT 507  
 ID ABD15601 standard; DNA; 2850 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14205.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 2850;  
 Best Local Similarity 43.9%; Pred. No. 9.4;  
 RESULT 508  
 ID ACA26098 standard; DNA; 2853 BP.  
 DE Prokaryotic essential gene #7755.  
 PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.6; DB 8; Length 2853;  
Best Local Similarity 45.4%; Pred. No. 9.4;  
RESULT 509  
ID ABX09933 standard; DNA; 2865 BP.  
DE DNA encoding maize Starch synthase Iia.  
PN WO200279410-A2.  
PD 10-OCT-2002.  
PA (BADI) BASF PLANT SCI GMBH.  
Query Match 5.2%; Score 51.6; DB 8; Length 2865;  
Best Local Similarity 49.6%; Pred. No. 9.4;  
RESULT 510  
ID ADG75175 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 9.1;  
RESULT 511  
ID ADG75118 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 9.1;  
RESULT 512  
ID AAV62154 standard; DNA; 21034 BP.  
DE HSV-2 strain SB5 Contig ID 10 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 21034;  
Best Local Similarity 44.9%; Pred. No. 8.9;  
RESULT 513  
ID AAV62134 standard; DNA; 26338 BP.  
DE HSV-2 strain SB5 Contig ID 104 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 26338;  
Best Local Similarity 44.9%; Pred. No. 8.9;  
RESULT 514  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOGA-) KOSAN BIOSCIENCES INC.  
Query Match 5.2%; Score 51.6; DB 12; Length 76994;  
Best Local Similarity 44.5%; Pred. No. 8.6;  
RESULT 515  
ID AAD54645 standard; DNA; 113193 BP.  
DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (UYDU-) UNIV COLLEGE DUBLIN.  
Query Match 5.2%; Score 51.6; DB 8; Length 113193;  
Best Local Similarity 44.0%; Pred. No. 8.5;  
RESULT 516  
ID AAV62176 standard; DNA; 117213 BP.  
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
Query Match 5.2%; Score 51.6; DB 2; Length 117213;  
Best Local Similarity 44.9%; Pred. No. 8.5;  
RESULT 517  
ID ABA99457 standard; DNA; 813 BP.  
DE Actinoplanes sp DNA encoding acarbose synthase AcboAasp.  
PN DE10021667-A1.  
PD 08-NOV-2001.  
PA (FARB) BAYER AG.  
Query Match 5.2%; Score 51.4; DB 6; Length 813;  
Best Local Similarity 44.7%; Pred. No. 11;

RESULT 518  
ID AAA29167 standard; cDNA; 1106 BP.  
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.  
PN WO200032757-A2.  
PD 08-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 5.2%; Score 51.4; DB 3; Length 1106;  
Best Local Similarity 45.0%; Pred. No. 10;  
RESULT 519  
ID ADC36364 standard; DNA; 1197 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:232.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1197;  
Best Local Similarity 43.9%; Pred. No. 10;  
RESULT 520  
ID ADC36374 standard; DNA; 1411 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:242.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1411;  
Best Local Similarity 43.9%; Pred. No. 10;  
RESULT 521  
ID ADJ27276 standard; cDNA; 1926 BP.  
DE Mouse HSP70.3 coding sequence.  
PN WO2003061684-A2.  
PD 31-JUL-2003.  
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 5.2%; Score 51.4; DB 11; Length 1926;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 522  
ID AAS10678 standard; cDNA; 1929 BP.  
DE Murine hsp70 cDNA sequence.  
PN WO200151081-A1.  
PD 19-JUL-2001.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 5.2%; Score 51.4; DB 4; Length 1929;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 523  
ID ACA23299 standard; DNA; 2307 BP.  
DE Prokaryotic essential gene #4956.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.4; DB 8; Length 2307;  
Best Local Similarity 49.8%; Pred. No. 10;  
RESULT 524  
ID ADQ18001 standard; DNA; 2526 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 818.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2526;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 525  
ID ADQ22602 standard; DNA; 2652 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5422.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2652;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 526  
ID AAD55818 standard; DNA; 4725 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #8.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.2%; Score 51.4; DB 10; Length 4725;  
Best Local Similarity 50.6%; Pred. No. 10;

RESULT 527  
ID ABZ11709 standard; cDNA; 7847 BP.  
DE Human polynucleotide SEQ ID NO 591.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.2%; Score 51.4; DB 6; Length 7847;  
Best Local Similarity 50.2%; Pred. No. 9.9;  
RESULT 528  
ID ADMA4227 standard; cDNA; 7847 BP.  
DE Novel human arginine-rich protein cDNA #591.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRWA/) DRMANAC R T.  
Query Match 5.2%; Score 51.4; DB 12; Length 7847;  
Best Local Similarity 50.2%; Pred. No. 9.9;  
RESULT 529  
ID ADP90617 standard; DNA; 34719 BP.  
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.  
PN JP2004180638-A.  
PD 02-JUL-2004.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.2%; Score 51.4; DB 12; Length 34719;  
Best Local Similarity 47.1%; Pred. No. 9.5;  
RESULT 530  
ID ABA99469 standard; DNA; 38064 BP.  
DE Actinoplanes sp SE 50/110 (CBS614.71) DNA encoding acarbose operon.  
PN DE10021667-A1.  
PD 08-NOV-2001.  
PA (FARB) BAYER AG.  
Query Match 5.2%; Score 51.4; DB 6; Length 38064;  
Best Local Similarity 44.7%; Pred. No. 9.5;  
RESULT 531  
ID ABX04971 standard; DNA; 103599 BP.  
DE S. cinnamomensis monensin type I polyketide synthase gene cluster.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.2%; Score 51.4; DB 4; Length 103599;  
Best Local Similarity 44.8%; Pred. No. 9.2;  
RESULT 532  
ID ADP95323 standard; cDNA; 447 BP.  
DE Cotton expressed sequence tag, EST, #4334.  
PN US2004123338-A1.  
PD 24-JUN-2004.  
PA (FINC/) FINCHER K L.  
Query Match 5.2%; Score 51.2; DB 12; Length 447;  
Best Local Similarity 50.8%; Pred. No. 12;  
RESULT 533  
ID ABZ13934 standard; DNA; 699 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.2%; Score 51.2; DB 6; Length 699;  
Best Local Similarity 47.5%; Pred. No. 11;  
RESULT 534  
ID ADGB7603 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.  
PN WO200222675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Query Match 5.2%; Score 51.2; DB 6; Length 699;  
Best Local Similarity 47.5%; Pred. No. 11;  
RESULT 535  
ID ADGB7604 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.  
PN WO200222675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Query Match 5.2%; Score 51.2; DB 6; Length 699;  
Best Local Similarity 47.5%; Pred. No. 11;  
RESULT 536  
ID ADA67907 standard; DNA; 699 BP.  
DE Arabidopsis thaliana gene, SEQ ID 151.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.2%; Score 51.2; DB 8; Length 699;  
Best Local Similarity 47.5%; Pred. No. 11;  
RESULT 537  
ID ABN99073 standard; DNA; 792 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANYV/) AN Y.  
PA (HAML/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYV/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 5.2%; Score 51.2; DB 6; Length 792;  
Best Local Similarity 47.5%; Pred. No. 11;  
RESULT 538  
ID ACA36840 standard; DNA; 1107 BP.  
DE Prokaryotic essential gene #8497.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.2; DB 8; Length 1107;  
Best Local Similarity 45.2%; Pred. No. 11;  
RESULT 539  
ID AAD55811 standard; DNA; 1683 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.2%; Score 51.2; DB 10; Length 1683;  
Best Local Similarity 48.3%; Pred. No. 11;  
RESULT 540  
ID AAS54365 standard; DNA; 2034 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #496.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.2; DB 4; Length 2034;  
Best Local Similarity 46.0%; Pred. No. 11;  
RESULT 541

ID AAV13836 standard; cDNA; 2277 BP.  
 DE Homo sapiens mammalian codon-optimized telomerase protein p105 gene.  
 PN WO9801543-A1.  
 PD 15-JAN-1998.  
 PA (TULA-) TULARIK INC.  
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
 Best Local Similarity 46.4%; Pred. No. 11;  
 RESULT 542  
 ID AAV05372 standard; RNA; 2277 BP.  
 DE Human telomerase p105 subunit mammalian optimised synthetic RNA.  
 PN WO9801542-A1.  
 PD 15-JAN-1998.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
 Best Local Similarity 46.4%; Pred. No. 11;  
 RESULT 543  
 ID AAA07385 standard; DNA; 4467 BP.  
 DE Heterosigma akashiwo Nat-ATPase gene.  
 PN JP2000050874-A.  
 PD 22-FEB-2000.  
 PA (NORO ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.  
 Query Match 5.2%; Score 51.2; DB 3; Length 4467;  
 Best Local Similarity 44.1%; Pred. No. 11;  
 RESULT 544  
 ID AAA58471 standard; DNA; 58857 BP.  
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.  
 PN WO200040704-A1.  
 PD 13-JUL-2000.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 5.2%; Score 51.2; DB 3; Length 58857;  
 Best Local Similarity 45.2%; Pred. No. 10;  
 RESULT 545  
 ID ADP03244 standard; DNA; 473 BP.  
 DE S. tridiae IF012773 L-glutamine DOI aminotransferase partial DNA.  
 PN JP20004089151-A.  
 PD 25-MAR-2004.  
 PA (TOKO ) TOKYO INST TECHNOLOGY.  
 Query Match 5.2%; Score 51; DB 12; Length 473;  
 Best Local Similarity 44.4%; Pred. No. 12;  
 RESULT 546  
 ID ABD13343 standard; DNA; 501 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11947.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51; DB 11; Length 501;  
 Best Local Similarity 48.5%; Pred. No. 12;  
 RESULT 547  
 ID AAV55831 standard; DNA; 799 BP.  
 DE Nucleotide sequence of the stabilising sequence-encoding insert.  
 PN WO9822577-A1.  
 PD 28-MAY-1998.  
 PA (MASU/) MASUCCI M G.  
 Query Match 5.2%; Score 51; DB 2; Length 799;  
 Best Local Similarity 46.1%; Pred. No. 12;  
 RESULT 548  
 ID ACA37639 standard; DNA; 1497 BP.  
 DE Prokaryotic essential gene #19296.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51; DB 8; Length 1497;  
 Best Local Similarity 48.0%; Pred. No. 12;  
 RESULT 549  
 ID ABD13303 standard; DNA; 1500 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11907.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51; DB 11; Length 1500;  
 Best Local Similarity 48.5%; Pred. No. 12;  
 RESULT 550  
 ID ADJ40244 standard; cDNA; 1503 BP.

DE Plant cDNA #1244.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAWER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.2%; Score 51; DB 12; Length 1503;  
 Best Local Similarity 47.6%; Pred. No. 12;  
 RESULT 551  
 ID AAL44275 standard; DNA; 1632 BP.  
 DE Micrococcus luteus crtI gene sequence.  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI ) CARGILL INC.  
 Query Match 5.2%; Score 51; DB 6; Length 1632;  
 Best Local Similarity 42.9%; Pred. No. 12;  
 RESULT 552  
 ID ADG93408 standard; DNA; 1632 BP.  
 DE Maize lipoxigenase (LOX) DNA #20.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51; DB 10; Length 1632;  
 Best Local Similarity 45.9%; Pred. No. 12;  
 RESULT 553  
 ID AAL61149 standard; DNA; 1713 BP.  
 DE Human mutant ARX gene #2.  
 PN WO2003045989-A1.  
 PD 05-JUN-2003.  
 PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
 Query Match 5.2%; Score 51; DB 9; Length 1713;  
 Best Local Similarity 46.2%; Pred. No. 12;  
 RESULT 554  
 ID ADS56497 standard; cDNA; 1755 BP.  
 DE Bacterial polynucleotide #8484.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.2%; Score 51; DB 13; Length 1755;  
 Best Local Similarity 47.9%; Pred. No. 12;  
 RESULT 555  
 ID ADG93406 standard; DNA; 1803 BP.  
 DE Maize lipoxigenase (LOX) DNA #19.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51; DB 10; Length 1803;  
 Best Local Similarity 45.9%; Pred. No. 12;  
 RESULT 556  
 ID AAH26500 standard; cDNA; 2561 BP.  
 DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
 PN WO200164874-A2.  
 PD 07-SEP-2001.  
 PA (BOST-) BOSTON HEART FOUND INC.  
 Query Match 5.2%; Score 51; DB 5; Length 2561;  
 Best Local Similarity 47.3%; Pred. No. 12;  
 RESULT 557  
 ID ABR85324 standard; cDNA; 2710 BP.  
 DE Human cytoskeleton-associated protein, CSAP-15, coding sequence.  
 PN WO200253719-A2.  
 PD 11-JUL-2002.

PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.1%; Score 51; DB 6; Length 2710;  
 Best Local Similarity 45.7%; Pred. No. 12;  
 RESULT 558  
 ID AAL44298 standard; DNA; 6941 BP.  
 DE Micrococcus luteus C50 carotenoid producing operon.  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI) CARGILL INC.  
 Query Match 5.2%; Score 51; DB 6; Length 6941;  
 Best Local Similarity 42.9%; Pred. No. 12;  
 RESULT 559  
 ID AAQ73500 standard; DNA; 8438 BP.  
 DE DNA encoding Pseudorabies virus large latency transcript.  
 PN US5352596-A.  
 PD 04-OCT-1994.  
 PA (USDA) US SEC OF AGRIC.  
 Query Match 5.2%; Score 51; DB 2; Length 8438;  
 Best Local Similarity 44.8%; Pred. No. 12;  
 RESULT 560  
 ID ABX56062 standard; DNA; 741 BP.  
 DE M. echinospira calicheamicin biosynthesis gene orfII.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.1%; Score 50.8; DB 8; Length 741;  
 Best Local Similarity 45.8%; Pred. No. 13;  
 RESULT 561  
 ID ACA43508 standard; DNA; 1125 BP.  
 DE Prokaryotic essential gene #25165.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1125;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 RESULT 562  
 ID AAT91453 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.  
 PN WO9709429-A2.  
 PD 13-MAR-1997.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 563  
 ID AAT91517 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.  
 PN WO9709428-A2.  
 PD 13-MAR-1997.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 564  
 ID AAV44350 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 DNA.  
 PN WO9816645-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 565  
 ID AAV64458 standard; DNA; 1155 BP.  
 DE M. tuberculosis immunogenic polypeptide Tbra28 DNA.  
 PN WO9816646-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 566  
 ID AAZ19048 standard; DNA; 1155 BP.  
 DE M. tuberculosis recombinant antigen DNA encoding Tbra28.  
 PN WO9942118-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.

Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 567  
 ID AAZ19260 standard; DNA; 1155 BP.  
 DE M. tuberculosis antigen Tbra28 DNA sequence.  
 PN WO9942076-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 568  
 ID ADA70376 standard; DNA; 1173 BP.  
 DE Rice gene, SEQ ID 3699.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1173;  
 Best Local Similarity 43.9%; Pred. No. 13;  
 RESULT 569  
 ID ADJ39706 standard; cDNA; 1173 BP.  
 DE Plant cDNA #706.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GORE/) GORE S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.1%; Score 50.8; DB 12; Length 1173;  
 Best Local Similarity 43.9%; Pred. No. 13;  
 RESULT 570  
 ID AAS51566 standard; DNA; 1317 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #151.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 4; Length 1317;  
 Best Local Similarity 51.0%; Pred. No. 13;  
 RESULT 571  
 ID ACA19467 standard; DNA; 1317 BP.  
 DE Prokaryotic essential gene #1124.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1317;  
 Best Local Similarity 51.0%; Pred. No. 13;  
 RESULT 572  
 ID ADA71150 standard; DNA; 1479 BP.  
 DE Rice gene, SEQ ID 4473.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1479;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 RESULT 573  
 ID AAL51696 standard; cDNA; 1682 BP.  
 DE Argiope trifasciata spider silk protein coding sequence #1.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1682;  
 Best Local Similarity 45.8%; Pred. No. 13;  
 RESULT 574  
 ID ABS78661 standard; DNA; 5760 BP.  
 DE M. echinospira DNA encoding PKSE protein.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.

PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.8; DB 6; Length 5760;  
Best Local Similarity 45.0%; Pred. No. 13;  
RESULT 575  
ID ABS63414 standard; cDNA; 508 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 5.1%; Score 50.6; DB 6; Length 508;  
Best Local Similarity 54.6%; Pred. No. 15;  
RESULT 576  
ID AAF74867 standard; DNA; 1313 BP.  
DE Leishmania major PPG nucleotide sequence.  
PN CN1272542-A.  
PD 08-NOV-2000.  
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.  
Query Match 5.1%; Score 50.6; DB 4; Length 1313;  
Best Local Similarity 47.1%; Pred. No. 14;  
RESULT 577  
ID ACA37566 standard; DNA; 1371 BP.  
DE Prokaryotic essential gene #19223.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.1%; Score 50.6; DB 8; Length 1371;  
Best Local Similarity 43.7%; Pred. No. 14;  
RESULT 578  
ID AAI92870 standard; cDNA; 2564 BP.  
DE Human polynucleotide SEQ ID NO 12930.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.1%; Score 50.6; DB 4; Length 2564;  
Best Local Similarity 48.6%; Pred. No. 14;  
RESULT 579  
ID ADQ21323 standard; DNA; 4233 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4143.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.1%; Score 50.6; DB 12; Length 4233;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 580  
ID ADQ25196 standard; DNA; 4244 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8016.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.1%; Score 50.6; DB 12; Length 4244;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 581  
ID ADQ91678 standard; DNA; 11740 BP.  
DE Polyketide synthase related DNA contig 1, SEQ ID 1.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.6; DB 13; Length 11740;  
Best Local Similarity 45.3%; Pred. No. 13;  
RESULT 582  
ID ADJ39239 standard; cDNA; 549 BP.  
DE Plant cDNA #239.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKS D.  
PA (ZHUT/) ZHU T.  
Query Match 5.1%; Score 50.4; DB 12; Length 549;  
Best Local Similarity 47.6%; Pred. No. 16;  
RESULT 583  
ID ABZ66752 standard; DNA; 669 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 166.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.4; DB 10; Length 669;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 584  
ID AAV62138 standard; DNA; 980 BP.  
DE HSV-2 strain SB5 Contig ID 53 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 5.1%; Score 50.4; DB 2; Length 980;  
Best Local Similarity 49.0%; Pred. No. 15;  
RESULT 585  
ID ADI42416 standard; DNA; 1159 BP.  
DE Plant transcription factor polynucleotide #544.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 5.1%; Score 50.4; DB 12; Length 1159;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 586  
ID ADC36273 standard; DNA; 1209 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:141.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 5.1%; Score 50.4; DB 10; Length 1209;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 587  
ID ADC36278 standard; DNA; 1473 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:146.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match 5.1%; Score 50.4; DB 10; Length 1473;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 588  
ID AAL61177 standard; DNA; 2247 BP.  
DE Actinosynnema pretiosum ABC transporter gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 5.1%; Score 50.4; DB 8; Length 2247;  
Best Local Similarity 43.7%; Pred. No. 15;  
RESULT 589  
ID ACN37449 standard; cDNA; 4755 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323899, SEQ ID NO:338.  
PN WO2004030615-A2.  
PD 15-APR-2004.



PA (GETH ) GENENTECH INC.  
 Query Match 5.1%; Score 50.4; DB 13; Length 4755;  
 Best Local Similarity 51.3%; Pred. No. 15;  
 RESULT 590  
 ID ADS14589 standard; DNA; 6375 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2302, SEQ ID 144.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 Query Match 5.1%; Score 50.4; DB 13; Length 6375;  
 Best Local Similarity 50.7%; Pred. No. 15;  
 RESULT 591  
 ID AAF81370 standard; DNA; 6390 BP.  
 DE Quorum sensing controlled gene qscI07 ORF.  
 PN WO200118248-A2.  
 PD 15-MAR-2001.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (QUOR-) QUORUM SCI INC.  
 Query Match 5.1%; Score 50.4; DB 4; Length 6390;  
 Best Local Similarity 50.7%; Pred. No. 15;  
 RESULT 592  
 ID ABZ75344 standard; DNA; 23673 BP.  
 DE Human R1128 gene cluster.  
 PN US634077A-B1.  
 PD 22-JAN-2002.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.1%; Score 50.4; DB 6; Length 23673;  
 Best Local Similarity 47.7%; Pred. No. 14;  
 RESULT 593  
 ID ABZ66808 standard; DNA; 45055 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 277.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.4; DB 10; Length 45055;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 594  
 Query Match 5.1%; Score 50.4; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 14;  
 RESULT 595  
 ID ADJ42262 standard; cDNA; 595 BP.  
 DE Plant cDNA #3262.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICKE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.1%; Score 50.2; DB 12; Length 595;  
 Best Local Similarity 50.5%; Pred. No. 17;  
 RESULT 596  
 ID ACA26748 standard; DNA; 841 BP.  
 DE Prokaryotic essential gene #8405.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.2; DB 8; Length 841;  
 Best Local Similarity 46.7%; Pred. No. 17;  
 RESULT 597  
 ID ABD12328 standard; DNA; 864 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10932.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 864;  
 Best Local Similarity 47.1%; Pred. No. 17;

RESULT 598  
 ID AAF61096 standard; DNA; 1545 BP.  
 DE P. putida KT2440-associated DNA ORF11200.  
 PN DE19935088-A1.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDT-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Query Match 5.1%; Score 50.2; DB 4; Length 1545;  
 Best Local Similarity 44.2%; Pred. No. 16;  
 RESULT 599  
 ID ADQ91680 standard; DNA; 2160 BP.  
 DE Polyketide synthase related ORF1, SEQ ID 3.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 2160;  
 Best Local Similarity 45.3%; Pred. No. 16;  
 RESULT 600  
 ID ABD12652 standard; DNA; 2211 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11256.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2211;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 601  
 ID ABD12391 standard; DNA; 2289 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10995.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2289;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 602  
 ID ADT43953 standard; cDNA; 3039 BP.  
 DE Bacterial polynucleotide #18704.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOX/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3039;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 603  
 ID ADS34438 standard; DNA; 3263 BP.  
 DE POSH protein associated DNA #192.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3263;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 604  
 ID AAH14472 standard; cDNA; 3269 BP.  
 DE Human cDNA sequence SEQ ID NO:11967.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.1%; Score 50.2; DB 4; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 605  
 ID ACN40510 standard; cDNA; 3269 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326614, SEQ ID NO:5332.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 606

ID ADS34443 standard; DNA; 3269 BP.  
DE POSH protein associated DNA #197.  
PN WO2004078130-A2.  
PD 16-SEP-2004.

PA (PROT-) PROTEOLOGICS INC.

Query Match 5.1%; Score 50.2; DB 13; Length 3269;  
Best Local Similarity 47.6%; Pred. No. 16;

RESULT 607

ID ADR31451 standard; DNA; 4826 BP.  
DE Streptomyces aureofaciens NRRL2209 Sau3A I genomic DNA fragment.  
PN US2004157303-A1.

PD 12-AUG-2004.

PA (MAHL/) MAHISHI L. H.

PA (TRIP/) TRIPATHI G.

PA (RAMC/) RAMCHANDER T V N.

PA (RAWA/) RAWAL S K.

Query Match

5.1%; Score 50.2; DB 13; Length 4826;  
Best Local Similarity 43.9%; Pred. No. 16;

RESULT 608

ID AAL61173 standard; DNA; 9975 BP.

DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.

PN WO2003045312-A2.

PD 05-JUN-2003.

PA (UNIW ) UNIV WASHINGTON.

Query Match

5.1%; Score 50.2; DB 8; Length 9975;  
Best Local Similarity 46.0%; Pred. No. 16;

RESULT 609

ID ABX4858 standard; cDNA; 390 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #14023.

PN US2002137139-A1.

PD 26-SEP-2002.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

Query Match

5.1%; Score 50; DB 8; Length 390;  
Best Local Similarity 52.2%; Pred. No. 18;

RESULT 610

ID AAZ52552 standard; cDNA; 888 BP.

DE Human secreted protein clone yd61\_1 nucleotide sequence SEQ ID NO:155.

PN WO9958642-A2.

PD 18-NOV-1999.

PA (GEMY ) GENETICS INST INC.

Query Match

5.1%; Score 50; DB 3; Length 888;  
Best Local Similarity 49.4%; Pred. No. 18;

RESULT 611

ID ADO00480 standard; cDNA; 1149 BP.

DE Novel human cDNA sequence #1295.

PN WO2004038003-A2.

PD 06-MAY-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match

5.1%; Score 50; DB 12; Length 1149;  
Best Local Similarity 47.8%; Pred. No. 18;

RESULT 612

ID ADN98911 standard; cDNA; 1149 BP.

DE Novel human cDNA sequence #511.

PN WO2004038003-A2.

PD 06-MAY-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match

5.1%; Score 50; DB 12; Length 1149;  
Best Local Similarity 47.8%; Pred. No. 18;

RESULT 613

ID ADS55971 standard; cDNA; 1317 BP.

DE Bacterial polynucleotide #7958.

PN US2003233675-A1.

PD 18-DEC-2003.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match

5.1%; Score 50; DB 13; Length 1317;  
Best Local Similarity 46.2%; Pred. No. 18;

RESULT 614

ID ADT44554 standard; cDNA; 1337 BP.

DE Bacterial polynucleotide #19305.

PN US2003233675-A1.

PD 18-DEC-2003.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match

5.1%; Score 50; DB 13; Length 1337;  
Best Local Similarity 49.2%; Pred. No. 18;

RESULT 615

ID ACA25880 standard; DNA; 1365 BP.

DE Prokaryotic essential gene #7537.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match

5.1%; Score 50; DB 8; Length 1365;  
Best Local Similarity 45.4%; Pred. No. 18;

RESULT 616

ID ADP28824 standard; DNA; 1470 BP.

DE Human secreted protein encoding sequence SEQ ID #822.

PN WO2004035732-A2.

PD 29-APR-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match

5.1%; Score 50; DB 12; Length 1470;  
Best Local Similarity 47.8%; Pred. No. 18;

RESULT 617

ID ADI23924 standard; DNA; 1806 BP.

DE Streptomyces refuineus 024A locus ORF2.

PN US2003198981-A1.

PD 23-OCT-2003.

PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match

5.1%; Score 50; DB 10; Length 1806;  
Best Local Similarity 46.3%; Pred. No. 18;

RESULT 618

ID ADG98257 standard; DNA; 1806 BP.

DE Acyl-specific C-domain DNA #13.

PN US2003211567-A1.

PD 13-NOV-2003.

PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match

5.1%; Score 50; DB 12; Length 1806;  
Best Local Similarity 46.3%; Pred. No. 18;

RESULT 619

ID ADT44505 standard; cDNA; 2148 BP.

DE Bacterial polynucleotide #19256.

PN US2003233675-A1.

PD 18-DEC-2003.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match

5.1%; Score 50; DB 13; Length 2148;  
Best Local Similarity 50.9%; Pred. No. 18;

RESULT 620

ID AAZ87297 standard; DNA; 13842 BP.

DE S. venezuelae macrolide biosynthetic gene pikAI, SEQ ID NO:30.

PN WO20000620-A2.

PD 06-JAN-2000.

PA (MINU ) UNIV MINNESOTA.

Query Match

5.1%; Score 50; DB 3; Length 13842;  
Best Local Similarity 44.7%; Pred. No. 17;

RESULT 621

ID ADL91915 standard; DNA; 13842 BP.

DE Streptomyces macrolide biosynthetic protein (PikR2) coding sequence.

PN US2003194784-A1.

PD 16-OCT-2003.

PA (SHER/) SHERMAN D H.

PA (LIUH/) LIU H.

PA (XUEY/) XUE Y.

PA (ZHAO/) ZHAO L.

Query Match 5.1%; Score 50; DB 12; Length 13842;  
Best Local Similarity 44.7%; Pred. No. 17;  
RESULT 622  
ID ADI23898 standard; DNA; 15738 BP.  
DE Streptomyces fradiae A541 locus ORF5.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 15738;  
Best Local Similarity 43.1%; Pred. No. 17;  
RESULT 623  
ID ADO51695 standard; DNA; 32329 BP.  
DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
PN US2004038250-A1.  
PD 26-FEB-2004.  
PA (ASTU-) ASTUR-PHARMA SA.  
PA (UYOV-) UNIV OVIEDO.  
Query Match 5.1%; Score 50; DB 12; Length 32329;  
Best Local Similarity 48.5%; Pred. No. 16;  
RESULT 624  
ID AAZ87318 standard; DNA; 36778 BP.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 5.1%; Score 50; DB 3; Length 36778;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 625  
ID ADL91933 standard; DNA; 36778 BP.  
DE Streptomyces venezuelae pik gene cluster coding sequence.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 5.1%; Score 50; DB 12; Length 36778;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 626  
ID ADI23892 standard; DNA; 37360 BP.  
DE Streptomyces fradiae A541 locus contig 2.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 37360;  
Best Local Similarity 43.1%; Pred. No. 16;  
RESULT 627  
ID AAZ87285 standard; DNA; 37948 BP.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 5.1%; Score 50; DB 3; Length 37948;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 628  
ID AAA75633 standard; DNA; 38506 BP.  
DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.  
PN US6117659-A.  
PD 12-SEP-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 3; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 629  
ID AAZ56001 standard; DNA; 38506 BP.  
DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.  
PN WO961599-A2.  
PD 02-DEC-1999.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 3; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 630  
ID ADA09418 standard; DNA; 38506 BP.  
DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.

PN US6509455-B1.  
PD 21-JAN-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 8; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 631  
ID ADH53462 standard; DNA; 38506 BP.  
DE S. venezuelae pKOS023-27 cosmid DNA.  
PN US2003162262-A1.  
PD 28-AUG-2003.  
PA (ASHL/) ASHLEY G.  
PA (BETL/) BETLACH M C.  
PA (BETL/) BETLACH M R.  
PA (MCDA/) MCDANIEL R.  
PA (TANG/) TANG L.  
Query Match 5.1%; Score 50; DB 10; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 632  
ID ABS56090 standard; DNA; 38506 BP.  
DE S. venezuelae DNA inserted into cosmid pKOS023-27.  
PN WO200297062-A2.  
PD 05-DEC-2002.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 633  
ID ABQ74179 standard; DNA; 229354 BP.  
DE Human cytomegalovirus strain AD169 genomic sequence SEQ ID NO:64.  
PN WO200257437-A2.  
PD 25-JUL-2002.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 5.1%; Score 50; DB 6; Length 229354;  
Best Local Similarity 46.1%; Pred. No. 15;  
RESULT 634  
ID ABQ90211 standard; DNA; 825 BP.  
DE M. capsulatus gene #196 for DNA array.  
PN WO200255655-A2.  
PD 18-JUL-2002.  
PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
PA (TIGR-) TIGR.  
Query Match 5.0%; Score 49.8; DB 6; Length 825;  
Best Local Similarity 49.2%; Pred. No. 19;  
RESULT 635  
ID ABK34330 standard; cDNA; 856 BP.  
DE Human cDNA for novel secreted protein, SEQ ID 99.  
PN WO200177290-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match 5.0%; Score 49.8; DB 6; Length 856;  
Best Local Similarity 50.5%; Pred. No. 19;  
RESULT 636  
ID ABZ66685 standard; DNA; 1272 BP.  
DE Orthomycin biosynthetic polynucleotide SEQ ID NO 32.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 10; Length 1272;  
Best Local Similarity 45.5%; Pred. No. 19;  
RESULT 637  
ID AAD53025 standard; DNA; 1293 BP.  
DE Streptomyces platensis ema9 gene.  
PN WO200292801-A2.  
PD 21-NOV-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49.8; DB 8; Length 1293;  
Best Local Similarity 48.7%; Pred. No. 19;  
RESULT 638  
ID ACA36585 standard; DNA; 1374 BP.  
DE Prokaryotic essential gene #8242.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.8; DB 8; Length 1374;

Best Local Similarity 51.1%; Pred. No. 19;  
 RESULT 639  
 ID ADA70992 standard; DNA; 1458 BP.  
 DE Rice gene, SEQ ID 4315.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.0%; Score 49.8; DB 8; Length 1458;  
 Best Local Similarity 48.1%; Pred. No. 19;  
 RESULT 640  
 ID ADI27212 standard; DNA; 1581 BP.  
 DE Rabbit LRP binding family protein DNA #1.  
 PN WO2003106657-A2.  
 PD 24-DEC-2003.  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 Query Match 5.0%; Score 49.8; DB 12; Length 1581;  
 Best Local Similarity 46.2%; Pred. No. 19;  
 RESULT 641  
 ID ABV94776 standard; cDNA; 1814 BP.  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 182.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 1814;  
 Best Local Similarity 47.5%; Pred. No. 19;  
 RESULT 642  
 ID ADP10373 standard; DNA; 1837 BP.  
 DE Reference mRNA sequences for marker probe #50.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Query Match 5.0%; Score 49.8; DB 12; Length 1837;  
 Best Local Similarity 47.5%; Pred. No. 19;  
 RESULT 643  
 ID AAF26295 standard; DNA; 2048 BP.  
 DE Pseudomonas sp Type II (xcp) secretion system DNA ORF04962a.  
 PN WO200107622-A2.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Query Match 5.0%; Score 49.8; DB 4; Length 2048;  
 Best Local Similarity 43.1%; Pred. No. 19;  
 RESULT 644  
 ID ADA71072 standard; DNA; 2136 BP.  
 DE Rice gene, SEQ ID 4395.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.0%; Score 49.8; DB 8; Length 2136;  
 Best Local Similarity 47.8%; Pred. No. 19;  
 RESULT 645  
 ID ABL61822 standard; DNA; 2520 BP.  
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:159.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
 Best Local Similarity 48.7%; Pred. No. 19;  
 RESULT 646  
 ID ABR84011 standard; cDNA; 2520 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #582.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
 Best Local Similarity 48.7%; Pred. No. 19;  
 RESULT 647  
 ID ABD16186 standard; DNA; 3003 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14790.  
 PN US6551795-B1.

PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.8; DB 11; Length 3003;  
 Best Local Similarity 49.1%; Pred. No. 19;  
 RESULT 648  
 ID AAD28566 standard; DNA; 3113 BP.  
 DE Herpes simplex virus type 2 UL46fragFl1F5 DNA.  
 PN WO200202131-A2.  
 PD 10-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 3113;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 649  
 ID ADG74980 standard; DNA; 3113 BP.  
 DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 52.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3113;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 650  
 ID ABD15936 standard; DNA; 3132 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14540.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.8; DB 11; Length 3132;  
 Best Local Similarity 49.1%; Pred. No. 19;  
 RESULT 651  
 ID AAT86704 standard; DNA; 3147 BP.  
 DE DNA encoding thermostable esterase TspA E101.  
 PN WO9725058-A1.  
 PD 17-JUL-1997.  
 PA (THER-) THERMOGEN INC.  
 Query Match 5.0%; Score 49.8; DB 2; Length 3147;  
 Best Local Similarity 46.4%; Pred. No. 19;  
 RESULT 652  
 ID AAO30399 standard; DNA; 3147 BP.  
 DE Thermus DNA encoding a thermostable esterase, TspA/E101.  
 PN US6218163-B1.  
 PD 17-APR-2001.  
 PA (THER-) THERMOGEN INC.  
 Query Match 5.0%; Score 49.8; DB 4; Length 3147;  
 Best Local Similarity 46.4%; Pred. No. 19;  
 RESULT 653  
 ID AAD28565 standard; DNA; 3345 BP.  
 DE Herpes simplex virus type 2 full length HSV-2 UL37 gene.  
 PN WO200202131-A2.  
 PD 10-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 654  
 ID ADG75117 standard; DNA; 3345 BP.  
 DE Human herpesvirus 2 UL37 ORF DNA - SEQ ID 189.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 655  
 ID ADG74977 standard; DNA; 3345 BP.  
 DE Human herpesvirus 2 UL37 DNA - SEQ ID 49.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 656  
 ID ABD16219 standard; DNA; 3411 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14823.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.8; DB 11; Length 3411;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 657  
ID ADO85407 standard; DNA; 3540 BP.  
DE Streptomycetes Phox/Phor operon containing DNA fragment, seq id 1.  
PN PR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.8; DB 12; Length 3540;  
Best Local Similarity 44.5%; Pred. No. 19;  
RESULT 658  
ID AAV62148 standard; DNA; 3663 BP.  
DE HSV-2 strain SBS Contig ID 94 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49.8; DB 2; Length 3663;  
Best Local Similarity 43.8%; Pred. No. 19;  
RESULT 659  
ID ACA38707 standard; DNA; 4323 BP.  
DE Prokaryotic essential gene #20364.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.8; DB 8; Length 4323;  
Best Local Similarity 43.3%; Pred. No. 19;  
RESULT 660  
ID ADO85409 standard; DNA; 4440 BP.  
DE Streptomycetes phor::omegaaac mutant, seq id 4.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.8; DB 12; Length 4440;  
Best Local Similarity 44.5%; Pred. No. 19;  
RESULT 661  
ID ADQ91711 standard; DNA; 9684 BP.  
DE Polyketide synthase ORF16, SEQ ID 34.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 13; Length 9684;  
Best Local Similarity 45.5%; Pred. No. 18;  
RESULT 662  
ID ABZ6810 standard; DNA; 37116 BP.  
DE Orthomycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 10; Length 37116;  
Best Local Similarity 45.5%; Pred. No. 18;  
RESULT 663  
ID AAD17184 standard; DNA; 65140 BP.  
DE Streptomycetes noursei nysl DNA of nystatin PKS gene cluster.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 5.0%; Score 49.8; DB 4; Length 65140;  
Best Local Similarity 46.4%; Pred. No. 17;  
RESULT 664  
ID AAD17186 standard; DNA; 125401 BP.  
DE Streptomycetes noursei nystatin PKS gene cluster DNA.  
PN WO200159126-A2.

PD 16-AUG-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 5.0%; Score 49.8; DB 4; Length 125401;  
Best Local Similarity 46.4%; Pred. No. 17;  
RESULT 665  
ID ADQ91695 standard; DNA; 164051 BP.  
DE Polyketide synthase related DNA contig 2, SEQ ID 18.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 13; Length 164051;  
Best Local Similarity 45.5%; Pred. No. 17;  
RESULT 666  
ID ADS65765 standard; cDNA; 242 BP.  
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 781.  
PN US2003237110-A9.  
PD 25-DEC-2003.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 5.0%; Score 49.6; DB 7; Length 242;  
Best Local Similarity 54.0%; Pred. No. 22;  
RESULT 667  
ID ABD03617 standard; DNA; 678 BP.  
DE Pseudomonas aeruginosa polynucleotide #2221.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.6; DB 11; Length 678;  
Best Local Similarity 44.8%; Pred. No. 21;  
RESULT 668  
ID ABD03778 standard; DNA; 753 BP.  
DE Pseudomonas aeruginosa polynucleotide #2382.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.6; DB 11; Length 753;  
Best Local Similarity 44.8%; Pred. No. 21;  
RESULT 669  
ID ACN45724 standard; DNA; 1362 BP.  
DE Prokaryotic essential gene #27381.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 8; Length 1362;  
Best Local Similarity 48.3%; Pred. No. 21;  
RESULT 670  
ID ADS56076 standard; cDNA; 1404 BP.  
DE Bacterial polynucleotide #8063.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.0%; Score 49.6; DB 13; Length 1404;  
Best Local Similarity 45.9%; Pred. No. 21;  
RESULT 671  
ID ADB58045 standard; DNA; 1531 BP.  
DE Toxicity-related gene, SEQ ID 3071.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.6; DB 10; Length 1531;

Best Local Similarity 47.2%; Pred. No. 21;  
RESULT 672  
ID ADB52519 standard; DNA; 1531 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
PN WO2003085993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.6; DB 10; Length 1531;  
Best Local Similarity 47.2%; Pred. No. 21;  
RESULT 673  
ID AAQ13305 standard; DNA; 1591 BP.  
DE Rat catechol-O-methyltransferase gene.  
PN WO9111513-A.  
PD 08-AUG-1991.  
PA (ORIN ) ORION YHTYMAE OY.  
Query Match 5.0%; Score 49.6; DB 2; Length 1591;  
Best Local Similarity 47.2%; Pred. No. 21;  
RESULT 674  
ID ADR25526 standard; DNA; 1743 BP.  
DE Breast cancer prognosis marker #1387.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 5.0%; Score 49.6; DB 13; Length 1743;  
Best Local Similarity 49.6%; Pred. No. 21;  
RESULT 675  
ID ADG75153 standard; DNA; 1765 BP.  
DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 225.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.6; DB 10; Length 1765;  
Best Local Similarity 45.6%; Pred. No. 21;  
RESULT 676  
ID AAS51445 standard; DNA; 2040 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #30.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 4; Length 2040;  
Best Local Similarity 44.6%; Pred. No. 21;  
RESULT 677  
ID ACA19446 standard; DNA; 2040 BP.  
DE Prokaryotic essential gene #1103.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 8; Length 2040;  
Best Local Similarity 44.6%; Pred. No. 21;  
RESULT 678  
ID ADM03489 standard; cDNA; 2218 BP.  
DE Human cDNA of the invention SEQ ID NO:2174.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.0%; Score 49.6; DB 11; Length 2218;  
Best Local Similarity 43.5%; Pred. No. 20;  
RESULT 679  
ID ABZ35021 standard; cDNA; 2271 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 133.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 5.0%; Score 49.6; DB 6; Length 2271;  
Best Local Similarity 47.2%; Pred. No. 20;  
RESULT 680  
ID ADB75311 standard; cDNA; 2487 BP.  
DE Prostate cancer marker cDNA.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.0%; Score 49.6; DB 10; Length 2487;  
Best Local Similarity 47.2%; Pred. No. 20;  
RESULT 681  
ID ADR25184 standard; DNA; 2487 BP.  
DE Breast cancer prognosis marker #1045.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 5.0%; Score 49.6; DB 13; Length 2487;  
Best Local Similarity 47.2%; Pred. No. 20;  
RESULT 682  
ID AAS51581 standard; DNA; 2742 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #166.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 4; Length 2742;  
Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 683  
ID ACA19538 standard; DNA; 2742 BP.  
DE Prokaryotic essential gene #1195.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 8; Length 2742;  
Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 684  
ID ABD03933 standard; DNA; 2814 BP.  
DE Pseudomonas aeruginosa polynucleotide #2537.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.6; DB 11; Length 2814;  
Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 685  
ID ADS55878 standard; cDNA; 3459 BP.  
DE Bacterial polynucleotide #7865.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.0%; Score 49.6; DB 13; Length 3459;  
Best Local Similarity 45.7%; Pred. No. 20;  
RESULT 686  
ID ADJ67856 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004038289-A1.  
PD 26-FEB-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 687  
ID ADJ68068 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004038290-A1.  
PD 26-FEB-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 688

ID ADK01146 standard; DNA; 3729 BP.  
DE DNA polymerase III-type enzyme subunit DNA #6.  
PN US2004043415-A1.  
PD 04-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 689  
ID ADJ79365 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004043414-A1.  
PD 04-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 690  
ID ADJ84805 standard; DNA; 3729 BP.  
DE T. thermophilus DNA polymerase III alpha subunit gene.  
PN US2004048309-A1.  
PD 11-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 691  
ID ADJ7593 standard; DNA; 3729 BP.  
DE DNA polymerase III-type enzyme related polynucleotide #4.  
PN US2004077012-A1.  
PD 22-APR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 692  
ID ADM66260 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004081995-A1.  
PD 29-APR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 693  
ID ADO04313 standard; DNA; 3729 BP.  
DE T. thermophilus DNA polymerase III dnaE gene.  
PN US2004106137-A1.  
PD 03-JUN-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;

PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 694  
ID ADP82390 standard; DNA; 3729 BP.  
DE Thermus thermophilus dnaE gene.  
PN US2004110210-A1.  
PD 10-JUN-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 695  
ID ABN59919 standard; cDNA; 5080 BP.  
DE Novel human coding sequence SEQ ID NO: 330.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49.6; DB 6; Length 5080;  
Best Local Similarity 44.2%; Pred. No. 20;  
RESULT 696  
ID ADF82340 standard; DNA; 5081 BP.  
DE Leukaemia-related DNA sequence #2896.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KEEN/) KEEN W.  
Query Match 5.0%; Score 49.6; DB 10; Length 5081;  
Best Local Similarity 44.2%; Pred. No. 20;  
RESULT 697  
ID ABL68935 standard; DNA; 5181 BP.  
DE DE kidney cancer related gene sequence SEQ ID NO:7272.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.0%; Score 49.6; DB 6; Length 5181;  
Best Local Similarity 47.2%; Pred. No. 20;  
RESULT 698  
ID ADJ11677 standard; DNA; 951 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 313.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
Query Match 5.0%; Score 49.4; DB 11; Length 951;  
Best Local Similarity 44.3%; Pred. No. 23;  
RESULT 699  
ID ADR01286 standard; DNA; 978 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF37 protein UNIQ DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 978;  
Best Local Similarity 49.4%; Pred. No. 23;  
RESULT 700

ID ABZ37556 standard; DNA; 1029 BP.  
DE Streptomyces viridochromogenes Avigt4 encoding polynucleotide.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 1029;  
Best Local Similarity 47.8%; Pred. No. 23;  
RESULT 701  
ID ADP88594 standard; DNA; 1149 BP.  
DE Human POU domain factor Brn3a gene exon 2.  
PN WO2004052186-A2.  
PD 24-JUN-2004.  
PA (FORS-) FORSYTH INST.  
Query Match 5.0%; Score 49.4; DB 12; Length 1149;  
Best Local Similarity 46.7%; Pred. No. 23;  
RESULT 702  
ID ACA38093 standard; DNA; 1173 BP.  
DE Prokaryotic essential gene #19750.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1173;  
Best Local Similarity 45.2%; Pred. No. 23;  
RESULT 703  
ID ACA27337 standard; DNA; 1191 BP.  
DE Prokaryotic essential gene #8994.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1191;  
Best Local Similarity 53.8%; Pred. No. 22;  
RESULT 704  
ID AAX09010 standard; cDNA; 1272 BP.  
DE Brn-3a polynucleotide.  
PN WO9905272-A1.  
PD 04-FEB-1999.  
PA (UNLO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.4; DB 2; Length 1272;  
Best Local Similarity 46.7%; Pred. No. 22;  
RESULT 705  
ID AAA29006 standard; cDNA; 1272 BP.  
DE Human transcription factor Brn-3a coding sequence.  
PN WO200034466-A1.  
PD 15-JUN-2000.  
PA (UNLO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.4; DB 3; Length 1272;  
Best Local Similarity 46.7%; Pred. No. 22;  
RESULT 706  
ID ADM80093 standard; DNA; 1398 BP.  
DE Spiramycin biosynthesis orf13c, SEQ ID 60.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.4; DB 12; Length 1398;  
Best Local Similarity 45.0%; Pred. No. 22;  
RESULT 707  
ID ADN97609 standard; DNA; 1398 BP.  
DE S ambotaciens spiramycin biosynthetic gene ORF13c.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS.  
Query Match 5.0%; Score 49.4; DB 12; Length 1398;  
Best Local Similarity 45.0%; Pred. No. 22;  
RESULT 708  
ID ABD01548 standard; DNA; 1419 BP.  
DE Pseudomonas aeruginosa polynucleotide #152.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1419;  
Best Local Similarity 46.2%; Pred. No. 22;

RESULT 709  
ID ACA40703 standard; DNA; 1587 BP.  
DE Prokaryotic essential gene #22360.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1587;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 710  
ID ACA38400 standard; DNA; 1590 BP.  
DE Prokaryotic essential gene #20057.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1590;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 711  
ID ABD01553 standard; DNA; 1692 BP.  
DE Pseudomonas aeruginosa polynucleotide #157.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1692;  
Best Local Similarity 46.2%; Pred. No. 22;  
RESULT 712  
ID ABD01582 standard; DNA; 1698 BP.  
DE Pseudomonas aeruginosa polynucleotide #186.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1698;  
Best Local Similarity 46.2%; Pred. No. 22;  
RESULT 713  
ID AAT40082 standard; DNA; 1724 BP.  
DE M. tuberculosis RNA polymerase Group I sigma subunit sigA gene.  
PN GB2298862-A.  
PD 18-SEP-1996.  
PA (ASTR) ASTRA AB.  
Query Match 5.0%; Score 49.4; DB 2; Length 1724;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 714  
ID ADG75006 standard; DNA; 2091 BP.  
DE Human herpesvirus 2 UL47 DNA - SEQ ID 78.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2091;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 715  
ID ADG75154 standard; DNA; 2091 BP.  
DE Human herpesvirus 2 strain HG52 UL47 DNA - SEQ ID 226.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2091;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 716  
ID ADG75015 standard; DNA; 2118 BP.  
DE Human herpesvirus 2 UL47 coding region DNA - SEQ ID 87.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2118;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 717  
ID ADG75014 standard; DNA; 2211 BP.  
DE Human herpesvirus 2 UL47-His construct DNA - SEQ ID 86.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2211;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 718



ID AAV22682 standard; DNA; 2214 BP.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JF10080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 5.0%; Score 49.4; DB 2; Length 2214;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 719  
ID ADC30095 standard; cDNA; 2382 BP.  
DE Human novel cDNA sequence, SEQ ID NO:177.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49.4; DB 10; Length 2382;  
Best Local Similarity 45.6%; Pred. No. 22;  
RESULT 720  
ID ACA30032 standard; DNA; 2502 BP.  
DE Prokaryotic essential gene #11689.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 2502;  
Best Local Similarity 55.6%; Pred. No. 22;  
RESULT 721  
ID ADT44784 standard; cDNA; 2517 BP.  
DE Bacterial polynucleotide #19535.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.0%; Score 49.4; DB 13; Length 2517;  
Best Local Similarity 46.4%; Pred. No. 22;  
RESULT 722  
ID AAQ2657 standard; DNA; 2745 BP.  
DE Virulence determinant rpov gene.  
PN WO9517511-A2.  
PD 29-JUN-1995.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 723  
ID AAQ2656 standard; DNA; 2745 BP.  
DE Virulence determinant rpov gene.  
PN WO9517511-A2.  
PD 29-JUN-1995.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 724  
ID AAV38109 standard; DNA; 2745 BP.  
DE Mycobacterium bovis large ORF WAG9200 DNA sequence.  
PN US783386-A.  
PD 21-JUL-1998.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 725  
ID AAV38108 standard; DNA; 2745 BP.  
DE Mycobacterium bovis virulence restoring DNA sequence.  
PN US783386-A.  
PD 21-JUL-1998.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 726  
ID AAS14697 standard; DNA; 3038 BP.

DE Human cDNA encoding neuroendocrine VGF.  
PN WO200174298-A2.  
PD 11-OCT-2001.  
PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
PA (HUGH-) HUGHES HOWARD MED INST.  
Query Match 5.0%; Score 49.4; DB 4; Length 3038;  
Best Local Similarity 44.2%; Pred. No. 22;  
RESULT 727  
ID ADD14800 standard; cDNA; 3038 BP.  
DE Human src biomarker polynucleotide SEQ ID NO:194.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.0%; Score 49.4; DB 10; Length 3038;  
Best Local Similarity 44.2%; Pred. No. 22;  
RESULT 728  
ID AAV22683 standard; cDNA to mRNA; 3331 BP.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JF10080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 729  
ID AAZ32021 standard; DNA; 3331 BP.  
DE Human METH1 related EST D86074.  
PN WO9937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 730  
ID AAC90078 standard; DNA; 3331 BP.  
DE D86074 cDNA clone.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Query Match 5.0%; Score 49.4; DB 5; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 731  
ID AAA30290 standard; DNA; 3489 BP.  
DE Kaposi's sarcoma-associated herpesvirus LANA gene.  
PN WO200029626-A1.  
PD 25-MAY-2000.  
PA (KIEF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 5.0%; Score 49.4; DB 3; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 732  
ID AAF82901 standard; DNA; 3489 BP.  
DE Nucleotide sequence of KSHV tethering protein, LANA.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.0%; Score 49.4; DB 4; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 733  
ID ABA93487 standard; DNA; 3489 BP.  
DE Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA.  
PN US6322792-B1.  
PD 27-NOV-2001.

PA (KIEFF/) KIEFF E D.  
Query Match 5.0%; Score 49.4; DB 6; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 734  
ID ADJ65095 standard; DNA; 3489 BP.  
DE HHV8 DNA encoding latency-associated nuclear antigen, LANNA.  
PN US2004037847-A1.  
PD 26-FEB-2004.  
PA (KIEFF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 5.0%; Score 49.4; DB 12; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 735  
ID ACA27005 standard; DNA; 4255 BP.  
DE Prokaryotic essential gene #8662.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 4255;  
Best Local Similarity 45.5%; Pred. No. 22;  
RESULT 736  
ID ADS19485 standard; DNA; 4353 BP.  
DE Modified HIV-1 GagPol polynucleotide sequence.  
PN US2004037780-A1.  
PD 26-FEB-2004.  
PA (PARS/) PARSONS D.  
PA (ANSO/) ANSON D.  
PA (LIMB/) LIMBERIS M.  
PA (FULL/) FULLER M.  
Query Match 5.0%; Score 49.4; DB 13; Length 4353;  
Best Local Similarity 48.1%; Pred. No. 22;  
RESULT 737  
ID AAV33912 standard; cDNA; 4524 BP.  
DE Nucleotide sequence of the SIAx DP2-64 (Oct-T1) gene.  
PN WO9849299-A1.  
PD 05-NOV-1998.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 5.0%; Score 49.4; DB 2; Length 4524;  
Best Local Similarity 47.5%; Pred. No. 22;  
RESULT 738  
ID ADRO1282 standard; DNA; 9762 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 3, SEQ ID 73.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 9762;  
Best Local Similarity 49.4%; Pred. No. 21;  
RESULT 739  
ID AAV62152 standard; DNA; 10211 BP.  
DE HSV-2 strain S85 Contig ID 99 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49.4; DB 2; Length 10211;  
Best Local Similarity 45.8%; Pred. No. 21;  
RESULT 740  
ID ABV99363 standard; DNA; 14061 BP.  
DE Human NOVI3b coding sequence.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.0%; Score 49.4; DB 6; Length 14061;  
Best Local Similarity 44.7%; Pred. No. 21;  
RESULT 741  
ID AAV73805 standard; DNA; 32207 BP.  
DE KSHV LUR DNA (nucleotides 105,301-137,507).  
PN US5849564-A.  
PD 15-DEC-1998.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.0%; Score 49.4; DB 2; Length 32207;  
Best Local Similarity 42.9%; Pred. No. 21;  
RESULT 742

ID ADR67012 standard; DNA; 32229 BP.  
DE Human cancer associated gene genomic sequence SEQ ID NO:58.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 32229;  
Best Local Similarity 45.0%; Pred. No. 21;  
RESULT 743  
ID ADO51695 standard; DNA; 32329 BP.  
DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
PN US2004038250-A1.  
PD 26-FEB-2004.  
PA (ASTU-) ASTUR-PHARMA SA.  
PA (UYOV-) UNIV OVIEDO.  
Query Match 5.0%; Score 49.4; DB 12; Length 32329;  
Best Local Similarity 44.7%; Pred. No. 21;  
RESULT 744  
ID ABZ37516 standard; DNA; 59816 BP.  
DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 745  
ID ABZ37515 standard; DNA; 59816 BP.  
DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 746  
ID ABX04971 standard; DNA; 103599 BP.  
DE S. cinamonensis monensin type I polyketide synthase gene cluster.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 747  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
Query Match 5.0%; Score 49.4; DB 5; Length 109519;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 748  
Query Match 5.0%; Score 49.4; DB 4; Length 110000;  
Best Local Similarity 47.6%; Pred. No. 20;  
RESULT 749  
Query Match 5.0%; Score 49.4; DB 4; Length 110000;  
Best Local Similarity 47.6%; Pred. No. 20;  
RESULT 750  
ID AA19941 standard; DNA; 137507 BP.  
DE KSHV long unique coding region and terminal repeat.  
PN WO9804576-A1.  
PD 05-FEB-1998.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.0%; Score 49.4; DB 2; Length 137507;  
Best Local Similarity 42.9%; Pred. No. 20;  
RESULT 751  
ID ADN12162 standard; DNA; 137508 BP.  
DE Human herpesvirus 8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO-) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match 5.0%; Score 49.4; DB 12; Length 137508;  
Best Local Similarity 42.9%; Pred. No. 20;  
RESULT 752  
ID ABD17309 standard; DNA; 789 BP.  
DE Pseudomonas aeruginosa polynucleotide #15913.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.0%; Score 49.2; DB 11; Length 789;  
 Best Local Similarity 48.3%; Pred. No. 25;  
 RESULT 753  
 ID ABD13248 standard; DNA; 795 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11852.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 795;  
 Best Local Similarity 46.1%; Pred. No. 25;  
 RESULT 754  
 ID ABD17908 standard; DNA; 888 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16512.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 888;  
 Best Local Similarity 50.7%; Pred. No. 24;  
 RESULT 755  
 ID ADS5666 standard; cDNA; 972 BP.  
 DE Bacterial polynucleotide #8653.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOV/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.0%; Score 49.2; DB 13; Length 972;  
 Best Local Similarity 47.2%; Pred. No. 24;  
 RESULT 756  
 ID AAS72681 standard; cDNA; 1074 BP.  
 DE DNA encoding novel human diagnostic protein #8485.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.0%; Score 49.2; DB 5; Length 1074;  
 Best Local Similarity 42.4%; Pred. No. 24;  
 RESULT 757  
 ID ABD12927 standard; DNA; 1221 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11531.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1221;  
 Best Local Similarity 46.1%; Pred. No. 24;  
 RESULT 758  
 ID ABD15054 standard; DNA; 1263 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13658.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
 Best Local Similarity 45.8%; Pred. No. 24;  
 RESULT 759  
 ID ABD14863 standard; DNA; 1263 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13467.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
 Best Local Similarity 45.6%; Pred. No. 24;  
 RESULT 760  
 ID AAX09011 standard; cDNA; 1266 BP.  
 DE Brn-3a polynucleotide.  
 PN WO9905272-A1.  
 PD 04-FEB-1999.  
 PA (UNLO) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.2; DB 2; Length 1366;  
 Best Local Similarity 47.4%; Pred. No. 24;  
 RESULT 761  
 ID AAA29007 standard; cDNA; 1266 BP.  
 DE Murine transcription factor Brn-3a coding sequence.

PN WO200034466-A1.  
 PD 15-JUN-2000.  
 PA (UNLO) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.2; DB 3; Length 1266;  
 Best Local Similarity 47.4%; Pred. No. 24;  
 RESULT 762  
 ID ABD17488 standard; DNA; 1512 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16092.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1512;  
 Best Local Similarity 50.7%; Pred. No. 24;  
 RESULT 763  
 ID ABD17174 standard; DNA; 1521 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15778.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1521;  
 Best Local Similarity 48.3%; Pred. No. 24;  
 RESULT 764  
 ID ABD17253 standard; DNA; 1569 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15857.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1569;  
 Best Local Similarity 48.3%; Pred. No. 24;  
 RESULT 765  
 ID AAD11112 standard; DNA; 1602 BP.  
 DE Human small cell lung cancer associated gene, ZIC2.  
 PN WO200153349-A2.  
 PD 26-JUL-2001.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 PA (CORR) CORNELL RES FOUND INC.  
 Query Match 5.0%; Score 49.2; DB 4; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 766  
 ID AAS61863 standard; cDNA; 1602 BP.  
 DE Lung small cell carcinoma antigen, cDNA #404.  
 PN WO200177168-A2.  
 PD 18-OCT-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.2; DB 6; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 767  
 ID ADD15207 standard; DNA; 1602 BP.  
 DE DNA encoding the human zinc finger protein ZIC2.  
 PN WO2003039490-A2.  
 PD 15-MAY-2003.  
 PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.  
 Query Match 5.0%; Score 49.2; DB 10; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 768  
 ID ADQ03085 standard; DNA; 1713 BP.  
 DE P. aeruginosa virulence gene, VIR17.  
 PN US2004122212-A1.  
 PD 24-JUN-2004.  
 PA (COSS/) COSSON P.  
 PA (KOHL/) KOHLER T.  
 PA (BENG/) BENGHEZAL M.  
 PA (MARC/) MARCHETTI A.  
 PA (DELD/) DELDEN C V.  
 Query Match 5.0%; Score 49.2; DB 12; Length 1713;  
 Best Local Similarity 43.8%; Pred. No. 24;  
 RESULT 769  
 ID ADP88591 standard; DNA; 2160 BP.  
 DE Murine class V POU transcription factor Brn3a gene.  
 PN WO2004052186-A2.  
 PD 24-JUN-2004.  
 PA (FORS-) FORSYTH INST.

Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2160;  
RESULT 770  
ID ABD17387 standard; DNA; 2400 BP.  
DE Pseudomonas aeruginosa polynucleotide #15991.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 11; Length 2400;  
RESULT 771  
ID ABK63479 standard; cDNA; 2455 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1386.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 6; Length 2455;  
RESULT 772  
ID ADB58687 standard; DNA; 2455 BP.  
DE Toxicity-related gene, SEQ ID 3713.  
PN WO2003084624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 773  
ID ADB53374 standard; DNA; 2455 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3916.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 774  
ID ADF30464 standard; cDNA; 2455 BP.  
DE Rat angiogenesis modulating protein cDNA #9.  
PN US2003162706-A1.  
PD 28-AUG-2003.  
PA (PROC) PROCTER & GAMBLE CO.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 775  
ID ABT42262 standard; DNA; 2455 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1364.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 776  
ID ADP72601 standard; DNA; 2455 BP.  
DE Renal toxin progression gene marker #1190.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2455;  
RESULT 777  
ID ADE25609 standard; cDNA; 2607 BP.  
DE Human cDNA differentially expressed in foam cells #13.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2607;  
RESULT 778  
ID ADK70215 standard; cDNA; 2680 BP.  
DE Human oesophageal cancer antigen cDNA SEQ ID NO:11.  
PN JP2003259872-A.  
PD 16-SEP-2003.  
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2680;

Best Local Similarity 53.0%; Pred. No. 24;  
RESULT 779  
ID ADQ25191 standard; DNA; 2717 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8011.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2717;  
RESULT 780  
ID ABA02191 standard; cDNA; 3318 BP.  
DE Human C/EBP alpha-encoding cDNA.  
PN US6306655-B1.  
PD 23-OCT-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 6; Length 3318;  
RESULT 781  
ID ADS56329 standard; cDNA; 3540 BP.  
DE Bacterial polynucleotide #8316.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 13; Length 3540;  
RESULT 782  
ID ADI39068 standard; DNA; 3597 BP.  
DE S. coelicolor meth DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI) BASF AG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 3597;  
RESULT 783  
ID ADI39145 standard; DNA; 8787 BP.  
DE Plasmid pCPHsdh meth\_SC DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI) BASF AG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 8787;  
RESULT 784  
ID ABL50991 standard; DNA; 35133 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 nucleotide sequence.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 4; Length 35133;  
RESULT 785  
ID ABL50990 standard; DNA; 35134 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 SEQ ID NO:1.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 4; Length 35134;  
RESULT 786  
ID ADP74816 standard; DNA; 137560 BP.  
DE Parapoxvirus ovis genome DNA sequence SeqID1.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 137560;  
RESULT 787  
ID AA68100 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

Query Match 5.0%; Score 49; DB 3; Length 399;  
Best Local Similarity 57.5%; Pred. No. 27;  
RESULT 788  
ID ADD41850 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #1.  
PN US200311373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 5.0%; Score 49; DB 10; Length 399;  
Best Local Similarity 57.5%; Pred. No. 27;  
RESULT 789  
ID ACA37827 standard; DNA; 717 BP.  
DE Prokaryotic essential gene #19484.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49; DB 8; Length 717;  
Best Local Similarity 44.8%; Pred. No. 27;  
RESULT 790  
ID ABX56042 standard; DNA; 843 BP.  
DE M. echinospira calicheamicin biosynthesis gene calr.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 5.0%; Score 49; DB 8; Length 843;  
Best Local Similarity 47.9%; Pred. No. 26;  
RESULT 791  
ID AAZ51697 standard; DNA; 1044 BP.  
DE Burkholderia cepacia reca gene (1).  
PN WO200014274-A1.  
PD 16-MAR-2000.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 5.0%; Score 49; DB 3; Length 1044;  
Best Local Similarity 43.8%; Pred. No. 26;  
RESULT 792  
ID AAT44494 standard; cDNA; 1355 BP.  
DE Murine cyclin-dependent kinase inhibitor p57KIP2 cDNA.  
PN WO9631534-A1.  
PD 10-OCT-1996.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 5.0%; Score 49; DB 2; Length 1355;  
Best Local Similarity 50.2%; Pred. No. 26;  
RESULT 793  
ID AAI72395 standard; cDNA; 1355 BP.  
DE p57-KIP2 cDNA.  
PN WO200204605-A2.  
PD 17-JAN-2002.  
PA (OTOG-) OTOGENE USA INC.  
PA (OTOG-) OTOGENE AG.  
Query Match 5.0%; Score 49; DB 6; Length 1355;  
Best Local Similarity 50.2%; Pred. No. 26;  
RESULT 794  
ID AAH26499 standard; DNA; 1614 BP.  
DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.0%; Score 49; DB 5; Length 1614;  
Best Local Similarity 43.7%; Pred. No. 26;  
RESULT 795  
ID ABS58306 standard; cDNA; 1852 BP.  
DE Spider dragline cDNA repetitive nucleotide sequence.  
PN US2002137211-A1.  
PD 26-SEP-2002.  
PA (UYSI-) UNIV SICHUAN TIANYOU BIOLOGIC ENG CO LTD.  
Query Match 5.0%; Score 49; DB 10; Length 1852;  
Best Local Similarity 46.6%; Pred. No. 26;  
RESULT 796  
ID ADM47862 standard; DNA; 1891 BP.  
DE Polynucleotide sequence #280 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.

PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 5.0%; Score 49; DB 12; Length 1891;  
Best Local Similarity 50.6%; Pred. No. 26;  
RESULT 797  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49; DB 8; Length 2000;  
Best Local Similarity 9.7%; Pred. No. 26;  
RESULT 798  
ID ADS10050 standard; DNA; 3070 BP.  
DE Human therapeutic DNA - SEQ ID 287.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 5.0%; Score 49; DB 13; Length 3070;  
Best Local Similarity 49.1%; Pred. No. 26;  
RESULT 799  
ID AAH98717 standard; cDNA; 4486 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 574.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49; DB 4; Length 4486;  
Best Local Similarity 47.5%; Pred. No. 25;  
RESULT 800  
ID AAV62153 standard; DNA; 7361 BP.  
DE HSV-2 strain SB5 Contig ID 1 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49; DB 2; Length 7361;  
Best Local Similarity 42.8%; Pred. No. 25;  
RESULT 801  
ID AAV62130 standard; DNA; 8952 BP.  
DE HSV-2 strain SB5 Contig ID 100 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49; DB 2; Length 8952;  
Best Local Similarity 42.8%; Pred. No. 25;  
RESULT 802  
ID AAL61171 standard; DNA; 9222 BP.  
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 5.0%; Score 49; DB 8; Length 9222;  
Best Local Similarity 46.0%; Pred. No. 25;  
RESULT 803  
ID AAH26495 standard; DNA; 12425 BP.  
DE Human low density lipoprotein binding protein 2 (LBP-2) gene.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.0%; Score 49; DB 5; Length 12425;  
Best Local Similarity 43.7%; Pred. No. 25;  
RESULT 804  
ID AAA14651 standard; DNA; 77536 BP.  
DE Nucleotide sequence of the PK-520 bioaynetic gene cluster.  
Query Match 5.0%; Score 49; DB 3; Length 77536;  
Best Local Similarity 44.4%; Pred. No. 23;  
RESULT 805  
Query Match 5.0%; Score 49; DB 4; Length 110000;  
Best Local Similarity 50.6%; Pred. No. 23;  
RESULT 806  
Query Match 5.0%; Score 49; DB 4; Length 110000;  
Best Local Similarity 45.0%; Pred. No. 23;  
RESULT 807

Query Match  
Best Local Similarity 5.0%; Score 49; DB 4; Length 110000;  
RESULT 808  
ID AAV62176 standard; DNA; 117213 BP.  
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
Query Match  
Best Local Similarity 5.0%; Score 49; DB 2; Length 117213;  
Best Local Similarity 42.8%; Pred. No. 23;  
RESULT 809  
ID ABD09003 standard; DNA; 852 BP.  
DE Pseudomonas aeruginosa polynucleotide #7607.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 852;  
Best Local Similarity 49.2%; Pred. No. 29;  
RESULT 810  
ID ABD10213 standard; DNA; 1083 BP.  
DE Pseudomonas aeruginosa polynucleotide #8817.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 1083;  
Best Local Similarity 50.3%; Pred. No. 28;  
RESULT 811  
ID ADQ87326 standard; cDNA; 1149 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4203.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 13; Length 1149;  
Best Local Similarity 49.6%; Pred. No. 28;  
RESULT 812  
ID ADQ87564 standard; cDNA; 1149 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4442.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 13; Length 1149;  
Best Local Similarity 49.6%; Pred. No. 28;  
RESULT 813  
ID ADC36141 standard; DNA; 1188 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:8.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 1188;  
Best Local Similarity 47.1%; Pred. No. 28;  
RESULT 814  
ID ACF06125 standard; DNA; 1194 BP.  
DE Bacterial P450 enzyme encoding DNA SEQ ID NO:33.  
PN WO2003052050-A2.  
PD 26-JUN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 9; Length 1194;  
Best Local Similarity 44.8%; Pred. No. 28;  
RESULT 815  
ID AAS09830 standard; DNA; 1209 BP.  
DE Pseudorabies virus DNA encoding glycoprotein 50, gp50.  
PN US6251634-B1.  
PD 26-JUN-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 4; Length 1209;  
Best Local Similarity 44.9%; Pred. No. 28;  
RESULT 816  
ID ABD10628 standard; DNA; 1227 BP.  
DE Pseudomonas aeruginosa polynucleotide #9232.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 1227;  
Best Local Similarity 50.3%; Pred. No. 28;  
RESULT 817  
ID ABZ66800 standard; DNA; 1272 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 262.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 1272;  
Best Local Similarity 47.6%; Pred. No. 28;  
RESULT 818  
ID ABD10546 standard; DNA; 1296 BP.  
DE Pseudomonas aeruginosa polynucleotide #9150.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 1296;  
Best Local Similarity 50.3%; Pred. No. 28;  
RESULT 819  
ID ADC36144 standard; DNA; 1418 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:11.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 1418;  
Best Local Similarity 47.1%; Pred. No. 28;  
RESULT 820  
ID ADC36202 standard; DNA; 1418 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:69.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 1418;  
Best Local Similarity 47.1%; Pred. No. 28;  
RESULT 821  
ID ACC47259 standard; cDNA; 1427 BP.  
DE Human SCAP encoding cDNA-Incyte Id. 6891852CB1.  
PN WO2003008625-A2.  
PD 30-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 8; Length 1427;  
Best Local Similarity 48.0%; Pred. No. 28;  
RESULT 822  
ID ABD13152 standard; DNA; 2232 BP.  
DE Pseudomonas aeruginosa polynucleotide #11756.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 2232;  
Best Local Similarity 43.4%; Pred. No. 28;  
RESULT 823  
ID ABD13005 standard; DNA; 2274 BP.  
DE Pseudomonas aeruginosa polynucleotide #11609.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 2274;  
Best Local Similarity 43.4%; Pred. No. 28;  
RESULT 824  
ID ABD13232 standard; DNA; 2613 BP.  
DE Pseudomonas aeruginosa polynucleotide #11836.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 2613;  
Best Local Similarity 43.4%; Pred. No. 28;  
RESULT 825  
ID ABD10111 standard; DNA; 2715 BP.  
DE Pseudomonas aeruginosa polynucleotide #8715.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.9%; Score 48.8; DB 11; Length 2715;

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Best Local Similarity 50.3%; Pred. No. 28;
RESULT 826
ID ABK93509 standard; DNA; 4826 BP.
DE DNA fragment containing poly-beta-hydroxybutyrate, PHB, synthesis genes.
PN US2002146785-A1.
PD 10-OCT-2002.
PA (MAHI/) MAHISHI L H.
PA (TRIP/) TRIPATHI G.
PA (RAMC/) RAMCHANDER T V N.
PA (RAWA/) RAWAL S K.
Query Match 4.9%; Score 48.8; DB 8; Length 4826;
Best Local Similarity 45.7%; Pred. No. 27;
RESULT 827
ID ABK91609 standard; DNA; 7897 BP.
DE Modified HIV protein-encoding plasmid DNA #161.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 7897;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 828
ID ABK91616 standard; DNA; 9166 BP.
DE Modified HIV protein-encoding plasmid DNA #168.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9166;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 829
ID ABK91619 standard; DNA; 9167 BP.
DE Modified HIV protein-encoding plasmid DNA #171.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9167;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 830
ID ABK91617 standard; DNA; 9169 BP.
DE Modified HIV protein-encoding plasmid DNA #169.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9169;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 831
ID ABK91614 standard; DNA; 9170 BP.
DE Modified HIV protein-encoding plasmid DNA #166.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9170;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 832
ID ABK91607 standard; DNA; 9189 BP.
DE Modified HIV protein-encoding plasmid DNA #159.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9189;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 833
ID ABK91612 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #164.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 834
ID ABK91611 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #163.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 835
ID ABK91623 standard; DNA; 9407 BP.
DE Modified HIV protein-encoding plasmid DNA #175.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9407;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 836
ID ABK91621 standard; DNA; 9782 BP.
DE Modified HIV protein-encoding plasmid DNA #173.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9782;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 837
ID ABK91620 standard; DNA; 9783 BP.
DE Modified HIV protein-encoding plasmid DNA #172.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9783;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 838
ID ABK91624 standard; DNA; 9785 BP.
DE Modified HIV protein-encoding plasmid DNA #176.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9785;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 839
ID ABK91622 standard; DNA; 9788 BP.
DE Modified HIV protein-encoding plasmid DNA #174.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9788;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 840
ID ABK91618 standard; DNA; 9792 BP.
DE Modified HIV protein-encoding plasmid DNA #170.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9792;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 841
ID ABZ66813 standard; DNA; 10035 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 282.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.8; DB 10; Length 10035;
Best Local Similarity 47.6%; Pred. No. 27;

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RESULT 842  
ID ADQ91701 standard; DNA; 10287 BP.  
DE Polyketide synthase ORF1, SEQ ID 24.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.8; DB 13; Length 10287;  
Best Local Similarity 47.4%; Pred. No. 27;  
RESULT 843  
ID ABK91613 standard; DNA; 12411 BP.  
DE Modified HIV protein-encoding plasmid DNA #165.  
PN WO200232943-A2.  
PD 25-APR-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (CHAD/) CHADRABARTI B K.  
Query Match 4.9%; Score 48.8; DB 6; Length 12411;  
Best Local Similarity 47.9%; Pred. No. 27;  
RESULT 844  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PN WO200277179-A2.  
PD 03-OCT-2002.  
PA (REGC ) UNIV CALIFORNIA.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 4.9%; Score 48.8; DB 10; Length 135638;  
Best Local Similarity 44.7%; Pred. No. 25;  
RESULT 845  
ID ABS63423 standard; cDNA; 528 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 4.9%; Score 48.6; DB 6; Length 528;  
Best Local Similarity 50.2%; Pred. No. 31;  
RESULT 846  
ID ACA38429 standard; DNA; 687 BP.  
DE Prokaryotic essential gene #20086.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 687;  
Best Local Similarity 45.3%; Pred. No. 31;  
RESULT 847  
ID ACA40639 standard; DNA; 690 BP.  
DE Prokaryotic essential gene #22296.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 690;  
Best Local Similarity 45.3%; Pred. No. 31;  
RESULT 848  
ID ADS58740 standard; cDNA; 1203 BP.  
DE Bacterial polynucleotide #10727.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.9%; Score 48.6; DB 13; Length 1203;  
Best Local Similarity 46.6%; Pred. No. 31;  
RESULT 849  
ID ABX56068 standard; DNA; 1320 BP.  
DE M. echinospora calicheamicin biosynthesis gene orfVIII.  
PN WO200279485-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 4.9%; Score 48.6; DB 8; Length 1320;  
Best Local Similarity 45.1%; Pred. No. 30;  
RESULT 850

ID ACC92989 standard; DNA; 1397 BP.  
DE HIV-1 subtype C isolate Dui51 reverse transcriptase codon optimised DNA.  
PN WO2003037919-A2.  
PD 08-MAY-2003.  
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
Query Match 4.9%; Score 48.6; DB 8; Length 1397;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 851  
ID AAT90471 standard; cDNA; 1479 BP.  
DE Human agrin cDNA.  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REG-) REGENERON PHARM INC.  
Query Match 4.9%; Score 48.6; DB 2; Length 1479;  
Best Local Similarity 43.8%; Pred. No. 30;  
RESULT 852  
ID ADL61985 standard; DNA; 1533 BP.  
DE Human ovarian cancer DNA marker #20197.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 48.6; DB 5; Length 1533;  
Best Local Similarity 48.4%; Pred. No. 30;  
RESULT 853  
ID ABD12608 standard; DNA; 1575 BP.  
DE Pseudomonas aeruginosa polynucleotide #11212.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1575;  
Best Local Similarity 46.6%; Pred. No. 30;  
RESULT 854  
ID ABD12542 standard; DNA; 1620 BP.  
DE Pseudomonas aeruginosa polynucleotide #11146.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1620;  
Best Local Similarity 46.6%; Pred. No. 30;  
RESULT 855  
ID AAT62137 standard; DNA; 2040 BP.  
DE Leishmania braziliensis Lbhsp83 antigen cDNA.  
PN WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 856  
ID AAV47557 standard; DNA; 2040 BP.  
DE Leishmania antigen Lbhsp83 coding sequence.  
PN WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 857  
ID AAD47114 standard; DNA; 2040 BP.  
DE Leishmania sp. 6H (Lbhsp83) DNA.  
PN WO200272792-A2.  
PD 19-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 858  
ID AAD40284 standard; DNA; 2040 BP.  
DE Leishmania braziliensis hsp83 antigenic protein encoding DNA.  
PN US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 859



ID AAS96021 standard; cDNA; 2040 BP.  
DE Leishmania antigen Lbhep83 DNA.  
PN WO200179276-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 860  
ID ABK81732 standard; cDNA; 2040 BP.  
DE Leishmania antigenic polynucleotide #3.  
PN US6365165-B1.  
PD 02-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 861  
ID AAF89523 standard; DNA; 2040 BP.  
DE L. braziliensis Hsp83 antigen DNA SEQ ID 5.  
PN US2002081320-A1.  
PD 27-JUN-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
PA (SKEI/) SKEIKY Y A W.  
PA (BHAT/) BHATIA A.  
PA (COLE/) COLER R N.  
PA (PROB/) PROBST P.  
PA (BRAN/) BRANNON M.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 862  
ID ADB78768 standard; cDNA; 2040 BP.  
DE Leishmania DNA encoding antigen Lbhep83.  
PN US2002189285-A1.  
PD 14-NOV-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
Query Match 4.9%; Score 48.6; DB 9; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 863  
ID AAH14403 standard; cDNA; 2279 BP.  
DE Human cDNA sequence SEQ ID NO:11841.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 4.9%; Score 48.6; DB 4; Length 2279;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 864  
ID ABX08845 standard; cDNA; 2279 BP.  
DE Angiogenesis-associated human polynucleotide sequence #107.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48.6; DB 10; Length 2279;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 865  
ID ADS34446 standard; DNA; 2279 BP.  
DE FOSH protein associated DNA #200.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 2279;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 866  
ID AAH17825 standard; cDNA; 2454 BP.  
DE Human cDNA sequence SEQ ID NO:17498.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 4.9%; Score 48.6; DB 4; Length 2454;

Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 867  
ID ADS34445 standard; DNA; 2454 BP.  
DE FOSH protein associated DNA #199.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 2454;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 868  
ID ABD12439 standard; DNA; 2472 BP.  
DE Pseudomonas aeruginosa polynucleotide #11043.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 2472;  
Best Local Similarity 46.6%; Pred. No. 30;  
RESULT 869  
ID ADS34441 standard; DNA; 2544 BP.  
DE FOSH protein associated DNA #195.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 2544;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 870  
ID AAL41592 standard; DNA; 2577 BP.  
DE HIV-1 subtype C isolate Du151 pol gene.  
PN WO200204494-A2.  
PD 17-JAN-2002.  
PA (MEDI-) MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
PA (UYNC-) UNIV NORTH CAROLINA.  
Query Match 4.9%; Score 48.6; DB 6; Length 2577;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 871  
ID AAZ06825 standard; DNA; 2712 BP.  
DE Streptomyces albidoflavus endochitinase DNA.  
PN WO9942594-A1.  
PD 26-AUG-1999.  
PA (CORR-) CORNELL RES FOUND INC.  
Query Match 4.9%; Score 48.6; DB 2; Length 2712;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 872  
ID AAH74538 standard; DNA; 2712 BP.  
DE Nucleotide sequence of an endochitinase polypeptide.  
PN WO200146387-A1.  
PD 28-JUN-2001.  
PA (CORR-) CORNELL RES FOUND INC.  
Query Match 4.9%; Score 48.6; DB 4; Length 2712;  
Best Local Similarity 47.6%; Pred. No. 30;  
RESULT 873  
ID ADS34444 standard; DNA; 3003 BP.  
DE FOSH protein associated DNA #198.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 3003;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 874  
ID ADQ85699 standard; cDNA; 3268 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2513.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.6; DB 12; Length 3268;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 875  
ID ADQ86774 standard; cDNA; 3268 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3649.  
PN WO2004060270-A2.

PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.6; DB 13; Length 3268;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 876  
ID ADS34439 standard; DNA; 3292 BP.  
DE POSH protein associated DNA #193.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 3292;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 877  
ID ABA95198 standard; cDNA; 3298 BP.  
DE Human MICAPTUB-2 polypeptide encoding cDNA (clone ID: 1593855CBI).  
PN WO200216587-A2.  
PD 28-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.9%; Score 48.6; DB 6; Length 3298;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 878  
ID ACC82987 standard; DNA; 3687 BP.  
DE HIV-1 Gtttnc DNA construct.  
PN WO2003037919-A2.  
PD 08-MAY-2003.  
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
Query Match 4.9%; Score 48.6; DB 8; Length 3687;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 879  
ID ADO85410 standard; DNA; 3720 BP.  
DE Streptomycetes phoK/phoR::omegaaac double mutant, seq id 5.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 4.9%; Score 48.6; DB 12; Length 3720;  
Best Local Similarity 49.4%; Pred. No. 30;  
RESULT 880  
ID ADQ85245 standard; cDNA; 4405 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2059.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.6; DB 13; Length 4405;  
Best Local Similarity 47.5%; Pred. No. 29;  
RESULT 881  
ID ADC39155 standard; cDNA; 4760 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 97.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 4760;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 882  
ID ADH72283 standard; DNA; 4760 BP.  
DE Human gene of the invention NOV60d SEQ ID NO:1179.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 4760;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 883  
ID ADO85408 standard; DNA; 4860 BP.  
DE Streptomycetes phoK::omegaaac mutant, seq id 3.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 4.9%; Score 48.6; DB 12; Length 4860;  
Best Local Similarity 49.4%; Pred. No. 29;

RESULT 884  
ID AAH48730 standard; cDNA; 5065 BP.  
DE Human HCN4 cDNA.  
PN WO200159153-A2.  
PD 16-AUG-2001.  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
Query Match 4.9%; Score 48.6; DB 4; Length 5065;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 885  
ID ADR86593 standard; cDNA; 5065 BP.  
DE Human HCN4 gene.  
PN JP2004254628-A.  
PD 16-SEP-2004.  
PA (KIMU/) KIMURA A.  
Query Match 4.9%; Score 48.6; DB 13; Length 5065;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 886  
ID ABA09197 standard; cDNA; 5499 BP.  
DE Human cation channel hHCN4 homologue cDNA, SEQ ID NO:973.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.6; DB 4; Length 5499;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 887  
ID ADC39153 standard; cDNA; 6224 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 95.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 888  
ID ADH72277 standard; DNA; 6224 BP.  
DE Human gene of the invention NOV60a SEQ ID NO:1173.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 889  
ID ADM74234 standard; DNA; 6224 BP.  
DE Human NOV8A gene sequence SeqID73.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 890  
ID ADC39163 standard; cDNA; 6494 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 105.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 6494;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 891  
ID ADH72291 standard; DNA; 6494 BP.  
DE Human gene of the invention NOV60h SEQ ID NO:1187.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6494;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 892  
ID AAV23873 standard; DNA; 562 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 4.9%; Score 48.4; DB 2; Length 562;  
 Best Local Similarity 49.2%; Pred. No. 34;  
 RESULT 894  
 ID AAZ06876 standard; cDNA; 562 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 2.  
 PN U5952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Query Match 4.9%; Score 48.4; DB 2; Length 562;  
 Best Local Similarity 49.2%; Pred. No. 34;  
 RESULT 895  
 ID AAA69580 standard; cDNA; 562 BP.  
 DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Query Match 4.9%; Score 48.4; DB 3; Length 562;  
 Best Local Similarity 49.2%; Pred. No. 34;  
 RESULT 896  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Query Match 4.9%; Score 48.4; DB 3; Length 562;  
 Best Local Similarity 49.2%; Pred. No. 34;  
 RESULT 897  
 ID ADD41710 standard; DNA; 562 BP.  
 DE O-methyl transferase DNA #6.  
 PN US2003131373-A1.  
 PD 10-JUL-2003  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 4.9%; Score 48.4; DB 10; Length 562;  
 Best Local Similarity 49.2%; Pred. No. 34;  
 RESULT 898  
 ID ADO52096 standard; DNA; 633 BP.  
 DE Novel canine microarray-related DNA sequence SeqID3398.  
 PN WO2004063324-A2.  
 PD 29-JUL-2004.  
 PA (GENE-) GENE LOGIC INC.  
 PA (PFIZ) PFIZER PROD INC.  
 Query Match 4.9%; Score 48.4; DB 13; Length 633;  
 Best Local Similarity 49.8%; Pred. No. 34;  
 RESULT 899  
 ID AAQ43032 standard; DNA; 756 BP.  
 DE Collagen-like polymer DCP3-C2 (AB12)C2 coding sequence.  
 PN WO9310154-A1.  
 PD 27-MAY-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 4.9%; Score 48.4; DB 2; Length 756;  
 Best Local Similarity 44.3%; Pred. No. 33;  
 RESULT 900  
 ID AAT16766 standard; DNA; 756 BP.  
 DE Collagen-like polymer sequence D gene 2 encoding unit C2A24C2.  
 PN U55496712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 4.9%; Score 48.4; DB 2; Length 756;  
 Best Local Similarity 44.3%; Pred. No. 33;  
 RESULT 901  
 ID AAA02484 standard; cDNA; 1000 BP.  
 DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.  
 PN WO9958675-A2.  
 PD 18-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.9%; Score 48.4; DB 3; Length 1000;  
 Best Local Similarity 33.5%; Pred. No. 33;

RESULT 902  
 ID ADA70207 standard; DNA; 1059 BP.  
 DE Rice gene, SEQ ID 3530.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.9%; Score 48.4; DB 8; Length 1059;  
 Best Local Similarity 43.8%; Pred. No. 33;  
 RESULT 903  
 ID ADJ11579 standard; DNA; 1059 BP.  
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 215.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBOOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICHKE D.  
 Query Match 4.9%; Score 48.4; DB 11; Length 1059;  
 Best Local Similarity 43.8%; Pred. No. 33;  
 RESULT 904  
 ID ADA71187 standard; DNA; 1482 BP.  
 DE Rice gene, SEQ ID 4510.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.9%; Score 48.4; DB 8; Length 1482;  
 Best Local Similarity 44.0%; Pred. No. 33;  
 RESULT 905  
 ID AAZ35999 standard; DNA; 1646 BP.  
 DE S. kitatoensis macrolide antibiotic acylation enzyme gene.  
 PN JP11285384-A.  
 PD 19-OCT-1999.  
 PA (ASAH) ASAHI KASEI KOGYO KK.  
 Query Match 4.9%; Score 48.4; DB 3; Length 1646;  
 Best Local Similarity 50.4%; Pred. No. 33;  
 RESULT 906  
 ID ACA37821 standard; DNA; 1650 BP.  
 DE Prokaryotic essential gene #19478.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 1650;  
 Best Local Similarity 45.0%; Pred. No. 33;  
 RESULT 907  
 ID ACA27358 standard; DNA; 2523 BP.  
 DE Prokaryotic essential gene #9015.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 2523;  
 Best Local Similarity 47.4%; Pred. No. 32;  
 RESULT 908  
 ID ADA70538 standard; DNA; 2562 BP.  
 DE Rice gene, SEQ ID 3861.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.9%; Score 48.4; DB 8; Length 2562;  
 Best Local Similarity 47.3%; Pred. No. 32;  
 RESULT 909  
 ID AAS06333 standard; cDNA; 2898 BP.  
 DE DNA encoding human glutamate receptor-like protein, MEM2.  
 PN WO200144473-A2.  
 PD 21-JUN-2001.  
 PA (CURA-) CURAGEN CORP.

Query Match 4.9%; Score 48.4; DB 4; Length 2898;  
 Best Local Similarity 43.0%; Pred. No. 32;  
 RESULT 910  
 ID AAD07033 standard; DNA; 3690 BP.  
 DE Methylobacterium extorquens PHA synthase DNA.  
 PN WO200123596-A2.  
 PD 05-APR-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 4.9%; Score 48.4; DB 4; Length 3690;  
 Best Local Similarity 48.2%; Pred. No. 32;  
 RESULT 911  
 ID AAZ09496 standard; DNA; 4751 BP.  
 DE Human heart tissue 1h ion channel DNA.  
 PN WO9942574-A1.  
 PD 26-AUG-1999.  
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.  
 Query Match 4.9%; Score 48.4; DB 2; Length 4751;  
 Best Local Similarity 53.8%; Pred. No. 32;  
 RESULT 912  
 ID AAD29757 standard; DNA; 4751 BP.  
 DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 4 DNA.  
 PN WO200202630-A2.  
 PD 10-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 Query Match 4.9%; Score 48.4; DB 6; Length 4751;  
 Best Local Similarity 53.8%; Pred. No. 32;  
 RESULT 913  
 ID ACA37735 standard; DNA; 4833 BP.  
 DE Prokaryotic essential gene #19392.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 4833;  
 Best Local Similarity 50.3%; Pred. No. 32;  
 RESULT 914  
 ID AAD54223 standard; DNA; 24081 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.4; DB 10; Length 24081;  
 Best Local Similarity 51.1%; Pred. No. 30;  
 RESULT 915  
 ID ACA37577 standard; DNA; 31263 BP.  
 DE Prokaryotic essential gene #19234.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 31263;  
 Best Local Similarity 46.2%; Pred. No. 30;  
 RESULT 916  
 ID AAD54217 standard; DNA; 52101 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.4; DB 10; Length 52101;  
 Best Local Similarity 51.1%; Pred. No. 30;  
 RESULT 917  
 Query Match 4.9%; Score 48.4; DB 4; Length 110000;  
 Best Local Similarity 45.6%; Pred. No. 29;  
 RESULT 918  
 ID ADQ54676 standard; DNA; 489 BP.  
 DE Novel canine microarray-related DNA sequence SeqID5978.  
 PN WO2004063324-A2.  
 PD 29-JUL-2004.  
 PA (GENE-) GENE LOGIC INC.  
 PA (PFIZ) PFIZER PROD INC.  
 Query Match 4.9%; Score 48.2; DB 13; Length 489;  
 Best Local Similarity 52.7%; Pred. No. 37;  
 RESULT 919  
 ID AAD57189 standard; DNA; 600 BP.

DE Mycobacterium avium subspecies paratuberculosis protein gene #2.  
 PN WO2003058248-A2.  
 PD 17-JUL-2003.  
 PA (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ.  
 Query Match 4.9%; Score 48.2; DB 9; Length 600;  
 Best Local Similarity 48.4%; Pred. No. 36;  
 RESULT 920  
 ID ADC30820 standard; cDNA; 663 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:902.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 663;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 921  
 ID ADK52175 standard; cDNA; 663 BP.  
 DE Full length cDNA clone MasP1 clone 3.  
 PN WO2004016651-A2.  
 PD 26-FEB-2004.  
 PA (UYVO-) UNIV YORK.  
 Query Match 4.9%; Score 48.2; DB 12; Length 663;  
 Best Local Similarity 44.0%; Pred. No. 36;  
 RESULT 922  
 ID ADJ39458 standard; cDNA; 786 BP.  
 DE Plant cDNA #458.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW) BUDWORTH P.  
 PA (MOUG) MOUGHAMER T.  
 PA (BRIG) BRIGGS S P.  
 PA (COOP) COOPER B.  
 PA (GLAZ) GLAZEBROOK J.  
 PA (GOFF) GOFF S A.  
 PA (KATA) KATAGIRI F.  
 PA (KREP) KREPS J.  
 PA (PROV) PROVART N.  
 PA (RICK) RICK D.  
 PA (ZHUT) ZHU T.  
 Query Match 4.9%; Score 48.2; DB 12; Length 786;  
 Best Local Similarity 49.8%; Pred. No. 36;  
 RESULT 923  
 ID ACC68993 standard; cDNA; 811 BP.  
 DE Human neurotension-associated protein NTRAN-15 cDNA SEQ ID NO:40.  
 PN WO2003025129-A2.  
 PD 27-MAR-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 811;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 924  
 ID ABD13103 standard; DNA; 822 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11707.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.2; DB 11; Length 822;  
 Best Local Similarity 46.5%; Pred. No. 36;  
 RESULT 925  
 ID ADG10464 standard; cDNA; 823 BP.  
 DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:54.  
 PN WO200296943-A1.  
 PD 05-DEC-2002.  
 PA (ASAH) ASAHI KASEI KOGYO KK.  
 Query Match 4.9%; Score 48.2; DB 10; Length 823;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 926  
 ID ADG10466 standard; cDNA; 823 BP.  
 DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:56.  
 PN WO200296943-A1.  
 PD 05-DEC-2002.  
 PA (ASAH) ASAHI KASEI KOGYO KK.  
 Query Match 4.9%; Score 48.2; DB 10; Length 823;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 927

ID ACA37950 standard; DNA; 825 BP.  
DE Prokaryotic essential gene #19607.  
PD WO200277183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 825;  
Best Local Similarity 48.9%; Pred. No. 36;  
RESULT 928  
ID AAI58255 standard; cDNA; 920 BP.  
DE Human polynucleotide SEQ ID NO 458.  
PD WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 4; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 929  
ID ADQ98462 standard; cDNA; 920 BP.  
DE DNA encoding human GPCR-like protein seqid 132.  
PD US659662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 5; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 930  
ID ADB48222 standard; cDNA; 920 BP.  
DE Novel human cDNA SEQ ID NO 132.  
PD US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 4.9%; Score 48.2; DB 9; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 931  
ID ACA42680 standard; DNA; 930 BP.  
DE Prokaryotic essential gene #24337.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 930;  
Best Local Similarity 48.1%; Pred. No. 36;  
RESULT 932  
ID ABK51403 standard; DNA; 969 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-2.  
PD WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 933  
ID AAD19181 standard; DNA; 969 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-2 isoform DNA.  
PD WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 934  
ID ADQ83726 standard; cDNA; 972 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #540.  
PD WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 12; Length 972;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 935  
ID ADQ87027 standard; cDNA; 972 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3903.  
PD WO2004060270-A2.

PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 13; Length 972;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 936  
ID ABK51402 standard; DNA; 1038 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-1.  
PD WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 937  
ID AAD19380 standard; DNA; 1038 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-1 isoform DNA.  
PD WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 938  
ID AAS14696 standard; DNA; 1038 BP.  
DE Human cDNA encoding transcription factor C/EBPbeta.  
PD WO200174298-A2.  
PD 11-OCT-2001.  
PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
PA (HUGH-) HUGHES HOWARD MED INST.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 939  
ID AAL44084 standard; DNA; 1038 BP.  
DE Human C/EBP-beta protein coding sequence 3.  
PD WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 940  
ID ABK51997 standard; DNA; 1038 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #3.  
PD WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 941  
ID ACF36516 standard; DNA; 1038 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PD WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 942  
ID ACN40795 standard; cDNA; 1038 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326852, SEQ ID NO:5808.  
PD WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 4.9%; Score 48.2; DB 13; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 943  
ID ABK51410 standard; DNA; 1042 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene mutant.  
PD WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1042;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 944  
ID ADS14749 standard; DNA; 1059 BP.

DE Pseudomonas aeruginosa quorum sensing controlled gene PA5161, SEQ ID 304.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA ) UNIV IOWA RES FOUND.  
Query Match 4.9%; Score 48.2; DB 13; Length 1059;  
Best Local Similarity 47.5%; Pred. No. 36;  
RESULT 945  
ID ADK71964 standard; DNA; 1260 BP.  
DE Human I Kappa B kinase (IKK) gamma DNA SeqID 22.  
PN WO2004016781-A1.  
PD 26-FEB-2004.  
PA (RIKE ) RIKEN KK.  
PA (KAZU-) KAZUSA DNA RES INST.  
Query Match 4.9%; Score 48.2; DB 12; Length 1260;  
Best Local Similarity 47.8%; Pred. No. 36;  
RESULT 946  
ID AAD55721 standard; DNA; 1336 BP.  
DE Argiope trifasciata major ampullate spidroin 2 (MaSp2) DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 4.9%; Score 48.2; DB 8; Length 1336;  
Best Local Similarity 43.2%; Pred. No. 36;  
RESULT 947  
ID ADP09651 standard; DNA; 1413 BP.  
DE Rice cinnamic acid 5-hydroxylase ORF DNA without the T-DNA insert Seq 42.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO.  
PA (POST-) POSTECH FOUND.  
Query Match 4.9%; Score 48.2; DB 12; Length 1413;  
Best Local Similarity 49.8%; Pred. No. 35;  
RESULT 948  
ID ADP75211 standard; cDNA; 1701 BP.  
DE Human ADAMTS2 cDNA splice variant 2.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 1701;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 949  
ID AAA35065 standard; DNA; 1910 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2754.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 950  
ID AAF21187 standard; DNA; 1910 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2754.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 951  
ID ABK51401 standard; DNA; 1910 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 952  
ID AAD19379 standard; DNA; 1910 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;

RESULT 953  
ID AAL44083 standard; DNA; 1910 BP.  
DE Human C/EBP-beta protein coding sequence 2.  
PN WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 954  
ID ABK84563 standard; cDNA; 1910 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1134.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 955  
ID ABL94237 standard; cDNA; 1910 BP.  
DE Human C/EBP beta-encoding cDNA, SEQ ID NO:3.  
PN US6271030-B1.  
PD 07-AUG-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 956  
ID ABK51996 standard; DNA; 1910 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #2.  
PN WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 957  
ID ACF36515 standard; DNA; 1910 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PN WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 958  
ID ABZ96881 standard; DNA; 1910 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 959  
ID ABD20730 standard; DNA; 1910 BP.  
DE Human pulmonary and inflammatory target DNA #341.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 960  
ID AAQ15015 standard; DNA; 1913 BP.  
DE Nuclear factor C/EBP2 DNA.  
PN JP03236782-A.  
PD 22-OCT-1991.  
PA (CHUZ-) CHUZO KISH IMOTO.  
Query Match 4.9%; Score 48.2; DB 2; Length 1913;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 961  
ID ADQ87415 standard; cDNA; 1967 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4292.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 13; Length 1967;

Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 962  
 ID A086256 standard; cDNA; 1967 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3128.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD//) WU T D.  
 PA (ZHOU//) ZHOU Y.  
 Query Match 4.9%; Score 48.2; DB 13; Length 1967;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 963  
 ID ADA44712 standard; DNA; 1975 BP.  
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.  
 PN WO2003031576-A2.  
 PD 17-APR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 1975;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 964  
 ID AAC81426 standard; cDNA; 1994 BP.  
 DE Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.  
 PN JP2000253884-A.  
 PD 19-SEP-2000.  
 PA (TOAG ) TOA GOSEI CHEM IND LTD.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 965  
 ID AAA35027 standard; DNA; 1994 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 966  
 ID AAF21149 standard; DNA; 1994 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2716.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 967  
 ID ADA44705 standard; DNA; 1994 BP.  
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.  
 PN WO2003031576-A2.  
 PD 17-APR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 968  
 ID ABZ96843 standard; DNA; 1994 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 969  
 ID ABV75393 standard; DNA; 1994 BP.  
 DE Human NEMO polypeptide encoding DNA.  
 PN WO200292761-A2.  
 PD 21-NOV-2002.  
 PA (IMMV ) IMMUNEX CORP.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 970  
 ID ABD20692 standard; DNA; 1994 BP.  
 DE Human pulmonary and inflammatory target DNA #303.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 11; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 971  
 ID AAZ07513 standard; DNA; 2009 BP.  
 DE Human RIP-associated protein (RAP-2) encoding DNA.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YEDH ) YEDA RES & DEV CO LTD.  
 PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2009;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 972  
 ID AAV06593 standard; cDNA; 2033 BP.  
 DE Human N-proteinase (short form) cDNA.  
 PN WO9800555-A1.  
 PD 08-JAN-1998.  
 PA (PROC/) PROCKOP D J.  
 PA (COLI/) COLIGE A.  
 PA (LAPI/) LAPIERE C.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2033;  
 Best Local Similarity 44.0%; Pred. No. 35;  
 RESULT 973  
 ID ABS57455 standard; cDNA; 2033 BP.  
 DE Human short form N-proteinase cDNA.  
 PN US6428998-B1.  
 PD 06-AUG-2002.  
 PA (UYLI-) UNIV LIEGE.  
 Query Match 4.9%; Score 48.2; DB 10; Length 2033;  
 Best Local Similarity 44.0%; Pred. No. 35;  
 RESULT 974  
 ID AAZ07514 standard; DNA; 2034 BP.  
 DE Human RIP-associated protein (RAP-2) clone #41072 nucleotide sequence.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YEDH ) YEDA RES & DEV CO LTD.  
 PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2034;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 975  
 ID ACD23012 standard; cDNA; 2035 BP.  
 DE Human NEMO cDNA.  
 PN US2003032055-A1.  
 PD 13-FEB-2003.  
 PA (KENW/) KENWRICK S J.  
 PA (WOLF/) WOFFENDIN H.  
 PA (MUNN/) MUNNICH A.  
 PA (SMAH/) SMAHI A.  
 PA (ISRA/) ISRAEL A.  
 PA (POUS/) POUSTKA A.  
 PA (HEIS/) HEISS N.  
 PA (DURS/) D'URSO M.  
 PA (LEWI/) LEWIS R A.  
 PA (NELS/) NELSON D L.  
 PA (ARAD/) ARADHYA S.  
 PA (LEVY/) LEVY M.  
 Query Match 4.9%; Score 48.2; DB 9; Length 2035;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 976  
 ID AAA35066 standard; DNA; 2171 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2755.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 35;  
 RESULT 977  
 ID AAF21188 standard; DNA; 2171 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2755.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.

Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 978  
ID ABZ96882 standard; DNA; 2171 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIC-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 979  
ID ABD20731 standard; DNA; 2171 BP.  
DE Human pulmonary and inflammatory target DNA #342.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIC-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 980  
ID ACA27128 standard; DNA; 2595 BP.  
DE Prokaryotic essential gene #8785.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 2595;  
Best Local Similarity 46.3%; Pred. No. 35;  
RESULT 981  
ID AAD28564 standard; DNA; 3350 BP.  
DE Herpes simplex virus type 2 G10\_UL37consensus DNA.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.2; DB 6; Length 3350;  
Best Local Similarity 44.5%; Pred. No. 35;  
RESULT 982  
ID ADG74976 standard; DNA; 3350 BP.  
DE Human herpesvirus 2 isolated clone DNA - SEQ ID 48.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.2; DB 10; Length 3350;  
Best Local Similarity 44.5%; Pred. No. 35;  
RESULT 983  
ID AAS77503 standard; cDNA; 3633 BP.  
DE DNA encoding novel human diagnostic protein #13307.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 5; Length 3633;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 984  
ID ACC72669 standard; cDNA; 3636 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:8.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 3636;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 985  
ID ACA40841 standard; DNA; 4146 BP.  
DE Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 4146;  
Best Local Similarity 46.1%; Pred. No. 34;  
RESULT 986  
ID ACA40804 standard; DNA; 4542 BP.  
DE Prokaryotic essential gene #22461.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 4542;

Best Local Similarity 43.2%; Pred. No. 34;  
RESULT 987  
ID ACN37449 standard; cDNA; 4755 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323899, SEQ ID NO:338.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.9%; Score 48.2; DB 13; Length 4755;  
Best Local Similarity 44.2%; Pred. No. 34;  
RESULT 988  
ID ADP09634 standard; DNA; 4941 BP.  
DE Rice cinnamic acid 5-hydroxylase genomic DNA without the T-DNA SeqID 25.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO.  
PA (POST-) POSTECH FOUND.  
Query Match 4.9%; Score 48.2; DB 12; Length 4941;  
Best Local Similarity 49.8%; Pred. No. 34;  
RESULT 989  
ID ADO10048 standard; cDNA; 5204 BP.  
DE Novel human protein NovId cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU/) KEKUDA R.  
PA (ALSO/) ALSOBOOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATI/) PATTURAJAN M.  
PA (GROS/) GROSSE W M.  
PA (LEPL/) LEFLEY D M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (EDIN/) EDINGER S R.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ROTH/) ROTHENBERG M E.  
PA (STON/) STONE D J.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (ANDE/) ANDERSON D W.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (EISE/) EISEN A.  
Query Match 4.9%; Score 48.2; DB 12; Length 5204;  
Best Local Similarity 48.9%; Pred. No. 34;  
RESULT 990  
ID ADP75209 standard; cDNA; 6642 BP.  
DE Human ADAMTS2 cDNA splice variant 1.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 6642;  
Best Local Similarity 44.0%; Pred. No. 34;  
RESULT 991  
ID AAV06592 standard; cDNA; 6692 BP.  
DE Human N-proteinase (long form) cDNA.  
PN WO9800555-A1.  
PD 08-JAN-1998.  
PA (PROC/) PROCKOP D J.  
PA (COLI/) COLIGE A.  
PA (LAPI/) LAPIERE C.  
Query Match 4.9%; Score 48.2; DB 2; Length 6692;  
Best Local Similarity 44.0%; Pred. No. 34;  
RESULT 992  
ID ABS57451 standard; cDNA; 6692 BP.  
DE Human long form N-proteinase cDNA.  
PN US6428998-B1.



PD 06-AUG-2002.  
PA (UYLI-) UNIV LIEGE.  
Query Match 4.9%; Score 48.2; DB 10; Length 6692;  
Best Local Similarity 44.0%; Pred. No. 34;  
RESULT 993  
ID AAA35028 standard; DNA; 8631 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 4.9%; Score 48.2; DB 3; Length 8631;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 994  
ID AAF21150 standard; DNA; 8631 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2717.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 4.9%; Score 48.2; DB 3; Length 8631;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 995  
ID ABZ96844 standard; DNA; 8631 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 8631;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 996  
ID ABD20693 standard; DNA; 8631 BP.  
DE Human pulmonary and inflammatory target DNA #304.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 8631;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 997  
ID AAD54222 standard; DNA; 9579 BP.  
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF5 DNA.  
PN WO20028176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 9579;  
Best Local Similarity 47.2%; Pred. No. 34;  
RESULT 998  
ID ADC26981 standard; DNA; 20922 BP.  
DE Sorangium cellulosum tmbA gene cluster tmbS DNA.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.9%; Score 48.2; DB 10; Length 20922;  
Best Local Similarity 46.3%; Pred. No. 33;  
RESULT 999  
ID AAD17185 standard; DNA; 27541 BP.  
DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF) SINTEF STIPELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAEVRIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 4.9%; Score 48.2; DB 4; Length 27541;  
Best Local Similarity 47.0%; Pred. No. 33;  
RESULT 1000  
ID AAD54217 standard; DNA; 52101 BP.

DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 52101;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 1001  
ID ADC26995 standard; DNA; 67251 BP.  
DE Sorangium cellulosum tmbA gene cluster.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.9%; Score 48.2; DB 10; Length 67251;  
Best Local Similarity 46.4%; Pred. No. 32;  
RESULT 1002  
ID AAL60437 standard; DNA; 70383 BP.  
DE Human kinase splice form 1 genomic DNA.  
Query Match 4.9%; Score 48.2; DB 9; Length 70383;  
Best Local Similarity 45.5%; Pred. No. 32;  
RESULT 1003  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 4.9%; Score 48.2; DB 12; Length 86941;  
Best Local Similarity 45.9%; Pred. No. 32;  
RESULT 1004  
Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
Best Local Similarity 43.2%; Pred. No. 31;  
RESULT 1005  
Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
Best Local Similarity 43.2%; Pred. No. 31;  
RESULT 1006  
ID ABD03629 standard; DNA; 465 BP.  
DE Pseudomonas aeruginosa polynucleotide #2233.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 465;  
Best Local Similarity 50.0%; Pred. No. 40;  
RESULT 1007  
ID ACF39326 standard; DNA; 660 BP.  
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:28.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 4.9%; Score 48; DB 8; Length 660;  
Best Local Similarity 51.4%; Pred. No. 39;  
RESULT 1008  
ID ABQ40859 standard; DNA; 712 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27450.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 48; DB 6; Length 712;  
Best Local Similarity 45.5%; Pred. No. 39;  
RESULT 1009  
ID ABQ40858 standard; DNA; 712 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27449.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 48; DB 6; Length 712;  
Best Local Similarity 45.5%; Pred. No. 39;  
RESULT 1010  
ID ABZ66735 standard; DNA; 756 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 132.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 10; Length 756;

Best Local Similarity 48.5%; Pred. No. 39;  
RESULT 1011  
ID ADS57559 standard; cDNA; 768 BP.  
DE Bacterial polynucleotide #9546.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.9%; Score 48; DB 13; Length 768;  
Best Local Similarity 46.2%; Pred. No. 39;  
RESULT 1012  
ID ABD08476 standard; DNA; 822 BP.  
DE Pseudomonas aeruginosa polynucleotide #7080.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 822;  
Best Local Similarity 45.2%; Pred. No. 39;  
RESULT 1013  
ID ABD03843 standard; DNA; 852 BP.  
DE Pseudomonas aeruginosa polynucleotide #2447.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 852;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1014  
ID ABD03031 standard; DNA; 1071 BP.  
DE Pseudomonas aeruginosa polynucleotide #1635.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1071;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1015  
ID AAA02477 standard; cDNA; 1127 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468.  
PN WO9958675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48; DB 3; Length 1127;  
Best Local Similarity 34.2%; Pred. No. 39;  
RESULT 1016  
ID AAZ10560 standard; DNA; 1128 BP.  
DE DNA encoding G protein-coupled receptor protein designated SREB1.  
PN WO9946378-A1.  
PD 16-SEP-1999.  
PA (YAWA) YAWANOUCI PHARM CO LTD.  
Query Match 4.9%; Score 48; DB 2; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1017  
ID AAA46026 standard; cDNA; 1128 BP.  
DE Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17.  
PN WO200022131-A2.  
PD 20-APR-2000.  
PA (ARENA) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1018  
ID AAD01125 standard; cDNA; 1128 BP.  
DE Human orphan G protein-coupled receptor hGPCR27 cDNA.  
PN WO200031258-A2.  
PD 02-JUN-2000.  
PA (ARENA) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1019  
ID AAD27892 standard; DNA; 1128 BP.  
DE Human G-protein coupled receptor 14266 DNA.

PN WO200212344-A2.  
PD 14-FEB-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1020  
ID AAS98049 standard; DNA; 1128 BP.  
DE Human DNA for potential G protein-coupled receptor #7.  
PN WO200185791-A1.  
PD 15-NOV-2001.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1021  
ID ACA93263 standard; cDNA; 1128 BP.  
DE Human cDNA encoding GPCR hGPCR27.  
PN US2003017528-A1.  
PD 23-JAN-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1022  
ID ABZ42853 standard; DNA; 1128 BP.  
DE Human G protein-coupled receptor GPR27 nucleotide SEQ ID NO:493.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1023  
ID ADG98761 standard; cDNA; 1128 BP.  
DE Human orphan GPCR cDNA, GPCR27.  
PN US2003148450-A1.  
PD 07-AUG-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 10; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1024  
ID ADJ26924 standard; cDNA; 1128 BP.  
DE Human endogenous orphan G-protein coupled receptor (GPCR) 27 cDNA.  
PN US2003175891-A1.  
PD 18-SEP-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1025  
ID ADN39803 standard; cDNA; 1128 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C175.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1026  
ID ADG86378 standard; DNA; 1128 BP.  
DE Human endogenous orphan GPCR hGPCR27 DNA.  
PN US2003229216-A1.  
PD 11-DEC-2003.  
PA (CHEN/) CHEN R.  
PA (LIAW/) LIAW C W.  
PA (LOWI) LOWITZ K. T.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
Query Match 4.9%; Score 48; DB 12; Length 1128;

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Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1027
ID ADO29912 standard; cDNA; 1128 BP.
DE Human GPCR GPR27 polynucleotide, SEQ ID NO:1014.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1028
ID ADP20171 standard; cDNA; 1128 BP.
DE Human G protein coupled receptor hGPCR27 cDNA.
PN US2004110238-A1.
PD 10-JUN-2004.
PA (CHEN/) CHEN R.
PA (LIAM/) LIAM C W.
PA (LOMI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
PA (BEHA/) BEHAN D P.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1029
ID ADO75075 standard; cDNA; 1128 BP.
DE Human cDNA encoding hGPCR27.
PN US2004137509-A1.
PD 15-JUL-2004.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1030
ID ADRA6633 standard; DNA; 1128 BP.
DE Cancer-associated protein coding sequence, SEQ ID 46.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 48; DB 13; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1031
ID ADT44450 standard; cDNA; 1155 BP.
DE Bacterial polynucleotide #19201.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1155;
Best Local Similarity 46.9%; Pred. No. 39;
RESULT 1032
ID ACC59401 standard; DNA; 1188 BP.
DE Microbial resistance gene PA1877 coding sequence.
PN WO2003041483-A2.
PD 22-MAY-2003.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.9%; Score 48; DB 9; Length 1188;
Best Local Similarity 46.8%; Pred. No. 39;
RESULT 1033
ID ADC36366 standard; DNA; 1197 BP.
DE Weed controller metabolism associated gene SEQ ID NO:234.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1197;
Best Local Similarity 44.1%; Pred. No. 39;
RESULT 1034
ID ACA37909 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #19566.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1275;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1035
ID ABD03924 standard; DNA; 1359 BP.
DE Pseudomonas aeruginosa polynucleotide #2528.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1359;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1036
ID ADC36376 standard; DNA; 1411 BP.
DE Weed controller metabolism associated gene SEQ ID NO:244.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1411;
Best Local Similarity 44.1%; Pred. No. 38;
RESULT 1037
ID ADT43932 standard; cDNA; 1437 BP.
DE Bacterial polynucleotide #18683.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1437;
Best Local Similarity 49.2%; Pred. No. 38;
RESULT 1038
ID ABD03787 standard; DNA; 1473 BP.
DE Pseudomonas aeruginosa polynucleotide #2391.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1473;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1039
ID ADT44593 standard; cDNA; 1677 BP.
DE Bacterial polynucleotide #19344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1677;
Best Local Similarity 47.4%; Pred. No. 38;
RESULT 1040
ID ABD03082 standard; DNA; 1695 BP.
DE Pseudomonas aeruginosa polynucleotide #1686.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1695;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1041
ID ABD02888 standard; DNA; 1740 BP.
DE Pseudomonas aeruginosa polynucleotide #1492.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1740;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1042
ID ACA25954 standard; DNA; 1782 BP.
DE Prokaryotic essential gene #7611.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1782;
Best Local Similarity 50.0%; Pred. No. 38;
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RESULT 1043  
ID ABD02930 standard; DNA; 1806 BP.  
DE Pseudomonas aeruginosa polynucleotide #1534.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1806;  
Best Local Similarity 50.0%; Pred. No. 38;  
RESULT 1044  
ID ADF070581 standard; DNA; 1842 BP.  
DE Orphan receptor ligand-related human protein gene SeqID204.  
PN WO2003071272-A1.  
PD 28-AUG-2003.  
PA (TAKA) TAKEDA CHEM IND LTD.  
Query Match 4.9%; Score 48; DB 10; Length 1842;  
Best Local Similarity 45.1%; Pred. No. 38;  
RESULT 1045  
ID AAX30924 standard; DNA; 1925 BP.  
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.  
PN WO9947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOPRIA INC.  
Query Match 4.9%; Score 48; DB 2; Length 1925;  
Best Local Similarity 51.4%; Pred. No. 38;  
RESULT 1046  
ID ABD08413 standard; DNA; 1929 BP.  
DE Pseudomonas aeruginosa polynucleotide #7017.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1929;  
Best Local Similarity 45.2%; Pred. No. 38;  
RESULT 1047  
ID ABD08507 standard; DNA; 1947 BP.  
DE Pseudomonas aeruginosa polynucleotide #7111.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1947;  
Best Local Similarity 45.2%; Pred. No. 38;  
RESULT 1048  
ID ABD08587 standard; DNA; 2253 BP.  
DE Pseudomonas aeruginosa polynucleotide #7191.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2253;  
Best Local Similarity 45.5%; Pred. No. 38;  
RESULT 1049  
ID ABD08649 standard; DNA; 2409 BP.  
DE Pseudomonas aeruginosa polynucleotide #7253.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2409;  
Best Local Similarity 45.5%; Pred. No. 38;  
RESULT 1050  
ID ADO24486 standard; cDNA; 2485 BP.  
DE Human PRO87344 encoding cDNA SEQ ID NO:125.  
PN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.9%; Score 48; DB 12; Length 2485;  
Best Local Similarity 45.1%; Pred. No. 38;  
RESULT 1051  
ID ABD08843 standard; DNA; 2490 BP.  
DE Pseudomonas aeruginosa polynucleotide #7447.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2490;  
Best Local Similarity 45.5%; Pred. No. 38;  
RESULT 1052

ID AAS54094 standard; DNA; 3489 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #225.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 4; Length 3489;  
Best Local Similarity 45.1%; Pred. No. 37;  
RESULT 1053  
ID ACA42240 standard; DNA; 3489 BP.  
DE Prokaryotic essential gene #23897.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 8; Length 3489;  
Best Local Similarity 45.1%; Pred. No. 37;  
RESULT 1054  
ID AAS08699 standard; DNA; 12152 BP.  
DE M. carbonacea DNA encoding Everninomicin biosynthetic enzymes.  
PN WO200151639-A2.  
PD 19-JUL-2001.  
PA (SCHE) SCHERING CORP.  
Query Match 4.9%; Score 48; DB 5; Length 12152;  
Best Local Similarity 48.5%; Pred. No. 36;  
RESULT 1055  
ID AAS17367 standard; DNA; 33529 BP.  
DE DNA sequence of S. celluloseum polyketide synthase cosmid, pKOS28-26.  
PN US6280399-B1.  
PD 28-AUG-2001.  
PA (KOSA-) KOSAN BIOSCIENCE.  
Query Match 4.9%; Score 48; DB 5; Length 33529;  
Best Local Similarity 46.4%; Pred. No. 35;  
RESULT 1056  
ID ABZ66810 standard; DNA; 37116 BP.  
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 10; Length 37116;  
Best Local Similarity 48.5%; Pred. No. 35;  
RESULT 1057  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 12; Length 76994;  
Best Local Similarity 44.4%; Pred. No. 34;  
RESULT 1058  
ID ABD08121 standard; DNA; 309 BP.  
DE Pseudomonas aeruginosa polynucleotide #6725.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 309;  
Best Local Similarity 49.4%; Pred. No. 43;  
RESULT 1059  
ID ADI42790 standard; DNA; 487 BP.  
DE Plant transcription factor polynucleotide #800.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIAN-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAAR-) HAAKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.

PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 4.8%; Score 47.8; DB 12; Length 487;  
Best Local Similarity 45.1%; Pred. No. 43;  
RESULT 1060  
ID ABK35609 standard; DNA; 777 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #28.  
PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 4.8%; Score 47.8; DB 6; Length 777;  
Best Local Similarity 51.8%; Pred. No. 42;  
RESULT 1061  
ID ADF58345 standard; cDNA; 777 BP.  
DE Human polynucleotide sequence SEQ ID NO:712.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 47.8; DB 10; Length 777;  
Best Local Similarity 51.8%; Pred. No. 42;  
RESULT 1062  
ID ABD17337 standard; DNA; 801 BP.  
DE Pseudomonas aeruginosa polynucleotide #15941.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 801;  
Best Local Similarity 47.5%; Pred. No. 42;  
RESULT 1063  
ID ABD15977 standard; DNA; 819 BP.  
DE Pseudomonas aeruginosa polynucleotide #14581.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 819;  
Best Local Similarity 47.1%; Pred. No. 42;  
RESULT 1064  
ID AAL61183 standard; DNA; 885 BP.  
DE Actinosynnema pretiosum methyltransferase gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 885;  
Best Local Similarity 44.9%; Pred. No. 42;  
RESULT 1065  
ID ABD08291 standard; DNA; 966 BP.  
DE Pseudomonas aeruginosa polynucleotide #6895.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 966;  
Best Local Similarity 49.4%; Pred. No. 42;  
RESULT 1066  
ID ACA37720 standard; DNA; 1029 BP.  
DE Prokaryotic essential gene #19377.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1029;  
Best Local Similarity 45.6%; Pred. No. 42;  
RESULT 1067  
ID ADB0220 standard; DNA; 1173 BP.  
DE Mycobacterium tuberculosis nutrient starvation-inducible gene #129.  
PN WO2003004520-A2.  
PD 16-JAN-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 4.8%; Score 47.8; DB 10; Length 1173;  
Best Local Similarity 47.0%; Pred. No. 42;  
RESULT 1068  
ID ABD17849 standard; DNA; 1218 BP.  
DE Pseudomonas aeruginosa polynucleotide #16453.

PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1218;  
Best Local Similarity 47.5%; Pred. No. 42;  
RESULT 1069  
ID ACA26886 standard; DNA; 1287 BP.  
DE Prokaryotic essential gene #8543.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1287;  
Best Local Similarity 45.4%; Pred. No. 41;  
RESULT 1070  
ID ABL15825 standard; cDNA; 1291 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41957.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Query Match 4.8%; Score 47.8; DB 4; Length 1291;  
Best Local Similarity 47.8%; Pred. No. 41;  
RESULT 1071  
ID ADS18615 standard; DNA; 1293 BP.  
DE Barley Ror2 DNA.  
PN WO2004081217-A2.  
PD 23-SEP-2004.  
PA (BADI ) BASF PLANT SCI GMBH.  
Query Match 4.8%; Score 47.8; DB 13; Length 1293;  
Best Local Similarity 46.7%; Pred. No. 41;  
RESULT 1072  
ID ABA16862 standard; DNA; 1343 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9193.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
Best Local Similarity 51.8%; Pred. No. 41;  
RESULT 1073  
ID ABA19759 standard; DNA; 1343 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12090.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
Best Local Similarity 51.8%; Pred. No. 41;  
RESULT 1074  
ID ACA37836 standard; DNA; 1404 BP.  
DE Prokaryotic essential gene #19493.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1404;  
Best Local Similarity 46.8%; Pred. No. 41;  
RESULT 1075  
ID ABD08211 standard; DNA; 1485 BP.  
DE Pseudomonas aeruginosa polynucleotide #6815.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1485;  
Best Local Similarity 49.4%; Pred. No. 41;  
RESULT 1076  
ID ABD08326 standard; DNA; 1509 BP.  
DE Pseudomonas aeruginosa polynucleotide #6930.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1509;  
Best Local Similarity 49.4%; Pred. No. 41;  
RESULT 1077  
ID ACA37879 standard; DNA; 1527 BP.  
DE Prokaryotic essential gene #19536.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1527;  
Best Local Similarity 47.2%; Pred. No. 41;  
RESULT 1078  
ID AAD36877 standard; DNA; 1686 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme encoding DNA, ORF15.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 1686;  
Best Local Similarity 46.3%; Pred. No. 41;  
RESULT 1079  
ID AAT62138 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-210 antigen cDNA.  
PN WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1080  
ID AAV47558 standard; DNA; 1771 BP.  
DE Leishmania antigen Lt-210 coding sequence.  
PN WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1081  
ID AA225621 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-210 nucleotide sequence.  
PN US965142-A.  
PD 12-OCT-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1082  
ID AAD40285 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-1 antigenic protein encoding DNA.  
PN US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1083  
ID AAS96022 standard; cDNA; 1771 BP.  
DE Leishmania antigen Lt-1 DNA.  
PN WO200179276-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1084  
ID ABK81733 standard; DNA; 1771 BP.  
DE Leishmania antigenic polynucleotide #4.  
PN US6365165-B1.  
PD 02-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1085  
ID AAF88524 standard; DNA; 1771 BP.  
DE L. tropica Lt-210 antigen DNA SEQ ID 7.  
PN US2002081320-A1.  
PD 27-JUN-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
PA (SKEI/) SKEIKY Y A W.  
PA (BHAT/) BHATIA A.  
PA (COL/) COLER R N.

PA (PROB/) PROBST P.  
PA (BRAN/) BRANNON M.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1086  
ID ADB78770 standard; DNA; 1771 BP.  
DE Leishmania DNA encoding antigen Lt-210.  
PN US2002169285-A1.  
PD 14-NOV-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
Query Match 4.8%; Score 47.8; DB 9; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1087  
ID ABD17433 standard; DNA; 1962 BP.  
DE Pseudomonas aeruginosa polynucleotide #16037.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1962;  
Best Local Similarity 47.5%; Pred. No. 41;  
RESULT 1088  
ID ABD17959 standard; DNA; 2526 BP.  
DE Pseudomonas aeruginosa polynucleotide #16563.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 2526;  
Best Local Similarity 47.5%; Pred. No. 41;  
RESULT 1089  
ID AAL61203 standard; DNA; 3018 BP.  
DE Actinosynnema pretiosum cytochrome P450 gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3018;  
Best Local Similarity 47.9%; Pred. No. 41;  
RESULT 1090  
ID ABD10462 standard; DNA; 3126 BP.  
DE Pseudomonas aeruginosa polynucleotide #9066.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 3126;  
Best Local Similarity 51.1%; Pred. No. 40;  
RESULT 1091  
ID AAL61181 standard; DNA; 3354 BP.  
DE Actinosynnema pretiosum transcriptional regulator gene #1.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3354;  
Best Local Similarity 41.5%; Pred. No. 40;  
RESULT 1092  
ID ADQ19781 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2600.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 40;  
RESULT 1093  
ID ADQ23914 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6734.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 40;  
RESULT 1094  
ID ABD16585 standard; DNA; 5121 BP.

DE Pseudomonas aeruginosa polynucleotide #15189.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 5121;  
Best Local Similarity 47.1%; Pred. No. 40;  
RESULT 1095  
ID ABD16327 standard; DNA; 6327 BP.  
DE Pseudomonas aeruginosa polynucleotide #14931.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 6327;  
Best Local Similarity 47.1%; Pred. No. 40;  
RESULT 1096  
ID ACF05731 standard; DNA; 7201 BP.  
DE Plasmid pEAK12G-IPAAA4548-6His.  
PN WO2003055913-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7201;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1097  
ID ACF06299 standard; DNA; 7231 BP.  
DE Plasmid pEAK12B-IPAAA26841-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7231;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1098  
ID ACF06300 standard; DNA; 7297 BP.  
DE SigptdIPAAA26841s-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7297;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1099  
ID ACF05558 standard; DNA; 7429 BP.  
DE Plasmid pEAK12G-IPAAA24020-6His.  
PN WO2003055912-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7429;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1100  
ID ACF06298 standard; DNA; 7456 BP.  
DE Plasmid pEAK12B-IPAAA26841long-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7456;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1101  
ID ADP28653 standard; DNA; 8973 BP.  
DE Human secreted protein encoding sequence SEQ ID #651.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 8973;  
Best Local Similarity 44.6%; Pred. No. 39;  
RESULT 1102  
ID AAD36874 standard; DNA; 29870 BP.  
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 29870;  
Best Local Similarity 46.3%; Pred. No. 38;  
RESULT 1103  
ID AAA29349 standard; DNA; 71989 BP.

DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.  
Query Match 4.8%; Score 47.8; DB 3; Length 71989;  
Best Local Similarity 48.2%; Pred. No. 37;  
RESULT 1104  
ID AAL61224 standard; DNA; 82746 BP.  
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 82746;  
Best Local Similarity 44.9%; Pred. No. 37;  
RESULT 1105  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 1106  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 45.4%; Pred. No. 37;  
RESULT 1107  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 1108  
ID ACL23251 standard; DNA; 422 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13242.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Query Match 4.8%; Score 47.6; DB 9; Length 422;  
Best Local Similarity 59.7%; Pred. No. 46;  
RESULT 1109  
ID ADT43053 standard; cDNA; 633 BP.  
DE Bacterial polynucleotide #17804.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 633;  
Best Local Similarity 46.6%; Pred. No. 46;  
RESULT 1110  
ID ADR01252 standard; DNA; 825 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF21 protein ALDB DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.8%; Score 47.6; DB 13; Length 825;  
Best Local Similarity 44.5%; Pred. No. 45;  
RESULT 1111  
ID ACA19654 standard; DNA; 921 BP.  
DE Prokaryotic essential gene #1311.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 921;  
Best Local Similarity 47.8%; Pred. No. 45;  
RESULT 1112  
ID ABD17059 standard; DNA; 930 BP.  
DE Pseudomonas aeruginosa polynucleotide #15663.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 930;  
Best Local Similarity 47.8%; Pred. No. 45;  
RESULT 1113  
ID ADI45687 standard; cDNA; 1002 BP.  
DE Corn isoprenoid biosynthesis-associated cDNA #30.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) GHASSEMIAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.

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PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1002;
    Best Local Similarity 47.0%; Pred. No. 45;
  RESULT 1114
  ID ADF31999 standard; DNA; 1170 BP.
  DE Transcriptional repressor of the ROK family.
  PN WO200309993-A2.
  PD 04-DEC-2003.
  PA (AVET ) AVENTIS PHARM INC.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1170;
    Best Local Similarity 43.8%; Pred. No. 45;
  RESULT 1115
  ID ADF32000 standard; DNA; 1170 BP.
  DE Transcriptional repressor of the ROK family complement.
  PN WO200309993-A2.
  PD 04-DEC-2003.
  PA (AVET ) AVENTIS PHARM INC.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1170;
    Best Local Similarity 43.8%; Pred. No. 45;
  RESULT 1116
  ID ADT42056 standard; cDNA; 1176 BP.
  DE Bacterial polynucleotide #16807.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1176;
    Best Local Similarity 45.3%; Pred. No. 45;
  RESULT 1117
  ID ACA37852 standard; DNA; 1203 BP.
  DE Prokaryotic essential gene #19509.
  PN WO200277183-A2.
  PD 03-OCT-2002.
  PA (ELIT-) ELITRA PHARM INC.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1203;
    Best Local Similarity 45.6%; Pred. No. 45;
  RESULT 1118
  ID ABD04031 standard; DNA; 1248 BP.
  DE Pseudomonas aeruginosa polynucleotide #2635.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1248;
    Best Local Similarity 46.4%; Pred. No. 45;
  RESULT 1119
  ID ABD05292 standard; DNA; 1278 BP.
  DE Pseudomonas aeruginosa polynucleotide #3896.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1278;
    Best Local Similarity 43.6%; Pred. No. 45;
  RESULT 1120
  ID ADT44381 standard; cDNA; 1410 BP.
  DE Bacterial polynucleotide #19132.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1410;
    Best Local Similarity 46.2%; Pred. No. 44;
  RESULT 1121
  ID ADS56254 standard; cDNA; 1572 BP.
  DE Bacterial polynucleotide #8241.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1572;
    Best Local Similarity 48.5%; Pred. No. 45;
  RESULT 1122
  ID ACA03563 standard; DNA; 1971 BP.
  DE Synthetic DNA encoding immunogenic HIV peptide #46.
  PN WO2003004657-A1.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
    Best Local Similarity 46.8%; Pred. No. 44;
  RESULT 1123
  ID ACA03557 standard; DNA; 1971 BP.
  DE Synthetic DNA encoding immunogenic HIV peptide #40.
  PN WO2003004657-A1.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
    Best Local Similarity 47.6%; Pred. No. 44;
  RESULT 1124
  ID ACC78513 standard; DNA; 1971 BP.
  DE HIV protInaRT YM.opt.SF2 nucleotide sequence.
  PN WO2003020876-A2.
  PD 13-MAR-2003.
  PA (CHIR ) CHIRON CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
    Best Local Similarity 47.6%; Pred. No. 44;
  RESULT 1125
  ID ADG13270 standard; DNA; 1971 BP.
  DE DNA of HIV construct protInaRT-YM-opt_C SEQ ID NO 49.
  PN WO2003004620-A2.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
  PA (UYST-) UNIV STELLENBOSCH.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 10; Length 1971;
    Best Local Similarity 46.8%; Pred. No. 44;
  RESULT 1126
  ID ABD03593 standard; DNA; 1971 BP.
  DE Pseudomonas aeruginosa polynucleotide #2197.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1971;
    Best Local Similarity 46.4%; Pred. No. 44;
  RESULT 1127
  ID ABD05320 standard; DNA; 1977 BP.
  DE Pseudomonas aeruginosa polynucleotide #3924.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1977;
    Best Local Similarity 43.6%; Pred. No. 44;
  RESULT 1128
  ID AAD55732 standard; DNA; 2078 BP.
  DE Dolomedes tenebrosus fibroin 2 DNA.
  PN WO2003020916-A2.
  PD 13-MAR-2003.
  PA (UYWY-) UNIV WYOMING.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 8; Length 2078;
    Best Local Similarity 46.2%; Pred. No. 44;
  RESULT 1129
  ID ABD05412 standard; DNA; 2091 BP.
  DE Pseudomonas aeruginosa polynucleotide #4016.

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PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2091;  
Best Local Similarity 43.6%; Pred. No. 44;  
RESULT 1130  
ID ADT42133 standard; cDNA; 2175 BP.  
DE Bacterial polynucleotide #16884.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 2175;  
Best Local Similarity 48.8%; Pred. No. 44;  
RESULT 1131  
ID ABD03873 standard; DNA; 2211 BP.  
DE Pseudomonas aeruginosa polynucleotide #2477.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2211;  
Best Local Similarity 46.4%; Pred. No. 44;  
RESULT 1132  
ID AAA70477 standard; DNA; 2305 BP.  
DE HIV FS(+/-) Protinact\_RTOpt\_YM coding sequence.  
PN WO200039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 3; Length 2305;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1133  
ID AAA70479 standard; DNA; 2306 BP.  
DE HIV FS(-) ProtMod\_RTOpt\_YM coding sequence.  
PN WO200039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 3; Length 2306;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1134  
ID ACA37615 standard; DNA; 2337 BP.  
DE Prokaryotic essential gene #19272.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 2337;  
Best Local Similarity 46.4%; Pred. No. 44;  
RESULT 1135  
ID ACA27167 standard; DNA; 2424 BP.  
DE Prokaryotic essential gene #8824.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 2424;  
Best Local Similarity 43.9%; Pred. No. 44;  
RESULT 1136  
ID ACA03547 standard; DNA; 2457 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #30.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2457;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1137  
ID ADC13265 standard; DNA; 2457 BP.  
DE DNA of HIV construct p2Pol-opt-YM\_C SEQ ID NO 44.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 4.8%; Score 47.6; DB 10; Length 2457;  
Best Local Similarity 44.5%; Pred. No. 44;

Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1138  
ID ABL39960 standard; DNA; 2463 BP.  
DE Synthetic construct PR975YM SEQ ID NO:31.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR ) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 4.8%; Score 47.6; DB 6; Length 2463;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1139  
ID ADM73765 standard; DNA; 2463 BP.  
DE HIV-1 polynucleotide #8.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBERG E J V.  
Query Match 4.8%; Score 47.6; DB 12; Length 2463;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1140  
ID ACA03542 standard; DNA; 2466 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #25.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1141  
ID ACC78506 standard; DNA; 2466 BP.  
DE HIV p2PolInaopt\_YM.SF2 nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1142  
ID AAD28560 standard; DNA; 2481 BP.  
DE Herpes simplex virus type 2 full-length HSV-2 RL2 gene.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.6; DB 6; Length 2481;  
Best Local Similarity 51.4%; Pred. No. 44;  
RESULT 1143  
ID ADG74963 standard; DNA; 2481 BP.  
DE Human herpesvirus 2 RL2 DNA - SEQ ID 35.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.6; DB 10; Length 2481;  
Best Local Similarity 51.4%; Pred. No. 44;  
RESULT 1144  
ID ACN40538 standard; cDNA; 2540 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326641, SEQ ID NO:5378.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 4.8%; Score 47.6; DB 13; Length 2540;  
Best Local Similarity 42.3%; Pred. No. 44;  
RESULT 1145  
ID ADT44483 standard; cDNA; 2652 BP.  
DE Bacterial polynucleotide #19234.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 2652;  
Best Local Similarity 44.5%; Pred. No. 44;

RESULT 1146  
 ID ADG75080 standard; DNA; 3066 BP.  
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 152.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3066;  
 Best Local Similarity 51.4%; Pred. No. 44;  
 RESULT 1147  
 ID ADT42075 standard; cDNA; 3090 BP.  
 DE Bacterial polynucleotide #16826.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.8%; Score 47.6; DB 13; Length 3090;  
 Best Local Similarity 49.1%; Pred. No. 44;  
 RESULT 1148  
 ID ADF30533 standard; cDNA; 3783 BP.  
 DE Rat angiogenesis modulating protein cDNA #24.  
 PN US2003162706-A1.  
 PD 28-AUG-2003.  
 PA (PROC) PROCTER & GAMBLE CO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3783;  
 Best Local Similarity 43.6%; Pred. No. 43;  
 RESULT 1149  
 ID ADE71207 standard; DNA; 5369 BP.  
 DE Novel human protein coding sequence #23.  
 PN JP2002345493-A.  
 PD 03-DEC-2002.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5369;  
 Best Local Similarity 45.6%; Pred. No. 43;  
 RESULT 1150  
 ID ADK18365 standard; DNA; 5780 BP.  
 DE Human NOVX protein encoding gene #10.  
 PN WO2003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5780;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1151  
 ID ABS78696 standard; DNA; 5802 BP.  
 DE S. kaniharraensis DNA encoding PKSE.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.6; DB 6; Length 5802;  
 Best Local Similarity 46.0%; Pred. No. 43;  
 RESULT 1152  
 ID ADS97707 standard; DNA; 5886 BP.  
 DE Rabbit alpha-myosin heavy chain coding sequence.  
 PN WO2004082370-A2.  
 PD 30-SEP-2004.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 4.8%; Score 47.6; DB 13; Length 5886;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1153  
 ID ADK18367 standard; DNA; 6008 BP.  
 DE Human NOVX protein encoding gene #11.  
 PN WO2003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1154  
 ID ADP13461 standard; DNA; 6008 BP.  
 DE Renal cell carcinoma differentially expressed gene #197.  
 PN WO2004048933-A2.  
 PD 10-JUN-2004.

PA (AMHP) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.  
 Query Match 4.8%; Score 47.6; DB 12; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1155  
 ID AAV58939 standard; DNA; 9960 BP.  
 DE Mycobacterium smegmatis embCAB operon.  
 PN WO9841533-A1.  
 PD 24-SEP-1998.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.8%; Score 47.6; DB 2; Length 9960;  
 Best Local Similarity 45.1%; Pred. No. 42;  
 RESULT 1156  
 ID ADS97709 standard; DNA; 12801 BP.  
 DE Rabbit alpha-myosin heavy chain expression cassette.  
 PN WO2004082370-A2.  
 PD 30-SEP-2004.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 4.8%; Score 47.6; DB 13; Length 12801;  
 Best Local Similarity 46.4%; Pred. No. 42;  
 RESULT 1157  
 ID AAD17185 standard; DNA; 27541 BP.  
 DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAERVIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 4.8%; Score 47.6; DB 4; Length 27541;  
 Best Local Similarity 47.2%; Pred. No. 41;  
 RESULT 1158  
 ID AAS59516 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 4; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 41;  
 RESULT 1159  
 ID ACF64445 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes DNA contig sequence #11.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 41;  
 RESULT 1160  
 ID ADJ12143 standard; DNA; 414 BP.  
 DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 779.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZERBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 414;  
Best Local Similarity 47.5%; Pred. No. 50;  
RESULT 1161  
ID ADJ44853 standard; cDNA; 504 BP.  
DE Plant cDNA #5853.  
PD US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 12; Length 504;  
Best Local Similarity 45.2%; Pred. No. 50;  
RESULT 1162  
ID ADG33398 standard; DNA; 670 BP.  
DE Maize lipoxygenase (LOX) DNA #15.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 10; Length 670;  
Best Local Similarity 49.0%; Pred. No. 49;  
RESULT 1163  
ID ADG33400 standard; DNA; 670 BP.  
DE Maize lipoxygenase (LOX) DNA #16.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 10; Length 670;  
Best Local Similarity 49.0%; Pred. No. 49;  
RESULT 1164  
ID ABD10158 standard; DNA; 918 BP.  
DE Pseudomonas aeruginosa polynucleotide #8762.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 918;  
Best Local Similarity 46.3%; Pred. No. 49;  
RESULT 1165  
ID ABD10588 standard; DNA; 948 BP.  
DE Pseudomonas aeruginosa polynucleotide #9192.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 948;  
Best Local Similarity 46.3%; Pred. No. 49;  
RESULT 1166  
ID ABD07203 standard; DNA; 954 BP.  
DE Pseudomonas aeruginosa polynucleotide #5807.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 948;  
Best Local Similarity 46.3%; Pred. No. 49;  
RESULT 1167  
ID AAZ51701 standard; DNA; 1044 BP.  
DE Burkholderia multivorans reca gene (1).  
PN WO200014274-A1.  
PD 16-MAR-2000.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 3; Length 1044;  
Best Local Similarity 43.6%; Pred. No. 49;  
RESULT 1168  
ID ABD12320 standard; DNA; 1116 BP.  
DE Pseudomonas aeruginosa polynucleotide #10924.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1116;  
Best Local Similarity 48.0%; Pred. No. 49;  
RESULT 1169  
ID ABD10379 standard; DNA; 1149 BP.  
DE Pseudomonas aeruginosa polynucleotide #8983.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1149;  
Best Local Similarity 46.3%; Pred. No. 49;  
RESULT 1170  
ID ABD12534 standard; DNA; 1209 BP.  
DE Pseudomonas aeruginosa polynucleotide #11138.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1209;  
Best Local Similarity 48.0%; Pred. No. 48;  
RESULT 1171  
ID ABX56037 standard; DNA; 1248 BP.  
DE M. echinospora calicheamicin biosynthesis gene calM.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1248;  
Best Local Similarity 49.3%; Pred. No. 48;  
RESULT 1172  
ID ABD07240 standard; DNA; 1251 BP.  
DE Pseudomonas aeruginosa polynucleotide #5844.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1251;  
Best Local Similarity 44.2%; Pred. No. 48;  
RESULT 1173  
ID ACA27319 standard; DNA; 1404 BP.  
DE Prokaryotic essential gene #8976.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1404;  
Best Local Similarity 44.6%; Pred. No. 48;  
RESULT 1174  
ID ABD04734 standard; DNA; 1650 BP.  
DE Pseudomonas aeruginosa polynucleotide #3338.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1650;  
Best Local Similarity 43.9%; Pred. No. 48;  
RESULT 1175  
ID ACA37851 standard; DNA; 1734 BP.  
DE Prokaryotic essential gene #19508.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1734;  
Best Local Similarity 52.8%; Pred. No. 48;  
RESULT 1176  
ID ABD04627 standard; DNA; 1869 BP.  
DE Pseudomonas aeruginosa polynucleotide #3231.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1869;  
Best Local Similarity 43.9%; Pred. No. 48;  
RESULT 1177  
ID ABD12660 standard; DNA; 1881 BP.  
DE Pseudomonas aeruginosa polynucleotide #11264.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 1881;  
 Best Local Similarity 48.0%; Pred. No. 48;  
 RESULT 1178  
 ID ABD07163 standard; DNA; 1986 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5767.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 1986;  
 Best Local Similarity 44.2%; Pred. No. 48;  
 RESULT 1179  
 ID ABD04694 standard; DNA; 2283 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3298.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 2283;  
 Best Local Similarity 43.9%; Pred. No. 48;  
 RESULT 1180  
 ID ADO26117 standard; DNA; 2354 BP.  
 DE Corn phenylalanine ammonia synthase (PAL) seqid 155.  
 PN WO2004046336-A2.  
 PD 03-JUN-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Query Match 4.8%; Score 47.4; DB 12; Length 2354;  
 Best Local Similarity 47.5%; Pred. No. 48;  
 RESULT 1181  
 ID ACA25940 standard; DNA; 2463 BP.  
 DE Prokaryotic essential gene #7597.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.4; DB 8; Length 2463;  
 Best Local Similarity 45.5%; Pred. No. 48;  
 RESULT 1182  
 ID ABD10506 standard; DNA; 2583 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9110.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 2583;  
 Best Local Similarity 46.3%; Pred. No. 47;  
 RESULT 1183  
 ID AAQ39093 standard; DNA; 2634 BP.  
 DE Streptomyces nodosus 2634bp BamHI fragment.  
 PN WO9306219-A1.  
 PD 01-APR-1993.  
 PA (FAEH) HOECHST AG.  
 Query Match 4.8%; Score 47.4; DB 2; Length 2634;  
 Best Local Similarity 44.9%; Pred. No. 47;  
 RESULT 1184  
 ID ACA23465 standard; DNA; 2883 BP.  
 DE Prokaryotic essential gene #5122.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.4; DB 8; Length 2883;  
 Best Local Similarity 44.9%; Pred. No. 47;  
 RESULT 1185  
 ID ADA71066 standard; DNA; 3153 BP.  
 DE Rice gene, SEQ ID 4389.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.4; DB 8; Length 3153;  
 Best Local Similarity 46.3%; Pred. No. 47;  
 RESULT 1186  
 ID ADA69900 standard; DNA; 3252 BP.  
 DE Rice gene, SEQ ID 3223.  
 PN WO2003000898-A1.

PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.4; DB 8; Length 3252;  
 Best Local Similarity 45.4%; Pred. No. 47;  
 RESULT 1187  
 ID ADC68517 standard; cDNA; 3629 BP.  
 DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:9.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 4.8%; Score 47.4; DB 10; Length 3629;  
 Best Local Similarity 46.1%; Pred. No. 47;  
 RESULT 1188  
 ID ADC68420 standard; cDNA; 3633 BP.  
 DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:130.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 4.8%; Score 47.4; DB 10; Length 3633;  
 Best Local Similarity 46.1%; Pred. No. 47;  
 RESULT 1189  
 ID AAD47222 standard; DNA; 19016 BP.  
 DE Streptococcus sp. H021 DNA fragment for rabelomycin biosynthetic pathway.  
 PN WO200274800-A1.  
 PD 26-SEP-2002.  
 PA (GALI-) GALILAEUS OY.  
 Query Match 4.8%; Score 47.4; DB 8; Length 19016;  
 Best Local Similarity 43.3%; Pred. No. 45;  
 RESULT 1190  
 ID ADE86070 standard; DNA; 47988 BP.  
 DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.  
 PN WO2003082909-A1.  
 PD 09-OCT-2003.  
 PA (AMHP) WYETH.  
 Query Match 4.8%; Score 47.4; DB 10; Length 47988;  
 Best Local Similarity 44.2%; Pred. No. 44;  
 RESULT 1191  
 ID AAA09469 standard; DNA; 50937 BP.  
 DE Streptococcus oleandomycin gene cluster.  
 PN WO200026349-A2.  
 PD 11-MAY-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
 Best Local Similarity 44.7%; Pred. No. 44;  
 RESULT 1192  
 ID AAA09469 standard; DNA; 50937 BP.  
 DE Streptococcus oleandomycin gene cluster.  
 PN WO200026349-A2.  
 PD 11-MAY-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
 Best Local Similarity 45.7%; Pred. No. 44;  
 RESULT 1193  
 ID ADP74816 standard; DNA; 137560 BP.  
 DE Parapoxvirus ovis genome DNA sequence SeqID1.  
 Query Match 4.8%; Score 47.4; DB 12; Length 137560;  
 Best Local Similarity 47.9%; Pred. No. 42;  
 RESULT 1194  
 ID ADC76153 standard; DNA; 607 BP.  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1422.  
 PN WO2003020905-A2.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1195  
 ID ADD17151 standard; DNA; 607 BP.  
 DE DNA (SeqID 1219) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1196  
 ID ADD17811 standard; DNA; 607 BP.  
 DE DNA (SeqID 1879) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1197  
 ID ADK58311 standard; DNA; 607 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #5694.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1198  
 ID ABD17417 standard; DNA; 714 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16021.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1199  
 ID ACA23687 standard; DNA; 852 BP.  
 DE Prokaryotic essential gene #5344.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 852;  
 Best Local Similarity 47.9%; Pred. No. 53;  
 RESULT 1200  
 ID ADC76149 standard; DNA; 873 BP.  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1418.  
 PN WO2003020905-A2.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1201  
 ID ADD17156 standard; DNA; 873 BP.  
 DE DNA (SeqID 1224) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW AGROSCIENCES LLC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1202  
 ID ADK58312 standard; DNA; 873 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #5695.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1203  
 ID RAT59269 standard; cDNA; 888 BP.  
 DE Streptomyces pristinaespiralis papC gene.  
 PN WO9601901-A1.  
 PD 25-JAN-1996.  
 PA (RHON ) RHONE-POULENC RORER SA.  
 Query Match 4.8%; Score 47.2; DB 2; Length 888;  
 Best Local Similarity 45.3%; Pred. No. 53;  
 RESULT 1204  
 ID ABD02366 standard; DNA; 999 BP.

DE Pseudomonas aeruginosa polynucleotide #970.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 999;  
 Best Local Similarity 46.4%; Pred. No. 53;  
 RESULT 1205  
 ID ADA48950 standard; DNA; 1044 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 9; Length 1044;  
 Best Local Similarity 44.5%; Pred. No. 53;  
 RESULT 1206  
 ID ABD02410 standard; DNA; 1110 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1014.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 1110;  
 Best Local Similarity 46.4%; Pred. No. 52;  
 RESULT 1207  
 ID ACA26954 standard; DNA; 1134 BP.  
 DE Prokaryotic essential gene #8611.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1134;  
 Best Local Similarity 46.7%; Pred. No. 52;  
 RESULT 1208  
 ID ADQ83738 standard; cDNA; 1178 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #552.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 4.8%; Score 47.2; DB 12; Length 1178;  
 Best Local Similarity 43.8%; Pred. No. 52;  
 RESULT 1209  
 ID ABX56038 standard; DNA; 1194 BP.  
 DE M. echinospora calicheamicin biosynthesis gene caln.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1194;  
 Best Local Similarity 43.0%; Pred. No. 52;  
 RESULT 1210  
 ID ABD02476 standard; DNA; 1275 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1080.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 1275;  
 Best Local Similarity 46.4%; Pred. No. 52;  
 RESULT 1211  
 ID ABX56047 standard; DNA; 1347 BP.  
 DE M. echinospora calicheamicin biosynthesis gene calw.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1347;  
 Best Local Similarity 47.0%; Pred. No. 52;  
 RESULT 1212  
 ID ACA23577 standard; DNA; 1374 BP.  
 DE Prokaryotic essential gene #5234.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1374;  
 Best Local Similarity 47.3%; Pred. No. 52;  
 RESULT 1213

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ID ADT43862 standard; cDNA; 1386 BP.
DE Bacterial polynucleotide #18613.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 13; Length 1386;
RESULT 1214
ID ACA26528 standard; DNA; 1395 BP.
DE Prokaryotic essential gene #8185.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1395;
RESULT 1215
ID ACA37685 standard; DNA; 1410 BP.
DE Prokaryotic essential gene #19342.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1410;
RESULT 1216
ID ABQ55009 standard; cDNA; 1616 BP.
DE Human ovarian antigen HUKJ46 cDNA, SEQ ID NO:889.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1616;
RESULT 1217
ID ABL39997 standard; DNA; 1680 BP.
DE Synthetic RT polynucleotide sequence SEQ ID NO:76.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1680;
RESULT 1218
ID ADM73810 standard; DNA; 1680 BP.
DE HIV-1 polynucleotide #45.
PN US2003233961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1680;
RESULT 1219
ID ACH91868 standard; DNA; 1737 BP.
DE Human genome derived single exon probe #25063.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1737;
RESULT 1220
ID ACH92275 standard; DNA; 1738 BP.
DE Human genome derived single exon probe #25470.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1738;
RESULT 1221
ID AAL40132 standard; DNA; 1896 BP.
DE Isoprenoid related nucleic acid sequence SEQ ID NO 16.
PN WO200226933-A2.
PD 04-APR-2002.
PA (CRGI) CARGILL INC.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1896;
RESULT 1222
ID ABD17641 standard; DNA; 1944 BP.
DE Pseudomonas aeruginosa polynucleotide #16245.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 11; Length 1944;
RESULT 1223
ID ACA03560 standard; DNA; 1977 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #43.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1977;
RESULT 1224
ID ACC78516 standard; DNA; 1977 BP.
DE HIV protRT.opt.SF2 nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1977;
RESULT 1225
ID ADM73804 standard; DNA; 1977 BP.
DE HIV-1 polynucleotide #39.
PN US2003233961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1977;
RESULT 1226
ID ABL39991 standard; DNA; 1978 BP.
DE Synthetic protease and RT polynucleotide sequence SEQ ID NO:70.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1978;
RESULT 1227
ID ACA03571 standard; DNA; 1989 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #54.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1989;
RESULT 1228
ID ACC78522 standard; DNA; 1989 BP.
DE HIV RT.opt.SF2 (native) nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.

Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1989;
RESULT 1229
ID ABD07303 standard; DNA; 2133 BP.
DE Pseudomonas aeruginosa polynucleotide #5907.

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PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2133;  
 Best Local Similarity 44.1%; Pred. No. 52;  
 RESULT 1230  
 ID ACA03552 standard; DNA; 2145 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #35.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
 Best Local Similarity 47.8%; Pred. No. 52;  
 RESULT 1231  
 ID ACC78510 standard; DNA; 2145 BP.  
 DE HIV pol.opt.SF2 nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
 Best Local Similarity 47.6%; Pred. No. 52;  
 RESULT 1232  
 ID AAA70481 standard; DNA; 2312 BP.  
 DE HIV FS(-) ProtMod\_RTopt(+) coding sequence.  
 PN WO200033302-A2.  
 PD 06-JUL-2000.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 3; Length 2312;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1233  
 ID ACA03543 standard; DNA; 2472 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #26.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2472;  
 Best Local Similarity 47.8%; Pred. No. 51;  
 RESULT 1234  
 ID ACC78507 standard; DNA; 2472 BP.  
 DE HIV p2Polopt.SF2 nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2472;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1235  
 ID ADA69874 standard; DNA; 2529 BP.  
 DE Rice gene, SEQ ID 3197.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2529;  
 Best Local Similarity 44.5%; Pred. No. 51;  
 RESULT 1236  
 ID ADC72236 standard; DNA; 2691 BP.  
 DE Human NR3B gene SEQ ID NO:9.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYTA ) UNIV YALE.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 4.8%; Score 47.2; DB 10; Length 2691;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1237  
 ID ADN49187 standard; cDNA; 2691 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match 4.8%; Score 47.2; DB 12; Length 2691;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1238

ID AAL47419 standard; cDNA; 2706 BP.  
 DE Human N-methyl-D-aspartate receptor coding sequence.  
 PN WO200240538-A2.  
 PD 23-MAY-2002.  
 PA (FARB ) BAYER AG.  
 Query Match 4.8%; Score 47.2; DB 6; Length 2706;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1239  
 ID ACC47899 standard; cDNA; 2706 BP.  
 DE Human NR3B subunit receptor polypeptide coding sequence.  
 PN WO2003033672-A2.  
 PD 24-APR-2003.  
 PA (RIKE ) RIKEN KK.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2706;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1240  
 ID ACA38169 standard; DNA; 2751 BP.  
 DE Prokaryotic essential gene #19826.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2751;  
 Best Local Similarity 47.1%; Pred. No. 51;  
 RESULT 1241  
 ID ADA69752 standard; DNA; 2763 BP.  
 DE Rice gene, SEQ ID 3075.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2763;  
 Best Local Similarity 48.2%; Pred. No. 51;  
 RESULT 1242  
 ID ABD17862 standard; DNA; 2808 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16466.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2808;  
 Best Local Similarity 48.8%; Pred. No. 51;  
 RESULT 1243  
 ID ABD12055 standard; DNA; 2862 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10659.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2862;  
 Best Local Similarity 43.1%; Pred. No. 51;  
 RESULT 1244  
 ID AAT59268 standard; cDNA; 2898 BP.  
 DE Streptomyces pristinaespiralis papA and papM intergenic region.  
 PN WO9601901-A1.  
 PD 25-JAN-1996.  
 PA (RHON ) RHONE-POULENC RORER SA.  
 Query Match 4.8%; Score 47.2; DB 2; Length 2898;  
 Best Local Similarity 45.3%; Pred. No. 51;  
 RESULT 1245  
 ID ADN49407 standard; DNA; 2898 BP.  
 DE Human glutamate receptor (MEM2) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD/) SPADERNA S K.  
 PA (QUIN/) QUINN K E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 Query Match 4.8%; Score 47.2; DB 12; Length 2898;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1246  
 ID ABD11810 standard; DNA; 2910 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10414.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 11; Length 2910;  
RESULT 1247  
ID AAS06334 standard; cDNA; 2916 BP.  
DE DNA encoding human glutamate receptor-like protein, MEM3.  
PN WO200144473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 4; Length 2916;  
RESULT 1248  
ID ADN49409 standard; DNA; 2916 BP.  
DE Human glutamate receptor (MEM3) DNA.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.  
PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 2916;  
RESULT 1249  
ID AAZ52054 standard; DNA; 3012 BP.  
DE Codon optimised Human immunodeficiency virus pol coding region.  
PN WO200015819-A1.  
PD 23-MAR-2000.  
PA (CHIL-) CHILDRENS MEDICAL CENT.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 3; Length 3012;  
RESULT 1250  
ID ABL3983 standard; DNA; 3015 BP.  
DE Synthetic Pol polynucleotide sequence SEQ ID NO:62.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR-) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 3015;  
RESULT 1251  
ID ACA03553 standard; DNA; 3015 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #36.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR-) CHIRON CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 3015;  
RESULT 1252  
ID ADM73796 standard; DNA; 3015 BP.  
DE HIV-1 polynucleotide #31.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBERG E J V.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3015;  
RESULT 1253  
ID ADC72232 standard; DNA; 3096 BP.  
DE Human NR3B gene SEQ ID NO:5.  
PN WO2003016479-A2.  
PD 27-FEB-2003.  
PA (BURN-) BURNHAM INST.  
PA (UYVA-) UNIV YALE.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 10; Length 3096;  
RESULT 1254  
ID ADN49183 standard; cDNA; 3096 BP.  
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.  
PN US2004033500-A1.  
PD 19-FEB-2004.

PA (BURN-) BURNHAM INST.  
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3096;  
RESULT 1255  
ID ADC72287 standard; DNA; 3097 BP.  
DE Human NR3B gene SEQ ID NO:61.  
PN WO2003016479-A2.  
PD 27-FEB-2003.  
PA (BURN-) BURNHAM INST.  
PA (UYVA-) UNIV YALE.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 10; Length 3097;  
RESULT 1256  
ID ADN49238 standard; cDNA; 3097 BP.  
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.  
PN US2004033500-A1.  
PD 19-FEB-2004.  
PA (BURN-) BURNHAM INST.  
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3097;  
RESULT 1257  
ID ABD11900 standard; DNA; 3111 BP.  
DE Pseudomonas aeruginosa polynucleotide #10504.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 11; Length 3111;  
RESULT 1258  
ID AAS06335 standard; cDNA; 3132 BP.  
DE DNA encoding human glutamate receptor-like protein, MEM4.  
PN WO200144473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 4; Length 3132;  
RESULT 1259  
ID ABZ33750 standard; cDNA; 3132 BP.  
DE Human TRICH encoding cDNA SEQ ID NO 56.  
PN WO200246415-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 3132;  
RESULT 1260  
ID ADN49411 standard; DNA; 3132 BP.  
DE Human glutamate receptor (MEM4) DNA.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.  
PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3132;  
RESULT 1261  
ID ABD07318 standard; DNA; 3135 BP.  
DE Pseudomonas aeruginosa polynucleotide #5922.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match  
Best Local Similarity 4.8%; Score 47.2; DB 11; Length 3135;  
RESULT 1262  
ID AAC76703 standard; cDNA; 3207 BP.  
DE Human ORFX ORF2258 polynucleotide sequence SEQ ID NO:4515.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.



Query Match 4.8%; Score 47.2; DB 3; Length 3207;  
Best Local Similarity 43.7%; Pred. No. 51;  
RESULT 1263  
ID ACA03544 standard; DNA; 3639 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #27.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
Best Local Similarity 47.6%; Pred. No. 51;  
RESULT 1264  
ID ACC78508 standard; DNA; 3639 BP.  
DE HIV p2PolTatRevNef.opt.native\_B nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
Best Local Similarity 47.6%; Pred. No. 51;  
RESULT 1265  
ID ADM02119 standard; cDNA; 3955 BP.  
DE Human cDNA of the invention SEQ ID NO:804.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 4.8%; Score 47.2; DB 11; Length 3955;  
Best Local Similarity 49.2%; Pred. No. 51;  
RESULT 1266  
ID AAA70414 standard; DNA; 4319 BP.  
DE HIV Gag-polymerase expression cassette coding sequence GagPol.ModSP.  
PN WO200039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 3; Length 4319;  
Best Local Similarity 47.6%; Pred. No. 51;  
RESULT 1267  
ID ADI60576 standard; DNA; 4532 BP.  
DE Secreted polypeptide encoding gene #115.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 4532;  
Best Local Similarity 49.2%; Pred. No. 50;  
RESULT 1268  
ID ADO24366 standard; cDNA; 4973 BP.  
DE Human PRO87327 encoding cDNA SEQ ID NO:5.  
PN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 4.8%; Score 47.2; DB 12; Length 4973;  
Best Local Similarity 49.2%; Pred. No. 50;  
RESULT 1269  
ID AAV21186 standard; DNA; 5676 BP.  
DE Mycolatopsis mediterranei strain wt3136 5.7 kb KpnI DNA fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS ) NOVARTIS AG.  
Query Match 4.8%; Score 47.2; DB 2; Length 5676;  
Best Local Similarity 44.9%; Pred. No. 50;  
RESULT 1270  
ID ADB53354 standard; DNA; 6402 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3896.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 6402;  
Best Local Similarity 43.0%; Pred. No. 50;  
RESULT 1271  
ID AAZ52055 standard; DNA; 8908 BP.  
DE Packaging construct pHDVgpm2 DNA.  
PN WO200015819-A1.  
PD 23-MAR-2000.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
Query Match 4.8%; Score 47.2; DB 3; Length 8908;

Best Local Similarity 47.6%; Pred. No. 50;  
RESULT 1272  
ID AAZ87298 standard; DNA; 11220 BP.  
DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINU ) UNIV MINNESOTA.  
Query Match 4.8%; Score 47.2; DB 3; Length 11220;  
Best Local Similarity 47.3%; Pred. No. 49;  
RESULT 1273  
ID ADL91917 standard; DNA; 11220 BP.  
DE Streptomycetes macrolide biosynthetic protein (PikAII) coding sequence.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 4.8%; Score 47.2; DB 12; Length 11220;  
Best Local Similarity 47.3%; Pred. No. 49;  
RESULT 1274  
ID ADJ72366 standard; DNA; 23949 BP.  
DE Streptomycetes roseosporus daptomycin biosynthesis gene fragment.  
PN WO2003014237-A2.  
PD 20-FEB-2003.  
PA (CUBI-) CUBIST PHARM INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 23949;  
Best Local Similarity 44.7%; Pred. No. 48;  
RESULT 1275  
ID ADC69979 standard; DNA; 27705 BP.  
DE Sorangium cellulosum tmba gene cluster tmba DNA.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.8%; Score 47.2; DB 10; Length 27705;  
Best Local Similarity 46.1%; Pred. No. 48;  
RESULT 1276  
ID AAV21187 standard; DNA; 53789 BP.  
DE Mycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS ) NOVARTIS AG.  
Query Match 4.8%; Score 47.2; DB 2; Length 53789;  
Best Local Similarity 44.9%; Pred. No. 47;  
RESULT 1277  
ID ABD16054 standard; DNA; 441 BP.  
DE Pseudomonas aeruginosa polynucleotide #14658.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47; DB 11; Length 441;  
Best Local Similarity 46.1%; Pred. No. 58;  
RESULT 1278  
ID ADB68842 standard; DNA; 536 BP.  
DE Minority luxI consensus sequence DNA 14.  
PN WO2003057902-A2.  
PD 17-JUL-2003.  
PA (FRAU ) FRAUNHOFER USA INC.  
Query Match 4.8%; Score 47; DB 10; Length 536;  
Best Local Similarity 12.9%; Pred. No. 58;  
RESULT 1279  
ID ADC08861 standard; DNA; 597 BP.  
DE Corn DNA sequence Seq ID1166 related to grain filling.  
PN WO2003000905-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47; DB 10; Length 597;  
Best Local Similarity 49.8%; Pred. No. 58;  
RESULT 1280  
ID ACA26778 standard; DNA; 675 BP.  
DE Prokaryotic essential gene #8435.  
PN WO200277183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 675;  
 Best Local Similarity 47.0%; Pred. No. 57;  
 RESULT 1281  
 ID ADO63457 standard; DNA; 715 BP.  
 DE Transcription factor G3083 orthologous sequence, SEQ ID 1924.  
 PN WO2004031349-A2.  
 PD 15-APR-2004.  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 Query Match 4.8%; Score 47; DB 12; Length 715;  
 Best Local Similarity 48.1%; Pred. No. 57;  
 RESULT 1282  
 ID ABQ78042 standard; cDNA; 758 BP.  
 DE Maize SCIP-1 orthologue encoding cDNA SEQ ID NO 5.  
 PN US2002069428-A1.  
 PD 06-JUN-2002.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 758;  
 Best Local Similarity 46.9%; Pred. No. 57;  
 RESULT 1283  
 ID ABX12766 standard; DNA; 930 BP.  
 DE DNA encoding murine ischaemia activated protein (IAP).  
 PN US2002160495-A1.  
 PD 31-OCT-2002.  
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 Query Match 4.8%; Score 47; DB 8; Length 930;  
 Best Local Similarity 50.7%; Pred. No. 57;  
 RESULT 1284  
 ID ADL17042 standard; cDNA; 1120 BP.  
 DE Streptomyces coelicolor Bcl-2 domain cDNA #1.  
 PN US2004023866-A1.  
 PD 05-FEB-2004.  
 PA (GODZ/) GODZIK A.  
 PA (REED/) REED J C.  
 Query Match 4.8%; Score 47; DB 12; Length 1120;  
 Best Local Similarity 48.7%; Pred. No. 57;  
 RESULT 1285  
 ID ABD15922 standard; DNA; 1260 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14526.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47; DB 11; Length 1260;  
 Best Local Similarity 46.1%; Pred. No. 56;  
 RESULT 1286  
 ID ABD16234 standard; DNA; 1260 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14838.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47; DB 11; Length 1260;  
 Best Local Similarity 46.1%; Pred. No. 56;  
 RESULT 1287  
 ID ABZ66692 standard; DNA; 1293 BP.  
 DE Orthostomycin biosynthetic polynucleotide SEQ ID NO 46.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.8%; Score 47; DB 10; Length 1293;  
 Best Local Similarity 44.1%; Pred. No. 56;  
 RESULT 1288  
 ID AAQ22481 standard; DNA; 1320 BP.  
 DE groEL-1 gene partial sequence.  
 PN WO2044452-A.  
 PD 19-MAR-1992.  
 PA (INSP-) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 1320;  
 Best Local Similarity 44.2%; Pred. No. 56;  
 RESULT 1289  
 ID ABQ54643 standard; cDNA; 1354 BP.  
 DE Human ovarian antigen HE2KN09 cDNA, SEQ ID NO:523.  
 PN WO20020677-A1.  
 PD 03-JAN-2002.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.8%; Score 47; DB 6; Length 1354;  
 Best Local Similarity 44.6%; Pred. No. 56;  
 RESULT 1290  
 ID AAV20099 standard; DNA; 1416 BP.  
 DE Pseudomonas LipR kinase coding sequence.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 2; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1291  
 ID AAAL3891 standard; DNA; 1416 BP.  
 DE Pseudomonas alcaligenes LipR nucleotide sequence SEQ ID NO:3.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 3; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1292  
 ID AAD22868 standard; DNA; 1416 BP.  
 DE Pseudomonas alcaligenes LipR DNA.  
 PN US6313283-B1.  
 PD 06-NOV-2001.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1293  
 ID ACA27226 standard; DNA; 1536 BP.  
 DE Prokaryotic essential gene #8883.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 1536;  
 Best Local Similarity 51.1%; Pred. No. 56;  
 RESULT 1294  
 ID AAQ22482 standard; DNA; 1620 BP.  
 DE groEL-1 gene coding region.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP-) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 1620;  
 Best Local Similarity 44.2%; Pred. No. 56;  
 RESULT 1295  
 ID ABX56033 standard; DNA; 1707 BP.  
 DE M. echinospira calicheamicin biosynthesis gene call.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47; DB 8; Length 1707;  
 Best Local Similarity 48.0%; Pred. No. 56;  
 RESULT 1296  
 ID AA64515 standard; cDNA; 1722 BP.  
 DE Nucleotide sequence of truncated FEZ1 transcript G3612.  
 PN WO200050565-A2.  
 PD 31-AUG-2000.  
 PA (UVJE-) UNIV JEFFERSON THOMAS.  
 Query Match 4.8%; Score 47; DB 3; Length 1722;  
 Best Local Similarity 45.9%; Pred. No. 56;  
 RESULT 1297  
 ID ADA71120 standard; DNA; 1790 BP.  
 DE Rice gene, SEQ ID 4443.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47; DB 8; Length 1790;  
 Best Local Similarity 50.2%; Pred. No. 56;  
 RESULT 1298  
 ID ACA23626 standard; DNA; 1968 BP.  
 DE Prokaryotic essential gene #5283.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.

Query Match 4.8%; Score 47; DB 8; Length 1968;  
 Best Local Similarity 45.2%; Pred. No. 56;  
 RESULT 1299  
 ID AAN92408 standard; DNA; 2061 BP.  
 DE Sequence encoding pseudorabies virus (PRV) glycoprotein gH.  
 PN WC8910965-A.  
 PD 16-NOV-1989.  
 PA (UPJO) UPJOHN CO.  
 Query Match 4.8%; Score 47; DB 1; Length 2061;  
 Best Local Similarity 44.7%; Pred. No. 56;  
 RESULT 1300  
 ID AAO22484 standard; DNA; 2167 BP.  
 DE gro es el operon with promoter sequence.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2167;  
 Best Local Similarity 44.2%; Pred. No. 56;  
 RESULT 1301  
 ID ADD22490 standard; DNA; 2335 BP.  
 DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ NO 140.  
 PN JP2003111595-A.  
 PD 15-APR-2003.  
 PA (ITOY/) ITO Y.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1302  
 ID ADI15967 standard; cDNA; 2335 BP.  
 DE Human PP 100 cDNA.  
 PN WO2003008450-A1.  
 PD 30-JAN-2003.  
 PA (ITOH/) ITOH K.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1303  
 ID ADS34440 standard; DNA; 2335 BP.  
 DE FOSH protein associated DNA #194.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.8%; Score 47; DB 13; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1304  
 ID AAO22485 standard; DNA; 2668 BP.  
 DE GROEL-1 gene.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2668;  
 Best Local Similarity 44.2%; Pred. No. 55;  
 RESULT 1305  
 ID AAV23493 standard; DNA; 4377 BP.  
 DE Pseudomonas LipQ, LipR, OrfV operon.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 2; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1306  
 ID AAA13504 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:28.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 3; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1307  
 ID AAF30869 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes LipQ, LipR and OrfZ gene region.  
 PN US6225106-B1.  
 PD 01-MAY-2001.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 4; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1308  
 ID AAD22881 standard; DNA; 4377 BP.  
 DE P. alcaligenes DNA comprising cosmids #71, #201, #505 and #726.  
 PN US6313283-B1.  
 PD 06-NOV-2001.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1309  
 ID AAF88336 standard; DNA; 6459 BP.  
 DE S. spinosa DNA fragment encoding ORF19, SEQ ID 43.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 6459;  
 Best Local Similarity 46.9%; Pred. No. 54;  
 RESULT 1310  
 ID AKS2418 standard; DNA; 6868 BP.  
 DE DNA encoding propionibacterium associated proteins.  
 PN JP2002112790-A.  
 PD 16-APR-2002.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 4.8%; Score 47; DB 6; Length 6868;  
 Best Local Similarity 51.7%; Pred. No. 54;  
 RESULT 1311  
 ID AAF88313 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 2.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 51;  
 RESULT 1312  
 ID AAF88316 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 5.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 51;  
 RESULT 1313  
 ID AAZ21501 standard; DNA; 80161 BP.  
 DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.  
 Query Match 4.8%; Score 47; DB 2; Length 80161;  
 Best Local Similarity 46.9%; Pred. No. 50;  
 RESULT 1314  
 ID ADI39159 standard; DNA; 85692 BP.  
 DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
 PN WO2003106653-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 PA (REID/) REID R C.  
 Query Match 4.8%; Score 47; DB 12; Length 85692;  
 Best Local Similarity 43.9%; Pred. No. 50;  
 RESULT 1315  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 50;  
 RESULT 1316  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 50;  
 RESULT 1317  
 ID AAA68102 standard; DNA; 296 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Query Match 4.7%; Score 46.8; DB 3; Length 296;  
 Best Local Similarity 54.7%; Pred. No. 63;  
 RESULT 1318  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.

PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 4.7%; Score 46.8; DB 10; Length 296;  
Best Local Similarity 54.7%; Pred. No. 63;  
RESULT 1319  
ID ADS14636 standard; DNA; 663 BP.  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA3181, SEQ ID 191.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA ) UNIV IOWA RES FOUND.  
Query Match 4.7%; Score 46.8; DB 13; Length 663;  
Best Local Similarity 50.4%; Pred. No. 62;  
RESULT 1320  
ID ABZ13007 standard; DNA; 768 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 812.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.7%; Score 46.8; DB 6; Length 768;  
Best Local Similarity 46.0%; Pred. No. 62;  
RESULT 1321  
ID ABD06367 standard; DNA; 792 BP.  
DE Pseudomonas aeruginosa polynucleotide #4971.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 792;  
Best Local Similarity 50.4%; Pred. No. 62;  
RESULT 1322  
ID AAV73801 standard; DNA; 801 BP.  
DE KSHV LUR terminal repeat unit DNA.  
PN US5849564-A.  
PD 15-DEC-1998.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 4.7%; Score 46.8; DB 2; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1323  
ID AAA30291 standard; DNA; 801 BP.  
DE Rhadino virus cis-acting element, RVCAE.  
PN WO20029626-A1.  
PD 25-MAY-2000.  
PA (KIEF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 4.7%; Score 46.8; DB 3; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1324  
ID ABA93488 standard; DNA; 801 BP.  
DE Kaposi's sarcoma-associated herpesvirus terminal repeat unit.  
PN US6322792-B1.  
PD 27-NOV-2001.  
PA (KIEF/) KIEFF E D.  
Query Match 4.7%; Score 46.8; DB 6; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1325  
ID ADJ65097 standard; DNA; 801 BP.  
DE HHV8 terminal repeat region, TR.  
PN US2004037847-A1.  
PD 26-FEB-2004.  
PA (KIEF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 4.7%; Score 46.8; DB 12; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1326  
ID ADD17814 standard; DNA; 872 BP.  
DE DNA (SeqID 1882) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.  
PD 13-NAR-2003.  
PA (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.  
Query Match 4.7%; Score 46.8; DB 10; Length 872;  
Best Local Similarity 48.8%; Pred. No. 62;  
RESULT 1327  
ID ACA37750 standard; DNA; 984 BP.  
DE Prokaryotic essential gene #19407.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 984;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1328  
ID ABD06351 standard; DNA; 1071 BP.  
DE Pseudomonas aeruginosa polynucleotide #4955.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1071;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1329  
ID ABD06390 standard; DNA; 1131 BP.  
DE Pseudomonas aeruginosa polynucleotide #4994.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1131;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1330  
ID ABD06380 standard; DNA; 1215 BP.  
DE Pseudomonas aeruginosa polynucleotide #4984.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1215;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1331  
ID ADA45210 standard; cDNA; 1358 BP.  
DE Recombinant Max & JLP N-terminal region protein, M2LZII coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1332  
ID ADA45206 standard; cDNA; 1358 BP.  
DE Recombinant Max and JLP N-terminal region protein, M2, coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1333  
ID ADA45208 standard; cDNA; 1358 BP.  
DE Recombinant Max and JLP N-terminal region protein, M2LZI coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1334  
ID ACA40293 standard; DNA; 1464 BP.  
DE Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 1464;  
Best Local Similarity 42.2%; Pred. No. 61;  
RESULT 1335  
ID ADR01290 standard; DNA; 1722 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF39 protein ABCA DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match 4.7%; Score 46.8; DB 13; Length 1722;  
 Best Local Similarity 46.3%; Pred. No. 60;  
 RESULT 1336  
 ID ADS55765 standard; cDNA; 2013 BP.  
 DE Bacterial polynucleotide #7752.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.7%; Score 46.8; DB 13; Length 2013;  
 Best Local Similarity 49.2%; Pred. No. 60;  
 RESULT 1337  
 ID ADT48680 standard; cDNA; 2226 BP.  
 DE Bacterial polynucleotide #23431.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.7%; Score 46.8; DB 13; Length 2226;  
 Best Local Similarity 44.3%; Pred. No. 60;  
 RESULT 1338  
 ID ACA37666 standard; DNA; 2739 BP.  
 DE Prokaryotic essential gene #19323.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.8; DB 8; Length 2739;  
 Best Local Similarity 45.1%; Pred. No. 60;  
 RESULT 1339  
 ID ABD08987 standard; DNA; 3171 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7591.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 3171;  
 Best Local Similarity 43.4%; Pred. No. 59;  
 RESULT 1340  
 ID ABD09358 standard; DNA; 3210 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7962.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 3210;  
 Best Local Similarity 43.4%; Pred. No. 59;  
 RESULT 1341  
 ID AAH47802 standard; DNA; 3535 BP.  
 DE Chimeric CBD-fused FR301379 acylase DNA.  
 PN WO200131038-A1.  
 PD 03-MAY-2001.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Query Match 4.7%; Score 46.8; DB 4; Length 3535;  
 Best Local Similarity 49.3%; Pred. No. 59;  
 RESULT 1342  
 ID AAI57831 standard; cDNA; 4176 BP.  
 DE Human polynucleotide SEQ ID NO 34.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.8; DB 4; Length 4176;  
 Best Local Similarity 49.4%; Pred. No. 59;  
 RESULT 1343  
 ID AAO95540 standard; DNA; 4356 BP.  
 DE Cardiac adenylyl cyclase gene.  
 PN TW243453-A.  
 PD 21-MAR-1995.  
 PA (AMCY) AMERICAN CYANAMID CO.  
 Query Match 4.7%; Score 46.8; DB 2; Length 4356;

Best Local Similarity 45.9%; Pred. No. 59;  
 RESULT 1344  
 ID ADA45191 standard; cDNA; 4667 BP.  
 DE Murine JLP coding sequence.  
 PN WO2003066652-A2.  
 PD 14-AUG-2003.  
 PA (UTEM) UNIV TEMPLE.  
 Query Match 4.7%; Score 46.8; DB 9; Length 4667;  
 Best Local Similarity 54.1%; Pred. No. 59;  
 RESULT 1345  
 ID ADC10001 standard; DNA; 5220 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
 PN WO2003000842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.7%; Score 46.8; DB 10; Length 5220;  
 Best Local Similarity 42.6%; Pred. No. 59;  
 RESULT 1346  
 ID AAF32248 standard; DNA; 5692 BP.  
 DE Streptomyces sp. cyclic lipopeptide acylase encoding DNA SEQ ID NO:1.  
 PN WO200102585-A1.  
 PD 11-JAN-2001.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Query Match 4.7%; Score 46.8; DB 4; Length 5692;  
 Best Local Similarity 49.3%; Pred. No. 58;  
 RESULT 1347  
 ID AAD54224 standard; DNA; 5862 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF7 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.8; DB 10; Length 5862;  
 Best Local Similarity 46.8%; Pred. No. 58;  
 RESULT 1348  
 ID ACA37617 standard; DNA; 10232 BP.  
 DE Prokaryotic essential gene #19274.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.8; DB 8; Length 10232;  
 Best Local Similarity 44.0%; Pred. No. 58;  
 RESULT 1349  
 ID AAA58472 standard; DNA; 18660 BP.  
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.  
 PN WO200040704-A1.  
 PD 13-JUL-2000.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 4.7%; Score 46.8; DB 3; Length 18660;  
 Best Local Similarity 47.5%; Pred. No. 57;  
 RESULT 1350  
 ID ABL68348 standard; DNA; 25000 BP.  
 DE Kidney cancer related gene sequence SEQ ID NO:6685.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 4.7%; Score 46.8; DB 6; Length 25000;  
 Best Local Similarity 47.3%; Pred. No. 56;  
 RESULT 1351  
 ID AAA11992 standard; DNA; 37856 BP.  
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
 PN DE19846493-A1.  
 PD 13-APR-2000.  
 PA (GBPB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 4.7%; Score 46.8; DB 3; Length 37856;  
 Best Local Similarity 48.2%; Pred. No. 55;  
 RESULT 1352  
 ID ADQ74672 standard; DNA; 74787 BP.  
 DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.  
 Query Match 4.7%; Score 46.8; DB 12; Length 74787;  
 Best Local Similarity 44.3%; Pred. No. 54;  
 RESULT 1353  
 Query Match 4.7%; Score 46.8; DB 4; Length 110000;  
 Best Local Similarity 42.2%; Pred. No. 54;

RESULT 1354  
ID ABD15774 standard; DNA; 270 BP.  
DE Pseudomonas aeruginosa polynucleotide #14378.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 270;  
Best Local Similarity 50.2%; Pred. No. 69;  
RESULT 1355  
ID ABD01848 standard; DNA; 489 BP.  
DE Pseudomonas aeruginosa polynucleotide #452.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 489;  
Best Local Similarity 50.2%; Pred. No. 69;  
RESULT 1356  
ID ACB38033 standard; DNA; 723 BP.  
DE Prokaryotic essential gene #19690.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.6; DB 8; Length 723;  
Best Local Similarity 45.3%; Pred. No. 67;  
RESULT 1357  
ID ADT44804 standard; cDNA; 762 BP.  
DE Bacterial polynucleotide #19555.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.7%; Score 46.6; DB 13; Length 762;  
Best Local Similarity 47.9%; Pred. No. 67;  
RESULT 1358  
ID ABD13964 standard; DNA; 777 BP.  
DE Pseudomonas aeruginosa polynucleotide #12568.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 777;  
Best Local Similarity 53.6%; Pred. No. 67;  
RESULT 1359  
ID ABD14635 standard; DNA; 786 BP.  
DE Pseudomonas aeruginosa polynucleotide #13239.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 786;  
Best Local Similarity 53.6%; Pred. No. 67;  
RESULT 1360  
ID ACC59353 standard; DNA; 948 BP.  
DE R ruber esterase estA coding sequence #1.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 948;  
Best Local Similarity 46.0%; Pred. No. 66;  
RESULT 1361  
ID ACC59354 standard; DNA; 948 BP.  
DE R ruber esterase estA coding sequence #2.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 948;  
Best Local Similarity 46.0%; Pred. No. 66;  
RESULT 1362  
ID ABD01827 standard; DNA; 981 BP.  
DE Pseudomonas aeruginosa polynucleotide #431.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 981;  
Best Local Similarity 47.9%; Pred. No. 66;  
RESULT 1363  
ID ABD11883 standard; DNA; 981 BP.  
DE Pseudomonas aeruginosa polynucleotide #10487.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 981;  
Best Local Similarity 47.7%; Pred. No. 66;  
RESULT 1364  
ID ADR13680 standard; DNA; 1032 BP.  
DE Amidase coding sequence, SEQ ID 17.  
PN WO2004069848-A2.  
PD 19-AUG-2004.  
PA (DIVE-) DIVERSA CORP.  
Query Match 4.7%; Score 46.6; DB 13; Length 1032;  
Best Local Similarity 44.3%; Pred. No. 66;  
RESULT 1365  
ID ABD08147 standard; DNA; 1062 BP.  
DE Pseudomonas aeruginosa polynucleotide #6751.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 1062;  
Best Local Similarity 47.2%; Pred. No. 66;  
RESULT 1366  
ID ACA38086 standard; DNA; 1224 BP.  
DE Prokaryotic essential gene #19743.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.6; DB 8; Length 1224;  
Best Local Similarity 52.3%; Pred. No. 66;  
RESULT 1367  
ID AAD33021 standard; DNA; 1299 BP.  
DE Streptomyces species ema5 gene.  
PN WO200292801-A2.  
PD 21-NOV-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.7%; Score 46.6; DB 10; Length 1299;  
Best Local Similarity 48.0%; Pred. No. 66;  
RESULT 1368  
ID ABD04946 standard; DNA; 1380 BP.  
DE Pseudomonas aeruginosa polynucleotide #3550.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 1380;  
Best Local Similarity 45.1%; Pred. No. 66;  
RESULT 1369  
ID ABZ71149 standard; DNA; 1473 BP.  
DE S. murayamaensis ATCC 21414 kinamycin encoding DNA SEQ ID NO.36.  
PN WO2003002066-A2.  
PD 09-JAN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 4.7%; Score 46.6; DB 8; Length 1473;  
Best Local Similarity 46.4%; Pred. No. 66;  
RESULT 1370  
ID ACC59357 standard; DNA; 1494 BP.  
DE R ruber vector pMSS12 coding sequence insert #4.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 1494;  
Best Local Similarity 46.0%; Pred. No. 65;  
RESULT 1371  
ID ACC59352 standard; DNA; 1494 BP.  
DE R ruber vector pMSS12 coding sequence insert #2.

PN WO2003031625-A1.  
 PD 17-APR-2003.  
 PA (DEGS ) DEGUSSA AG.  
 PA (SCHW/) SCHWAB H.  
 Query Match 4.7%; Score 46.6; DB 10; Length 1494;  
 Best Local Similarity 46.0%; Pred. No. 65;  
 RESULT 1372  
 ID ABD08270 standard; DNA; 1530 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6874.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 1530;  
 Best Local Similarity 47.2%; Pred. No. 65;  
 RESULT 1373  
 ID AAL61148 standard; DNA; 1710 BP.  
 DE Human mutant ARX gene #1.  
 PN WO2003045989-A1.  
 PD 05-JUN-2003.  
 PA (WOMB-) WOMEN'S & CHILDREN'S HOSPITAL.  
 Query Match 4.7%; Score 46.6; DB 9; Length 1710;  
 Best Local Similarity 46.3%; Pred. No. 65;  
 RESULT 1374  
 ID ABD04953 standard; DNA; 1947 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3557.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 1947;  
 Best Local Similarity 45.1%; Pred. No. 65;  
 RESULT 1375  
 ID ABD14312 standard; DNA; 2325 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12916.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 2325;  
 Best Local Similarity 53.6%; Pred. No. 65;  
 RESULT 1376  
 ID ADB87421 standard; DNA; 2500 BP.  
 DE Transgene expression regulatory element, STAR66F.  
 PN WO2003004704-A2.  
 PD 16-JAN-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 10; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1377  
 ID ADJ35230 standard; DNA; 2500 BP.  
 DE Human stabilising anti-repression, STAR, element #66.  
 PN WO2003106674-A2.  
 PD 24-DEC-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1378  
 ID ADL96848 standard; DNA; 2500 BP.  
 DE Stabilizing Anti-Repressor DNA sequence, T2F STAR 66F.  
 PN WO2003106684-A2.  
 PD 24-DEC-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1379  
 ID ACC44572 standard; cDNA; 3285 BP.  
 DE Alpha-amylase/glucosylase fusion nucleotide sequence SEQ ID NO:46.  
 PN WO2003018766-A2.  
 PD 06-MAR-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.7%; Score 46.6; DB 8; Length 3285;  
 Best Local Similarity 48.7%; Pred. No. 64;  
 RESULT 1380  
 ID ABL15824 standard; cDNA; 3790 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO:41954.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 4.7%; Score 46.6; DB 4; Length 3790;  
 Best Local Similarity 47.2%; Pred. No. 64;  
 RESULT 1381  
 ID ACA28449 standard; DNA; 3963 BP.  
 DE Prokaryotic essential gene #8106.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.6; DB 8; Length 3963;  
 Best Local Similarity 43.1%; Pred. No. 64;  
 RESULT 1382  
 ID AAL61172 standard; DNA; 4770 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #3.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 4.7%; Score 46.6; DB 8; Length 4770;  
 Best Local Similarity 44.8%; Pred. No. 63;  
 RESULT 1383  
 ID ADC10001 standard; DNA; 5220 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
 PN WO2003000842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.7%; Score 46.6; DB 10; Length 5220;  
 Best Local Similarity 44.2%; Pred. No. 63;  
 RESULT 1384  
 ID ABS78655 standard; DNA; 5811 BP.  
 DE S. macromyceticus DNA encoding PKSE protein macromycin.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.6; DB 6; Length 5811;  
 Best Local Similarity 47.6%; Pred. No. 63;  
 RESULT 1385  
 ID ABD01877 standard; DNA; 7419 BP.  
 DE Pseudomonas aeruginosa polynucleotide #481.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 7419;  
 Best Local Similarity 47.9%; Pred. No. 63;  
 RESULT 1386  
 ID ABD01792 standard; DNA; 7449 BP.  
 DE Pseudomonas aeruginosa polynucleotide #396.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 7449;  
 Best Local Similarity 47.9%; Pred. No. 63;  
 RESULT 1387  
 ID ABL66291 standard; DNA; 14800 BP.  
 DE Lung cancer related gene sequence SEQ ID NO:4628.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 4.7%; Score 46.6; DB 6; Length 14800;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1388  
 ID ADP13447 standard; DNA; 14800 BP.  
 DE Renal cell carcinoma differentially expressed gene #183.  
 PN WO20004048933-A2.  
 PD 10-JUN-2004.  
 PA (AMHP ) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TRBP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.

Query Match 4.7%; Score 46.6; DB 12; Length 14800;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1389  
 ID AAS94858 standard; DNA; 14835 BP.  
 DE Human DNA sequence #113 expressed during foam cell differentiation.  
 PN WO200177389-A2.  
 PD 18-OCT-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.7%; Score 46.6; DB 6; Length 14835;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1390  
 ID AAD54223 standard; DNA; 24081 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.6; DB 10; Length 24081;  
 Best Local Similarity 46.7%; Pred. No. 61;  
 RESULT 1391  
 ID AD007566 standard; DNA; 25467 BP.  
 DE Streptomyces kanamyceticus kanamycin biosynthesis genes SEQ ID NO:1.  
 PN JP2004173537-A.  
 PD 24-JUN-2004.  
 PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
 Query Match 4.7%; Score 46.6; DB 12; Length 25467;  
 Best Local Similarity 46.9%; Pred. No. 61;  
 RESULT 1392  
 ID ABZ71131 standard; DNA; 36321 BP.  
 DE Streptomyces murayamaensis ATCC 21414 kinamycin related DNA SEQ ID NO:1.  
 PN WO2003002066-A2.  
 PD 09-JAN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 4.7%; Score 46.6; DB 8; Length 36321;  
 Best Local Similarity 46.4%; Pred. No. 60;  
 RESULT 1393  
 ID ACF30939 standard; DNA; 53905 BP.  
 DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
 PN WO2003027290-A1.  
 PD 03-APR-2003.  
 PA (NISE) JAPAN TOBACCO INC.  
 PA (SYGN) SYNGENTA LTD.  
 Query Match 4.7%; Score 46.6; DB 8; Length 53905;  
 Best Local Similarity 46.2%; Pred. No. 59;  
 RESULT 1394  
 ID ADI09998 standard; DNA; 53905 BP.  
 DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
 PN WO2004005515-A1.  
 PD 15-JAN-2004.  
 PA (NISE) JAPAN TOBACCO INC.  
 PA (SYGN) SYNGENTA LTD.  
 Query Match 4.7%; Score 46.6; DB 12; Length 53905;  
 Best Local Similarity 46.2%; Pred. No. 59;  
 RESULT 1395  
 ID ABQ81849 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC PROD NESTLE SA.  
 Query Match 4.7%; Score 46.6; DB 6; Length 349980;  
 Best Local Similarity 48.7%; Pred. No. 56;  
 RESULT 1397  
 ID AAU51695 standard; cDNA; 314 BP.  
 DE Kukulcania hibernalis spider silk protein coding sequence #3.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 4.7%; Score 46.4; DB 8; Length 314;  
 Best Local Similarity 51.4%; Pred. No. 74;  
 RESULT 1398  
 ID ACH87193 standard; DNA; 461 BP.

DE Human genome derived single exon probe #20388.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match 4.7%; Score 46.4; DB 12; Length 461;  
 Best Local Similarity 50.7%; Pred. No. 73;  
 RESULT 1399  
 ID ACH73807 standard; DNA; 529 BP.  
 DE Human genome derived single exon probe #7002.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match 4.7%; Score 46.4; DB 12; Length 529;  
 Best Local Similarity 49.6%; Pred. No. 73;  
 RESULT 1400  
 ID AAH06810 standard; cDNA; 872 BP.  
 DE Human cDNA clone (5'-primer) SEQ ID NO:3645.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 4.7%; Score 46.4; DB 4; Length 872;  
 Best Local Similarity 50.0%; Pred. No. 72;  
 RESULT 1401  
 ID ABD15695 standard; DNA; 981 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14299.  
 PN US651795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.4; DB 11; Length 981;  
 Best Local Similarity 44.2%; Pred. No. 72;  
 RESULT 1402  
 ID ACA37963 standard; DNA; 1065 BP.  
 DE Prokaryotic essential gene #19620.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 8; Length 1065;  
 Best Local Similarity 47.3%; Pred. No. 71;  
 RESULT 1403  
 ID AAH46980 standard; cDNA; 1072 BP.  
 DE Human glutathione peroxidase (GPx6) encoding cDNA.  
 PN US6231853-B1.  
 PD 15-MAY-2001.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1404  
 ID ABU59157 standard; cDNA; 1072 BP.  
 DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
 PN US2002031506-A1.  
 PD 14-MAR-2002.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 6; Length 1072;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1405  
 ID AAI58027 standard; cDNA; 1100 BP.  
 DE Human polynucleotide SEQ ID NO 230.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1100;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1406  
 ID AAI59813 standard; cDNA; 1205 BP.  
 DE Human polynucleotide SEQ ID NO 3802.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1205;



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Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1407
ID ADI42681 standard; DNA; 1219 BP.
DE Plant transcription factor polynucleotide #735.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 4.7%; Score 46.4; DB 12; Length 1219;
Best Local Similarity 44.2%; Pred. No. 71;
RESULT 1408
ID ADO02930 standard; cDNA; 1219 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #98.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.7%; Score 46.4; DB 12; Length 1219;
Best Local Similarity 44.2%; Pred. No. 71;
RESULT 1409
ID AAZ65013 standard; cDNA; 1227 BP.
DE Membrane-bound protein PRO828 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 12; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1410
ID AAS46137 standard; cDNA; 1227 BP.
DE Human DNA encoding PRO polypeptide sequence #213.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1411
ID AAF44159 standard; cDNA; 1227 BP.
DE Human PRO828 (UNQ469) nucleotide sequence SEQ ID NO:188.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 5; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1412
ID ABL86133 standard; cDNA; 1227 BP.
DE Human PRO828 cDNA sequence SEQ ID NO:123.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1413
ID ABK28599 standard; cDNA; 1227 BP.
DE Human DNA57037-1444 encoding PRO828.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1414
ID ABL95622 standard; cDNA; 1227 BP.
DE Human angiogenesis related cDNA PRO828 SEQ ID NO: 123.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH/) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1415
ID ACA89587 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1416
ID ACA73597 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1417
ID ACA05912 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1418
ID ACA66746 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO protein #213.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH/) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 1419
ID ACA64292 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003003531-A1.
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PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
ID AC88795 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1431  
ID AC970237 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1432  
ID AC12459 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1433  
ID ACC74374 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1434  
ID AC16002 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1435  
ID AC25570 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1436  
ID AC18047 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1437  
ID ACC88334 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1438  
ID AC21688 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1439  
ID AC18755 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
PD 27-FEB-2003.

PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
ID ACF20321 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1421  
ID ACF19707 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1422  
ID ACD1995 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1423  
ID ACF13160 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1424  
ID ACD25263 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1425  
ID ACF00312 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1426  
ID AC972369 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1427  
ID ACD04893 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1428  
ID ACD18354 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1429  
ID ACD08361 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040054-A1.  
PD 27-FEB-2003.

RESULT 1440  
ID ABX98365 standard; cDNA; 1227 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 425.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1441  
ID ACD14116 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1442  
ID ACD09896 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1443  
ID ACC8641 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027286-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1444  
ID ACD21381 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1445  
ID ABX75753 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO828.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1446  
ID ABX97956 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1447  
ID ACA97432 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1448  
ID ACA57895 standard; cDNA; 1227 BP.  
DE Human PRO828 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1449  
ID ACD14423 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1450  
ID ACC91206 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1451  
ID ACC88948 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1452  
ID ACD07145 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1453  
ID ACA67596 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1454  
ID ACC81651 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1455  
ID ACC89255 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1456  
ID ACC86611 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1457  
ID ACC9869 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1458  
ID ACC93048 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1459  
ID ABX80751 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1460  
ID ACA72676 standard; cDNA; 1227 BP.

DE Human PRO polynucleotide #213.  
PN US2003022255-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1461  
ID ACA9194 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003022237-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1462  
ID ACA6930 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1463  
ID ACA97073 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1464  
ID ACA91069 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1465  
ID ACA70851 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1466  
ID ACA95361 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1467  
ID ACDA4260 standard; cDNA; 1227 BP.  
DE CDNA encoding human PRO828 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1468  
ID ACC86304 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1469  
ID ACC90176 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1470  
ID ACID12784 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1471  
ID ACF20014 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1472  
ID ABX76958 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1473  
ID ACA73290 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1474  
ID ACA68833 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1475  
ID ACA74677 standard; cDNA; 1227 BP.  
DE CDNA encoding human PRO polypeptide #213.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1476  
ID ACA70544 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1477  
ID ACID14730 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1478  
ID ACA68402 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1479  
ID ABX98867 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1480  
ID ACC81344 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;

Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1481  
ID ACA95668 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1482  
ID ACDO4586 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1483  
ID ACC88027 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1484  
ID ACF12689 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1485  
ID ABX79431 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1486  
ID ACA96404 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1487  
ID ACA65178 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1488  
ID ACA73904 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1489  
ID ACA74316 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1490  
ID ACA96711 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;

RESULT 1491  
ID ACD10817 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1492  
ID ACC91513 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1493  
ID ACA93452 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1494  
ID ACD02848 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1495  
ID ACC87413 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1496  
ID ACC85997 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1497  
ID ABX81134 standard; cDNA; 1227 BP.  
DE Human secreted or transmembrane protein related PCR primer #48.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1498  
ID ACA65485 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1499  
ID ACA94302 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1500  
ID ACA98046 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 16:05:28 ; Search time 7487 Seconds  
(without alignments)  
6400.722 Million cell updates/sec

Title: US-10-017-407A-305

Perfect score: 989

Sequence: 1 gggggccgcggtccgaga.....Caataaaaaaaaaaaaaaa 989

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989	100.0	989	6	AX201342 Sequence
2	989	100.0	989	6	AX697237 Sequence
3	989	100.0	989	9	AY358476 Homo sapi
4	985.8	99.7	1037	6	AX338454 Sequence
5	985.8	99.7	1041	9	BC047774 Homo sapi
6	981.8	99.3	985	6	BD222712 Human sig
7	938.2	94.9	988	9	AK074421 Homo sapi
8	907.8	91.8	913	9	BC023663 Homo sapi
9	789	79.8	789	6	CQ721501 Sequence
10	789	79.8	789	6	AX338456 Sequence
11	625	63.2	946	10	BC049670 Mus muscu
12	312	31.5	326	6	AX407985 Sequence
13	309.2	31.3	237829	2	AC120475 Rattus no
14	256.8	26.0	38679	9	AL3390034 Human DNA
15	256.8	26.0	169612	2	AC027393 Homo sapi
16	224.6	22.7	157428	10	AL606832 Mouse DNA
17	224.6	22.7	209643	10	AC080018
18	200	20.2	14100	1	MXU24657 Myxococcu
19	194.8	19.7	11171	6	CQ801141 Sequence

20	193.8	19.6	675	6	CQ801150 Sequence
21	188.8	19.1	10840	1	AE004550 Pseudomon
22	185.8	18.8	2381	1	STMWMBEC
23	185.8	18.8	2381	6	E06690 DNA encodin
24	185.4	18.7	304282	1	AE016910 Chromobac
25	185	18.7	663	12	AV657514 Synthetic
26	182.4	18.4	69644	1	AY179507 Streptomy
27	161.8	16.4	953	6	AR236716 Sequence
28	161.8	16.4	953	8	BT009394 Triticum
29	159.6	16.1	976	8	AB110168 Oryza sat
30	159.6	16.1	996	8	AK104326 Oryza sat
31	159.6	16.1	1096	8	AK104801 Oryza sat
32	159.6	16.1	1098	8	AK071482 Oryza sat
33	159.2	16.1	1049	6	AR236715 Sequence
34	158.6	16.0	997	6	AR236700 Sequence
35	158.6	16.0	1338	6	AX654529 Sequence
36	157.2	15.9	1078	6	AR236714 Sequence
37	157.2	15.9	1078	8	BT009389 Triticum
38	155.6	15.7	1018	6	AR236711 Sequence
39	154	15.6	891	6	AR236694 Sequence
40	154	15.6	1167	8	ZMA242981 Zea mays
41	153	15.5	77534	1	AF235504 Streptomy
42	153	15.5	77536	6	BD235937 Polyketid
43	153	15.5	77536	6	AR271638 Sequence
44	153	15.5	77536	6	AR564393 Sequence
45	152.8	15.4	1112	6	AX660732 Sequence
46	152.4	15.4	1218	6	AX146637 Sequence
47	151.4	15.3	82746	1	AF453501 Actinosyn
48	150.2	15.2	1158	8	AF644637 Oryza sat
49	150.2	15.2	1895	8	AK106735 Oryza sat
50	150.2	15.2	137354	8	AP000364 Oryza sat
51	148	15.0	798	6	AX660925 Sequence
52	148	15.0	1118	6	AR236712 Sequence
53	148	15.0	1118	8	BT009186 Triticum
54	148	15.0	1136	8	ZMA242980 Zea mays
55	148	15.0	1146	6	AR236695 Sequence
56	147.6	14.9	1252	6	CQ857676 Sequence
57	146.8	14.8	10882	1	AE002493 Neisseria
58	146.8	14.8	349980	6	AX044032 Sequence
59	146.2	14.8	875	8	AB158406 Triticum
60	146.2	14.8	1018	8	BT009093 Triticum
61	145	14.7	959	8	AK108479 Oryza sat
62	144.6	14.6	329861	1	NMA522491 Neisseria
63	144.4	14.6	1057	6	AR236696 Sequence
64	143.6	14.5	1052	8	AK065744 Oryza sat
65	141.8	14.3	783	6	AX654528 Sequence
66	141.8	14.3	1149	8	AK061757 Oryza sat
67	140.6	14.2	1058	6	AR236699 Sequence
68	140	14.2	783	6	AX654276 Sequence
69	137	13.9	1116	8	AY644638 Oryza sat
70	129.6	13.1	1466	8	AK065515 Oryza sat
71	128.2	13.0	237221	1	AP003599 Nostoc sp
72	127.4	12.9	651	6	AX196012 Sequence
73	127.4	12.9	109519	6	AX195929 Sequence
74	126	12.7	923	6	AR236697 Sequence
75	125.4	12.7	835	6	AX660084 Sequence
76	123.2	12.5	300465	1	AE016962 Coxiiella
77	122.8	12.4	1810	6	E09625 Streptomyce
78	122.8	12.4	3267	1	STMACYA
79	118.6	12.0	201	11	BV202015 Continuation (4 of
80	118.6	12.0	89888	2	AY294423.3 Mus muscu
81	118.6	12.0	161371	10	AC132590 Rattus no
82	116.8	11.8	188267	2	AC137230 Rattus no
83	116.8	11.8	228354	2	AC137429 Rattus no
84	116.8	11.8	266834	2	AC123487 Rucalyptu
85	110	11.1	1013	8	AF168780 Rhodother
86	110	11.1	1944	1	AF145250 Eucalyptu
87	109.8	11.1	1006	8	AF046122 E. gunni nr
88	109.8	11.1	1068	8	EG122228 Continuation (4 of
89	109.6	11.1	110000	2	AC105718.3 Boehmeria
90	107.8	10.9	486	8	AY651026 Chromobac
91	107.4	10.9	304282	1	AE016910 Chromobac
92	106.2	10.7	976	8	VVCCOAMT Z542233 V.vinifera

c	93	103.6	10.5	343	6	AX400599	Sequence	166	84	8.5	1026	8	AY057554	AY057554 Arabidops
	94	102	10.3	134199	1	SYCSLRF	D64004 Synchocyst	167	84	8.5	110000	1	CR628336_25	Continuation (26 o
c	95	101.4	10.3	300425	1	AP005044	AP005044 Streptomy	168	83.6	8.5	1033	8	AY088577	Arabidops
c	96	99.4	10.1	300800	1	SC0939112	AL939112 Streptomy	169	83.2	8.4	110000	1	AP006618_26	Continuation (27 o
	97	98.4	9.9	772	6	FVAJ1447	AD001447 Fragaria	170	82.8	8.4	1258	6	ARI22016	Sequence
	98	96.8	9.8	1012	6	BD224370	BD224370 Materials	171	82.8	8.4	1258	6	I92681	Sequence 1
	99	96.8	9.8	1012	6	AR4312820	AR4312820 Sequence	172	82.8	8.4	1258	8	PUMCCOAMT	M69184 Petroselinu
	100	96.8	9.8	1012	6	AR4326420	AR4326420 Sequence	173	82.6	8.4	125020	9	AF429315	AF429315 Homo sapi
	101	96.8	9.8	1026	6	AR0666484	AR0666484 Sequence	174	82.2	8.3	105815	8	AY644636	AY644636 Oryza sat
	102	96.8	9.8	1026	6	AR074097	AR074097 Sequence	175	82.2	8.3	105815	8	AP002536	AP002536 Oryza sat
	103	96.8	9.8	1026	6	AR143609	AR143609 Sequence	176	82.2	8.3	156054	8	AB023482	AB023482 Oryza sat
	104	96.8	9.8	1026	6	BD224282	BD224282 Materials	177	81	8.2	622	8	AB076979	AB076979 Avena sat
	105	96.8	9.8	1026	6	AR216332	AR216332 Sequence	178	79.6	8.0	1258	6	A22706	A22706 Caffeoyl-Co
	106	96.8	9.8	1026	6	AR432734	AR432734 Sequence	179	79.2	8.0	980	6	AR236704	AR236704 Sequence
	107	96.8	9.8	1026	6	BD005645	BD005645 Materials	180	78	7.9	1098	8	AY128822	AY128822 Arabidops
	108	96.8	9.8	1172	8	AY279007	AY279007 Zea mays	181	78	7.9	1185	8	AY087981	AY087981 Arabidops
	109	96.4	9.7	1136	8	AY279011	AY279011 Zea mays	182	78	7.9	1201	8	AY093172	AY093172 Arabidops
	110	96.4	9.7	1145	8	AY279031	AY279031 Zea mays	183	77.4	7.8	837	8	AY094008	AY094008 Arabidops
	111	96.4	9.7	1150	8	AY279012	AY279012 Zea mays	184	77.4	7.8	1107	8	AY070483	AY070483 Arabidops
	112	96.4	9.7	1150	8	AY279013	AY279013 Zea mays	c	185	7.7	110000	1	AP006618_48	Continuation (49 o
	113	96.4	9.7	1150	8	AY279030	AY279030 Zea mays	186	76.2	7.7	760	6	AR074116	Continuation (49 o
	114	96.4	9.7	1150	8	AY279033	AY279033 Zea mays	187	76.2	7.7	760	6	AR074116	Sequence
	115	96.4	9.7	1150	8	AY279033	AY279033 Zea mays	188	76.2	7.7	760	6	BD224301	BD224301 Materials
	116	95.2	9.6	1172	8	AY279006	AY279006 Zea mays	189	76.2	7.7	760	6	BD272991	BD272991 Materials
	117	95.2	9.6	1172	8	AY279025	AY279025 Zea mays	190	76.2	7.7	760	6	AR216351	AR216351 Sequence
	118	95.2	9.6	1172	8	AY279027	AY279027 Zea mays	191	76.2	7.7	760	6	AR432753	AR432753 Sequence
	119	95.2	9.6	1180	6	AY798857	AY798857 Sequence	192	75.8	7.7	1046	8	BD005664	BD005664 Materials
	120	95.2	9.6	1182	8	AY279009	AY279009 Zea mays	193	74.8	7.6	816	8	PTU27116	U27116 Populus tre
	121	95.2	9.6	1438	8	AY279021	AY279021 Zea mays	194	74.4	7.5	929	6	AF022775	AF022775 Nicotiana
	122	95.2	9.6	1442	8	AY279019	AY279019 Zea mays	195	74.4	7.5	1104	8	AR236703	AR236703 Sequence
	123	95.2	9.6	1444	8	AY279017	AY279017 Zea mays	196	74.2	7.5	726	8	AF053553	AF053553 Mesembrya
	124	95.2	9.6	1445	8	AY279018	AY279018 Zea mays	197	73.8	7.5	920	4	AF240466	AF240466 Populus t
	125	95.2	9.6	1445	8	AY279022	AY279022 Zea mays	198	73.8	7.5	1834	8	AY340812	AY340812 Canis fam
	126	95.2	9.6	1451	8	AY279004	AY279004 Zea mays	c	199	7.5	2768	8	AK105550	AK105550 Oryza sat
	127	95.2	9.6	1451	8	AY279020	AY279020 Zea mays	c	200	7.5	170021	8	AK109619	AK109619 Oryza sat
	128	95.2	9.6	1463	8	AY279016	AY279016 Zea mays	c	201	7.5	176261	8	AP003256	AP003256 Oryza sat
	129	95.2	9.6	1464	8	AY279015	AY279015 Zea mays	c	202	7.5	145828	8	AP003274	AP003274 Oryza sat
	130	94.8	9.6	110000	1	BX571966_17	Continuation (18 o	c	203	7.4	154188	8	AP005392	AP005392 Oryza sat
	131	94.8	9.6	110000	1	CP000011_09	Continuation (10 o	c	204	7.4	870	6	AP005633	AP005633 Oryza sat
	132	94.8	9.6	110000	1	CP000011_10	Continuation (10 o	c	205	7.4	706	8	AR225246	AR225246 Sequence
	133	94.6	9.6	1152	8	AY279023	AY279023 Zea mays	c	206	7.4	706	8	PBA130841	PBA130841 Populus b
	134	94.6	9.6	1152	8	AY279032	AY279032 Zea mays	c	207	7.3	1213	9	BC011935	BC011935 Homo sapi
	135	93.6	9.5	110000	1	CR628337_25	Continuation (26 o	c	208	7.3	280558	1	AE017301	AE017301 Thersmus t
	136	93.4	9.4	675	6	AR390021	AR390021 Sequence	c	209	7.2	744	8	AF327458	AF327458 Populus a
	137	93	9.4	1136	8	AY279034	AY279034 Zea mays	c	210	7.2	2084	11	BV167609	BV167609 sqm6022
	138	93	9.4	1153	8	AY279010	AY279010 Zea mays	c	211	7.2	2084	11	BV177509	BV177509 sqm95100
	139	93	9.4	1181	6	AY798855	AY798855 Sequence	c	212	7.2	816	9	CR456997	CR456997 Homo sapi
	140	93	9.4	1181	8	AY279024	AY279024 Zea mays	c	213	7.2	1025	8	CR456997	CR456997 Homo sapi
	141	93	9.4	1181	8	AY279024	AY279024 Zea mays	c	214	7.2	1025	8	PBTJ4894	PBTJ4894 Populus b
	142	93	9.4	1181	8	AY279026	AY279026 Zea mays	c	215	7.2	1107	6	Q812330	Q812330 Sequence
	143	93	9.4	1206	8	AY279008	AY279008 Zea mays	c	216	7.2	1107	9	HUMCOMTA	HUMCOMTA M65212 Homo sapien
	144	93	9.4	1209	8	AY279028	AY279028 Zea mays	c	217	7.2	1291	6	Q0716680	Q0716680 Sequence
	145	93	9.4	1222	8	AY279029	AY279029 Zea mays	c	218	7.1	918	8	ZEU13151	ZEU13151 Zimnia eleg
	146	93	9.4	1232	8	AF036095	AF036095 Pinus tae	c	219	7.1	2084	11	BV177077	BV177077 sqm92606
	147	93	9.4	1434	8	AY279014	AY279014 Zea mays	c	220	7.1	189038	2	AC120323	AC120323 Rattus no
	148	88	8.9	931	6	AR236702	AR236702 Sequence	c	221	7.1	811	6	AR225247	AR225247 Sequence
	149	87.8	8.9	534	6	AR236717	AR236717 Sequence	c	222	7.1	5222	1	DRU52145	DRU52145 Deinococcus
	150	87.4	8.8	1210	8	AK063541	AK063541 Oryza sat	c	223	7.0	591	8	AY607699	AY607699 Apium gra
	151	87.2	8.8	2955	1	AF075724	AF075724 Legionell	c	224	7.0	6090	1	U30252	U30252 Synchococ
	152	87.2	8.8	110000	1	AP017354_25	Continuation (26 o	c	225	7.0	873	9	CR456422	CR456422 Homo sapi
	153	86.2	8.7	347660	1	AE002994	Continuation (26 o	c	226	7.0	1206	6	AX774876	AX774876 Sequence
	154	85.6	8.7	962	6	AR236705	AR236705 Mesorhizo	c	227	7.0	1206	6	HUMCOMTC	HUMCOMTC M58212 Homo sapien
	155	85.6	8.7	1023	6	AR236706	AR236706 Sequence	c	228	6.9	297850	1	AP006577	AP006577 Gloebact
	156	85.4	8.6	607	8	AY098515	AY098515 Ananas co	c	229	6.9	976	11	PM12D6G	PM12D6G Penicilli
	157	85.4	8.6	125020	9	AF429315	AF429315 Homo sapi	c	230	6.9	1217	9	BC000419	BC000419 Homo sapi
	158	84.4	8.5	939	8	PBTJ4896	AY224896 Populus b	c	231	6.9	1217	9	BC005867	BC005867 Mus muscu
	159	84.4	8.5	963	8	AY620245	AY620245 Ammi maju	c	232	6.8	239130	2	AC079420	AC079420 Mus muscu
	160	84.4	8.5	1049	8	PBTJ4895	AY224895 Populus b	c	233	6.8	890	8	AB000408	AB000408 Populus k
	161	84	8.5	780	6	Q804646	Q804646 Sequence	c	234	6.8	930	8	AB000408	AB000408 Populus k
	162	84	8.5	780	6	Q805684	Q805684 Sequence	c	235	6.8	12454	1	AE002019	AE002019 Deinococ
	163	84	8.5	780	6	AY143979	AY143979 Arabidops	c	236	6.8	13151	8	AC144491	AC144491 Oryza sat
	164	84	8.5	815	8	AY081457	AY081457 Arabidops	c	237	6.8	160738	8	AC073556	AC073556 Oryza sat
	165	84	8.5	999	8	AY062630	AY062630 Arabidops	c	238	6.8	323	8	AF534905	AF534905 Coffea ca
								c	239	6.8	110000	2	LMFLCHR32_06	Continuation (7 of



c 239	67	6.8	110000	2	LMFLCHR36_31	Continuation (32 o	312	62.4	6.3	219952	2	AC084804	AC084804 Mus muscu
240	67	6.8	175837	2	AC022045	AP001972 Homo sapi	313	62.4	6.3	341957	1	EX842572	EX842572 Mycobacte
241	67	6.8	215235	9	AP001972	AB0611268 Solanum t	314	62.4	6.3	343050	1	EX248334	EX248334 Porphyrom
242	66.8	6.8	1023	8	AB0611268	AB074145 Sequence	c 315	62.2	6.3	300029	1	AE017178	AE017178 Mycobacte
243	66.8	6.8	1074	6	AB074145	BD224330 Materials	316	62.2	6.3	301332	1	AE017237	AE017237 Sus scrofa
244	66.8	6.8	1074	6	BD224330	AR216380 Sequence	c 317	62	6.3	175963	2	AC148913	AC148913 Streptomy
245	66.8	6.8	1074	6	AR216380	BD005694 Materials	c 318	62	6.3	295150	1	SC0939126	AL939126 Streptomy
246	66.8	6.8	1074	6	AR432782	BD005693 Materials	c 319	61.8	6.2	186752	9	AC111200	AC111200 Homo sapi
247	66.8	6.8	1074	6	BD005693	AR074146 Sequence	c 320	61.6	6.2	281450	6	AP005032	AP005032 Streptomy
248	66.8	6.8	1075	6	AR074146	BD224331 Materials	c 321	61.6	6.2	845	6	AR225248	AR225248 Sequence
249	66.8	6.8	1075	6	BD224331	AR216381 Sequence	c 322	61.6	6.2	110000	1	AP006840_30	Continuation (31 o
250	66.8	6.8	1075	6	AR216381	AR432783 Sequence	c 323	61.6	6.2	276289	1	AE017306	AE017306 Thermus t
251	66.8	6.8	1075	6	AR432783	BD005694 Materials	c 324	61.4	6.2	146111	10	AC132340	AC132340 Mus muscu
252	66.8	6.8	1075	6	BD005694	AL939108 Streptomy	c 325	61.4	6.2	215342	4	AC149292	AC149292 Sus scrofa
253	66.8	6.8	339650	1	SC0939108	AF257324 Streptomy	c 326	61.2	6.2	302325	1	AE017236	AE017236 Mycobacte
c 254	66.6	6.7	13533	1	CF257324	Q0760958 Sequence	c 327	61	6.2	976	11	PM12D6G	AL684370 Penicilli
255	66.4	6.7	744	6	AX259371	AX259371 Sequence	c 328	61	6.2	110000	1	AP006618_49	Continuation (50 o
256	66.4	6.7	744	6	AX259371	U20736 Medicago sa	c 329	61	6.2	151085	8	AP003239	AP003239 Oryza sat
257	66.4	6.7	966	8	MSU20736	Q0760964 Sequence	c 330	61	6.2	292100	1	SC0939121	Streptomy
258	66.4	6.7	1906	6	Q0760964	AX36951 Leishmani	c 331	60.8	6.1	1578	6	A38265	Sequence 1
259	66.4	6.7	86000	2	AC136951	EX640432 Bordetell	c 332	60.8	6.1	2357	14	AY363172	AY363172 Pseudorab
c 260	66.4	6.7	346301	1	EX640432	EX640446 Bordetell	c 333	60.8	6.1	2510	14	SH1UL2XA	M95285 Suid herpes
c 261	66.4	6.7	348642	1	EX640446	AR236707 Sequence	c 334	60.8	6.1	9382	14	SH1ULGNS	L00676 Pseudorabie
c 262	66.2	6.7	912	6	AR236707	AP005041 Streptomy	c 335	60.8	6.1	110000	8	AE016818_02	Continuation (3 of
c 263	66	6.7	300425	1	AP005041	AL939112 Streptomy	c 336	60.6	6.1	917	8	AY087244	AY087244 Arabidops
c 264	66	6.7	300800	1	SC0939112	AY632768 Mycobacte	c 337	60.6	6.1	7413	1	PAAPR4PG	X64558 Pseudomonas
265	65.8	6.7	6375	1	AY632768	BV185588 sqm14856	c 338	60.6	6.1	11588	1	AE004554	AE004554 Pseudom
266	65.4	6.6	101	11	BV185588	Continuation (16 o	c 339	60.6	6.1	201050	1	AL646064	AL646064 Ralstonia
267	65.4	6.6	110000	1	AP006840_15	AY500159 Corthorus	c 340	60.6	6.1	298550	1	AP005029	AP005029 Streptomy
268	64.8	6.6	908	8	AY500159	AR25249 Sequence	c 341	60.6	6.1	301068	1	AE017231	AE017231 Mycobacte
269	64.8	6.6	967	6	AR25249	AL939110 Streptomy	c 342	60.6	6.1	1094	11	PM7G11B	AL685196 Penicilli
270	64.8	6.6	283100	1	SC0939110	AY452532 Chlamydom	c 343	60.4	6.1	10445	1	AB008466	AB008466 Streptomy
271	64.6	6.5	2832	8	AY452532	Continuation (8 of	c 344	60.4	6.1	25883	1	AB008466	AB008466 Streptomy
272	64.6	6.5	110000	2	LMFLCHR36_07	AL939122 Streptomy	c 345	60.4	6.1	136753	2	AC149968	AC149968 Strongylo
273	64.6	6.5	311000	1	SC0939122	BD035032 Sequence	c 346	60.4	6.1	349980	6	AX492784	AX492784 Sequence
274	64.4	6.5	143	6	AX899499	BD035032 Sequence	c 347	60.4	6.1	349980	6	AX492784	AX533951 Sequence
275	64.4	6.5	143	6	BD035032	AX640439 Bordetell	c 348	60.2	6.1	1007	11	PM3H11G	AL685749 Penicilli
276	64.4	6.5	600	6	AR236713	EX640439 Bordetell	c 349	60.2	6.1	1062	6	BD180422	BD180422 Highly th
277	64.2	6.5	346362	1	EX640439	EX640439 Bordetell	c 350	60.2	6.1	1007	11	PM3H11G	AY162971 Micromono
c 278	64.2	6.5	346362	1	EX640439	AK058441 Oryza sat	c 351	60.2	6.1	3797	14	PVULSGENE	AY162971 Micromono
c 279	64	6.5	346362	1	EX640439	AK058441 Oryza sat	c 352	60.2	6.1	6653	1	AY162971	AC098271 Rattus no
280	64	6.5	954	8	AK058441	AC074054 Oryza sat	c 353	60.2	6.1	211161	2	AC098271	AC098271 Rattus no
c 281	64	6.5	1543	8	AK058441	AC113337 Genomic s	c 354	60	6.1	729	6	AX507705	AX507705 Sequence
c 282	64	6.5	85130	2	AC074054	AC148515 Sus scrofa	c 355	60	6.1	730	8	AY056313	AY056313 Arabidops
c 283	64	6.5	135876	8	AC113337	AC148515 Sus scrofa	c 356	60	6.1	956	8	AF360317	AF360317 Arabidops
c 284	64	6.5	145510	8	AC148515	AE017240 Mycobacte	c 357	60	6.1	982	6	AR236709	AR236709 Sequence
c 285	64	6.5	172407	2	AC148515	AE017240 Mycobacte	c 358	60	6.1	1065	11	PM2B12B	AL684695 Penicilli
c 286	64	6.5	299886	1	AE017240	AE017082 Oryza sat	c 359	60	6.1	1227	8	NT282982	Z82982 Nicotiana ta
c 287	63.8	6.5	306096	8	AE017082	AE001956 Deinococc	c 360	60	6.1	1279	11	PM2H12G	AL684840 Penicilli
288	63.6	6.4	510	6	AR236698	AL684840 Penicilli	c 361	60	6.1	123019	9	AC111006	AC111006 Homo sapi
289	63.6	6.4	12541	1	AE001956	AK130031 Homo sapi	c 362	60	6.1	277000	1	SC0939109	AL939109 Streptomy
c 290	63.6	6.4	1279	11	PM2H12G	Z56282 N.tabacum m	c 363	59.8	6.0	1242	6	BD180349	BD180349 Highly th
c 291	63.4	6.4	2039	9	AK130031	Continuation (32 o	c 364	59.6	6.0	399	6	BD224470	BD224470 Materiale
c 292	63.4	6.4	296300	1	AP005035	Continuation (33 o	c 365	59.6	6.0	399	6	AR216520	AR216520 Sequence
c 293	63.2	6.4	1016	8	NTCCOAMT	AL684695 Penicilli	c 366	59.6	6.0	956	11	PM2D12B	AL684743 Penicilli
c 294	63.2	6.4	1065	11	PM2B12B	Continuation (32 o	c 367	59.6	6.0	1980	14	AC2NK24	M18041 Avian trans
c 295	63.2	6.4	110000	1	AP006618_31	Continuation (32 o	c 368	59.6	6.0	2253	5	CHFCPOSA	M37000 Chicken c-f
c 296	63.2	6.4	110000	1	AP006618_32	Continuation (33 o	c 369	59.6	6.0	2253	5	CHFCPOSA	Y00659 Chicken fos
c 297	63.2	6.4	136753	2	AC149968	CR628364 Danio rer	c 370	59.6	6.0	7185	6	AX803764	AX803764 Sequence
c 298	63.2	6.4	176704	2	CR628364	AP005037 Streptomy	c 371	59.6	6.0	48177	7	AY369485	AY369485 Burkholde
c 299	63.2	6.4	299425	1	AP005037	AE017231 Mycobacte	c 372	59.6	6.0	61944	6	AX803750	AX803750 Sequence
c 300	63.2	6.4	301068	1	AE017231	EX640419 Bordetell	c 373	59.6	6.0	110000	1	AE016822_23	Continuation (24 o
c 301	63	6.4	349672	1	AX8460F19	AL035460 Human DNA	c 374	59.6	6.0	110000	1	AE016822_24	Continuation (25 o
c 302	62.8	6.3	135005	9	HS860F19	M06647 Rat tropel	c 375	59.6	6.0	110000	1	AP006618_55	Continuation (56 o
c 303	62.8	6.3	2595	10	RATREBA	AX704275 Sequence	c 376	59.6	6.0	283100	1	SC0939110	AL939110 Streptomy
c 304	62.8	6.3	75216	6	AX704275	Continuation (14 o	c 377	59.6	6.0	295150	1	SC0939125	AL939125 Streptomy
c 305	62.8	6.3	110000	1	AE000516_13	Continuation (14 o	c 378	59.6	6.0	308015	1	AE016783	AE016783 Pseudom
c 306	62.8	6.3	299450	1	EX248338	EX248338 Mycobacte	c 379	59.4	6.0	110000	1	AP006618_09	Continuation (10 o
c 307	62.6	6.3	349306	1	EX248338	EX248338 Mycobacte	c 380	59.4	6.0	110000	1	AP006618_10	Continuation (11 o
c 308	62.6	6.3	1014	8	NTU62734	U62734 Nicotiana t	c 381	59.4	6.0	116305	8	AP003992	AP003992 Oryza sat
c 309	62.6	6.3	216050	1	AL646076	AL646076 Ralstonia	c 382	59.4	6.0	141477	8	AP005456	AP005456 Oryza sat
c 310	62.6	6.3	348257	1	EX640425	Continuation (3 of	c 383	59.4	6.0	170051	2	AC148233	AC148233 Oryctolag
c 311	62.4	6.3	110000	1	AP000516_02	Continuation (53 o	c 384	59.4	6.0	189910	2	AC148233	

385	59.4	6.0	196834	8	AP005458	Oryza sat	458	57.4	5.8	1298	8	AY323261	Zea mays
386	59.4	6.0	197050	1	AL646081	Ralstonia	459	57.4	5.8	1298	8	AY323263	Zea mays
c 387	59.4	6.0	296500	1	SC0939128	Streptomy	460	57.4	5.8	1298	8	AY323265	Zea mays
388	59.2	6.0	1791	6	BD179866	Highly th	461	57.4	5.8	1311	8	AY323252	Zea mays
389	59.2	6.0	196950	2	CR589874	Danio rer	462	57.4	5.8	1311	8	AY323257	Zea mays
390	59.2	6.0	273285	1	AE017304	Thermus t	463	57.4	5.8	1311	8	AY323264	Zea mays
391	59.2	6.0	298450	1	SC0939107	Streptomy	464	57.4	5.8	1536	8	AY323241	Zea mays
392	59	6.0	2531	8	AY341851	Oryza sat	465	57.4	5.8	1536	8	AY323243	Zea mays
393	59	6.0	3152	8	AY341843	Oryza sat	466	57.4	5.8	1536	8	AY323245	Zea mays
394	59	6.0	10800	6	AX512249	Sequence	467	57.4	5.8	1536	8	AY323247	Zea mays
395	59	6.0	10809	6	AX512245	Sequence	468	57.4	5.8	1536	8	AY323248	Zea mays
396	59	6.0	110000	2	LMFLCHR36_03	Continuation (4 of	469	57.4	5.8	1536	8	AY323250	Zea mays
c 397	59	6.0	139298	8	OSJN00012	Continuation (4 of	470	57.4	5.8	1537	8	AY323242	Zea mays
398	59	6.0	277000	1	SC0939109	Streptomy	471	57.4	5.8	1537	8	AY323251	Zea mays
399	58.8	5.9	1393	11	PM11H12G	AL684264	472	57.4	5.8	1549	8	AY323249	Zea mays
c 400	58.8	5.9	2320	8	AK069799	Oryza sat	473	57.4	5.8	1597	1	AF306513	Pseudomon
c 401	58.8	5.9	2793	8	AK067140	Oryza sat	474	57.4	5.8	23451	1	AB070952	Streptomy
402	58.8	5.9	3849	6	AX058889	Sequence	475	57.4	5.8	66637	3	AC090053	Leishmani
403	58.8	5.9	5958	3	AF350276	Nephila m	c 476	57.4	5.8	131563	9	HS212310	BS322561
404	58.8	5.9	12744	1	AF204401	Streptomy	c 477	57.4	5.8	195859	14	AF281817	Homo sapi
405	58.8	5.9	187517	5	AY519500	Gallus ga	c 478	57.4	5.8	223201	9	HS531110	Tupaia he
c 406	58.8	5.9	247910	1	AE017307	Thermus t	c 479	57.4	5.8	276289	1	AE017306	Homo sapi
c 407	58.8	5.9	299800	1	AP005040	Streptomy	c 480	57.4	5.8	302300	1	AP005034	Streptomy
c 408	58.8	5.9	311000	1	SC0939122	Streptomy	c 481	57.4	5.8	310550	1	SC0939113	Streptomy
c 409	58.8	5.9	48024	7	AY368235	Burkholde	c 482	57.4	5.8	340000	9	HS21C102	Homo sapi
410	58.6	5.9	110000	1	AP006840_11	Continuation (12 o	c 483	57.2	5.8	584	6	AX660579	Sequence
c 411	58.6	5.9	274676	1	AE017305	Thermus t	c 484	57.2	5.8	987	6	BD180315	Highly th
c 412	58.6	5.9	289308	1	AE017242	Mycobacte	485	57.2	5.8	1143	11	PM12A11G	Penicilli
c 413	58.6	5.9	293050	1	SC0939116	Streptomy	486	57.2	5.8	1506	10	MUSHSP63A	Mouse heat
c 414	58.6	5.9	299925	1	AP005045	Streptomy	487	57.2	5.8	73882	6	CQ870950	Sequence
415	58.6	5.9	300327	1	AE017228	Mycobacte	488	57.2	5.8	89713	1	AF605139	Actinopa
416	58.4	5.9	1288	6	AE007563	Sequence	c 489	57.2	5.8	110000	1	AP006840_06	Continuation (7 of
c 417	58.4	5.9	3858	5	CHKCFOS	M18043	c 490	57.2	5.8	110000	1	AP006840_07	Continuation (8 of
c 418	58.4	5.9	7413	14	PVUL50S	X87246	c 491	57.2	5.8	110000	2	LMFLCHR28_1	Continuation (2 of
419	58.4	5.9	127304	2	AC119051	Suid herpes	c 492	57.2	5.8	272101	1	AE017302	Thermus t
c 420	58.4	5.9	309050	1	SC0939117	Streptomy	493	57	5.8	10136	1	AF546156	Micromono
c 421	58.2	5.9	1970	5	GGY17794	Y17794	494	57	5.8	11133	6	CQ879023	Sequence
422	58.2	5.9	4237	8	D84400	Oryza sativ	495	57	5.8	11219	1	SERERYAA	Saccharopol
423	58.2	5.9	89376	1	AJ632270	Actinopia	496	57	5.8	11219	6	AR049367	Sequence
424	58.2	5.9	91839	2	AC098688	Bos tauru	497	57	5.8	11219	6	AR095528	Sequence
c 425	58.2	5.9	197805	2	AC105307	Bos tauru	498	57	5.8	36602	6	CQ878999	Sequence
426	58.2	5.9	295150	1	SC0939125	Streptomy	c 499	57	5.8	38494	6	AR345349	Sequence
427	58.2	5.9	299925	1	AP005039	Streptomy	c 500	57	5.8	38503	1	MSGB1912CS	Sequence
428	58	5.9	897	6	AX654732	Sequence	c 501	57	5.8	38675	1	MLU15180	Mycobacteri
429	58	5.9	2329	1	SGHRDT	X79979	c 502	57	5.8	38675	6	AR345367	Sequence
430	58	5.9	2396	1	AF425994	Streptomy	c 503	57	5.8	281450	1	AP005032	Streptomy
431	58	5.9	10444	14	PVI422133	AF422133	c 504	57	5.8	348450	1	MLEPRTN4	Mycobacte
c 432	58	5.9	88421	6	AX417445	Sequence	505	56.8	5.7	990	6	BD179631	Nicotiana t
c 433	58	5.9	110000	1	AP006840_20	Continuation (21 o	506	56.8	5.7	1003	8	NTU62735	Sequence
434	58	5.9	186752	9	AC111200	Homo sapi	507	56.8	5.7	1182	6	AR151710	Sequence
435	58	5.9	290850	1	SC0939127	Streptomy	508	56.8	5.7	1182	6	AR352531	Sequence
c 436	58	5.9	308050	1	SC0939124	Streptomy	509	56.8	5.7	1306	8	AY323238	Zea mays
437	57.8	5.8	9678	1	AB110645	Streptomy	510	56.8	5.7	1306	8	AY323240	Zea mays
438	57.8	5.8	110000	1	AP006618_38	Continuation (39 o	511	56.8	5.7	1306	8	AY323262	Zea mays
439	57.8	5.8	110000	1	AP006618_39	Continuation (40 o	512	56.8	5.7	1306	8	AY323270	Zea mays
c 440	57.8	5.8	110000	1	AP006840_27	Continuation (28 o	513	56.8	5.7	1308	8	AY323269	Zea mays
441	57.8	5.8	245210	2	AC137771	Homo sapi	514	56.8	5.7	1309	8	AY323239	Zea mays
c 442	57.8	5.8	299550	1	AP005031	Streptomy	515	56.8	5.7	1309	8	AY323256	Zea mays
c 443	57.8	5.8	347894	1	BX640431	Bordetelli	516	56.8	5.7	1309	8	AY323266	Zea mays
444	57.6	5.8	2358	8	AJ635325	Spermatoz	517	56.8	5.7	1311	8	AY323267	Zea mays
445	57.6	5.8	3297	6	BD180129	Highly th	518	56.8	5.7	1314	8	AY323253	Zea mays
c 446	57.6	5.8	106873	14	AB096160	Cercopith	519	56.8	5.7	1314	8	AY323268	Zea mays
447	57.6	5.8	110000	1	AP006618_19	Continuation (20 o	520	56.8	5.7	1320	8	AY323271	Zea mays
c 448	57.6	5.8	156789	14	AF533768	Cercopith	521	56.8	5.7	1544	8	AY323246	Zea mays
449	57.6	5.8	166036	2	AC145332	Felis cat	522	56.8	5.7	2000	6	AX655393	Zea mays
c 450	57.6	5.8	299050	1	SC0939119	Streptomy	523	56.8	5.7	2000	6	AX655393	Sequence
451	57.6	5.8	321250	1	SC0939111	Streptomy	524	56.8	5.7	3900	1	AF262754	Amocolato
452	57.4	5.8	1029	6	BD174410	DNA resto	c 525	56.8	5.7	5269	1	AB001610	Deinococc
453	57.4	5.8	1298	8	AY323254	Zea mays	526	56.8	5.7	6584	1	SCPACAS	Streptomyes
454	57.4	5.8	1298	8	AY323255	Zea mays	527	56.8	5.7	11604	6	AR151704	Sequence
455	57.4	5.8	1298	8	AY323258	Zea mays	528	56.8	5.7	11604	6	AR352525	Sequence
456	57.4	5.8	1298	8	AY323259	Zea mays	529	56.8	5.7	15079	6	AR151702	Sequence
457	57.4	5.8	1298	8	AY323260	Zea mays	530	56.8	5.7	15120	1	SCU87786	Streptomyce

531	56.8	5.7	15120	6	AR352523	Sequence	604	5.7	2109	6	AX321622	Sequence
C 532	56.8	5.7	22976	6	AR410057	Sequence	605	5.7	2142	6	BD157246	Primer fo
C 533	56.8	5.7	22976	6	AX000035	Sequence	606	5.7	2142	6	AX878471	Sequence
C 534	56.8	5.7	22976	6	AX969142	Sequence	607	5.7	2142	9	AK021532	Homo sapi
C 535	56.8	5.7	22976	6	BD062419	LSR recep	608	5.7	2198	6	BD156336	Primer fo
536	56.8	5.7	29870	6	AX763606	Sequence	609	5.7	2198	6	AX876825	Sequence
537	56.8	5.7	36401	1	AX263398	Sequence	610	5.7	2198	9	AK001474	Homo sapi
C 538	56.8	5.7	41936	6	AX335752	Sequence	611	5.7	2347	9	BC009372	Homo sapi
C 539	56.8	5.7	41936	9	CH19R30879	Sequence	612	5.7	2360	9	BC043619	Homo sapi
C 540	56.8	5.7	55972	1	AF386507	Streptomy	613	5.7	2392	6	AX003881	Sequence
541	56.8	5.7	65351	2	AC139773	Homo sapi	614	5.7	2392	9	BD086467	DNA demet
C 542	56.8	5.7	102230	8	AP004045	Oryza sat	615	5.7	2392	9	AF072247	Homo sapi
543	56.8	5.7	110000	1	AP006840_04	Continuation (5 of	616	5.7	2885	9	HUMHBA3	Homo sapien
544	56.8	5.7	110000	1	AP006840_10	Continuation (11 of	617	5.7	4257	6	ARI44708	Sequence
545	56.8	5.7	110000	1	AP006840_34	Continuation (35 of	618	5.7	4257	6	ARI45616	Sequence
546	56.8	5.7	138289	2	AP0044873	AP046073 Oryza sat	619	5.7	4257	6	AR526866	Sequence
C 547	56.8	5.7	188050	1	AL646072	Ralstonia	620	5.7	4943	6	BD188749	Novel tyr
548	56.8	5.7	299925	1	AP005048	Streptomy	621	5.7	4943	9	AB067470	Homo sapi
C 549	56.8	5.7	300800	1	AP005036	Streptomy	622	5.7	4988	6	AX766352	Sequence
C 550	56.8	5.7	303550	1	SC0339131	Streptomy	623	5.7	6633	14	HEHSVIG3	Herpes simp
551	56.8	5.7	313800	1	SC0339114	Streptomy	624	5.7	12001	6	AR048721	Sequence
552	56.6	5.7	976	8	AK073885	Oryza sat	625	5.7	12561	1	AE004557	Pseudomon
553	56.6	5.7	2450	6	AX654813	Sequence	626	5.7	15559	1	AF074603	Streptomy
554	56.6	5.7	25085	6	AX598627	Sequence	627	5.7	26245	14	HSIUS	Human herpe
555	56.6	5.7	50543	6	AX598617	Sequence	628	5.7	26245	14	HSIUS	Human herpe
556	56.6	5.7	92392	8	AC128647	Oryza sat	629	5.7	32668	1	SPU575934	Micromono
557	56.6	5.7	110000	1	AP006618_51	Continuation (52 of	630	5.7	33676	1	SCARDIGN	Saccharothr
C 558	56.6	5.7	110000	1	AP006840_08	Continuation (9 of	631	5.7	38146	1	AY524043	Micromono
559	56.6	5.7	110000	1	AP006840_17	Continuation (18 of	632	5.7	43058	6	AX332810	Sequence
C 560	56.6	5.7	110000	1	AP006840_19	Continuation (20 of	633	5.7	43058	6	AX333047	Sequence
C 561	56.6	5.7	110000	2	BX284653_2	Continuation (3 of	634	5.7	43058	6	AX411306	Sequence
C 562	56.6	5.7	110000	8	AC145127_06	Continuation (7 of	635	5.7	43058	9	HSGGI	Human DNA s
563	56.6	5.7	114184	8	AP003984	Oryza sat	636	5.7	107955	2	AP005551	Oryza sat
C 564	56.6	5.7	150336	9	HSJ395C13	Human DNA	637	5.7	110000	2	LMFLCHR36_13	Continuation (14 o
C 565	56.6	5.7	154082	8	AC108756	Oryza sat	638	5.7	121849	8	AC092779	Oryza sat
C 566	56.6	5.7	189349	8	AC068654	Genomic S	639	5.7	150155	8	AC092777	Oryza sat
567	56.6	5.7	216050	1	AL646076	Ralstonia	640	5.7	152261	14	HEICG	Human herpe
C 568	56.6	5.7	245210	2	AC137771	Homo sapi	641	5.7	152261	14	HEICG	Human herpe
C 569	56.6	5.7	304564	8	AE017049	Oryza sat	642	5.7	170020	8	AC138001	Oryza sat
570	56.4	5.7	1013	8	SLASADRN	Stellaria l	643	5.7	172238	8	AC145381	Oryza sat
571	56.4	5.7	1230	8	AK105901	Oryza sat	644	5.7	190076	9	AC008403	Homo sapi
572	56.4	5.7	1392	6	BD180195	Highly th	645	5.7	258002	9	AE006462	Homo sapi
573	56.4	5.7	3957	6	A45258	Sequence 2	646	5.7	276800	1	SC0939115	Streptomy
574	56.4	5.7	9450	1	AF190463	Comanonas	647	5.7	299925	1	AP005043	Streptomy
575	56.4	5.7	15738	6	AX803762	Sequence	648	5.7	300100	1	SC0939123	Streptomy
576	56.4	5.7	110000	1	AP006618_16	Continuation (17 of	649	5.7	302898	1	AE017238	Mycobacte
C 577	56.4	5.7	150715	14	AY714813	Cercopith	650	5.6	890	8	NTU38612	Nicotiana t
578	56.4	5.7	154746	14	HSV2HG52	Herpes simp	651	5.6	1150	14	HSUALIR3	epstein-bar
C 579	56.4	5.7	154746	14	HSV2HG52	Herpes simp	652	5.6	1152	6	AX653506	Sequence
580	56.4	5.7	172368	2	CR450819	Danio rer	653	5.6	1393	11	PM11H12G	Penicilli
581	56.4	5.7	187829	2	AC025388	Homo sapi	654	5.6	1427	8	AK109606	Oryza sat
582	56.4	5.7	289308	1	AE017242	Mycobacte	655	5.6	1926	6	AR217866	Sequence
C 583	56.4	5.7	348866	1	BE640426	Bordetell	656	5.6	1926	6	AR254714	Sequence
584	56.2	5.7	1143	6	AX574142	Sequence	657	5.6	1926	6	AK107940	Sequence
585	56.2	5.7	2793	6	AR009990	Sequence	658	5.6	2860	6	AR108994	Sequence
586	56.2	5.7	2793	6	195876	Sequence 1	659	5.6	2860	10	MMU08210	Mus musculu
587	56.2	5.7	3060	3	AF027735	Nephila c	660	5.6	2810	1	STWTCR3	Streptomyce
588	56.2	5.7	13513	1	AY423269	Streptomy	661	5.6	3281	3	LMA243459	Legishmani
589	56.2	5.7	14186	6	AX204987	Sequence	662	5.6	3643	10	BC051649	Mus muscu
590	56.2	5.7	48221	6	AX574200	Sequence	663	5.6	5452	6	AR083151	Sequence
C 591	56.2	5.7	58996	1	AB034704	Rubriviva	664	5.6	5452	12	U02454	Cloning vec
592	56.2	5.7	110000	1	AP006618_14	Continuation (15 of	665	5.6	8705	6	BD225380	Targeting
593	56.2	5.7	226251	10	AL833803	Mouse DNA	666	5.6	8705	6	BD225380	Targeting
594	56.2	5.7	300425	1	SC095038	Streptomy	667	5.6	9482	6	AR349578	Sequence
C 595	56.2	5.7	339650	1	SC0939108	Streptomy	668	5.6	9551	6	CQ829527	Sequence
C 596	56.2	5.7	343243	1	BE640414	Bordetell	669	5.6	9551	6	AR076233	Sequence
C 597	56.2	5.7	349260	1	BX572595	Rhodosphe	670	5.6	9551	9	HUMTRHYAL	Human trich
598	56	5.7	1104	5	AF364329	Coturnix	671	5.6	9600	6	AR2665	Sequence 1
599	56	5.7	1302	8	AK070743	Oryza sat	672	5.6	9600	6	AR158345	Sequence
600	56	5.7	2043	9	BC032443	Homo sapi	673	5.6	9600	6	AR241207	Sequence
601	56	5.7	2109	6	BD237101	Compounds	674	5.6	10285	6	AX551315	Sequence
602	56	5.7	2109	6	AR225501	Sequence	675	5.6	10285	6	AX552015	Sequence
603	56	5.7	2109	6	AR562924	Sequence	676	5.6	10330	6	CQ789661	Sequence

C 677	55.8	5.6	10477	6	CQ789659	Sequence	750	55.2	5.6	66669	1	AME16952	Y16952 Amycolatops
C 678	55.8	5.6	10516	6	CQ789657	Sequence	751	55.2	5.6	85163	1	AY048670	AY048670 Streptomy
C 679	55.8	5.6	10561	6	CQ789655	Sequence	752	55.2	5.6	95209	2	AP004323	AP004323 Oryza sat
C 680	55.8	5.6	10596	6	I25041	Sequence 15	C 753	55.2	5.6	110000	1	AP006618	Continuation (54 o
C 681	55.8	5.6	10596	6	I30503	Sequence 15	C 754	55.2	5.6	110000	1	AP006840	Continuation (18 o
C 682	55.8	5.6	10615	6	CQ789682	Sequence	C 755	55.2	5.6	110000	1	EX571966	Continuation (7 of
C 683	55.8	5.6	10737	12	XXU02428	U02428 Cloning vec	C 756	55.2	5.6	110000	2	LMFLCHR16_02	Continuation (3 of
C 684	55.8	5.6	10774	6	CQ789660	Sequence	C 757	55.2	5.6	110000	2	LMFLCHR16_03	Continuation (4 of
C 685	55.8	5.6	10850	12	U02455	U02455 Cloning vec	C 758	55.2	5.6	110000	8	AE016815	Continuation (5 of
C 686	55.8	5.6	10921	6	CQ789658	Sequence	C 759	55.2	5.6	137860	10	AC122407	AC122407 Mus muscu
C 687	55.8	5.6	10961	6	CQ789656	Sequence	C 760	55.2	5.6	145796	8	AC130598	AC130598 Oryza sat
C 688	55.8	5.6	11006	6	CQ789654	Sequence	C 761	55.2	5.6	146408	8	AC130610	AC130610 Oryza sat
C 689	55.8	5.6	11059	6	CQ789683	Sequence	C 762	55.2	5.6	154728	9	AC018730	AC018730 Homo sapi
C 690	55.8	5.6	13750	1	AY260903	AY260903 Rhodospir	C 763	55.2	5.6	187956	8	AC135425	AC135425 Oryza sat
C 691	55.8	5.6	16080	6	AR404205	Sequence	C 764	55.2	5.6	299300	1	AP005026	AP005026 Streptomy
C 692	55.8	5.6	17753	6	CQ790449	Sequence	C 765	55.2	5.6	348257	1	EX640425	EX640425 Bordetell
C 693	55.8	5.6	22960	12	AY192024	AY192024 BAC cloni	C 766	55.2	5.6	349497	1	EX640440	EX640440 Bordetell
C 694	55.8	5.6	115245	8	AP005682	AP005682 Oryza sat	C 767	55	5.6	2205	9	BC009438	BC009438 Homo sapi
C 695	55.8	5.6	128525	8	AP003118	AP003118 Oryza sat	C 768	55	5.6	2490	8	AK100050	AK100050 Oryza sat
C 696	55.8	5.6	132733	8	CNS08CA4	AL772426 Oryza sat	C 769	55	5.6	2559	6	AR488839	AR488839 Sequence
C 697	55.8	5.6	135793	8	CNS08CA5	AL772427 Oryza sat	C 770	55	5.6	2562	6	CQ720385	CQ720385 Sequence
C 698	55.8	5.6	141983	8	AP003047	AP003047 Oryza sat	C 771	55	5.6	28890	1	AF512431	AF512431 Saccharot
C 699	55.8	5.6	151578	9	AL589986	AL589986 Human DNA	C 772	55	5.6	30943	6	CQ801140	CQ801140 Sequence
C 700	55.8	5.6	171823	14	HHV507799	AJ507799 Human her	C 773	55	5.6	53784	1	AMM223012	AJ223012 Amycolato
C 701	55.8	5.6	172281	14	EBV	VO1555 Epstein-Bar	C 774	55	5.6	53789	6	A69720	A69720 Sequence 3
C 702	55.8	5.6	184113	14	HS4B958RAJ	M80517 Epstein-Bar	C 775	55	5.6	66280	1	AF195122	AF195122 Rhodobact
C 703	55.8	5.6	196950	2	CR589874	CR589874 Danio rer	C 776	55	5.6	103576	8	YUP8H12	AC000098 Arabidops
C 704	55.8	5.6	232605	1	AE017222	AE017222 Thermus t	C 777	55	5.6	109528	1	AF040570	AF040570 Amycolato
C 705	55.8	5.6	251872	2	AE0125998	AE012598 Rattus no	C 778	55	5.6	110000	1	AP006618	Continuation (9 of
C 706	55.8	5.6	270418	1	AE017303	AE017303 Thermus t	C 779	55	5.6	110000	2	EX255276	Continuation (16 o
C 707	55.8	5.6	280558	1	AE017301	AE017301 Thermus t	C 780	55	5.6	188050	1	AL646072	AL646072 Ralstonia
C 708	55.8	5.6	313800	1	SC0939114	AL939114 Streptomy	C 781	55	5.6	292200	1	SC0939129	AL939129 Streptomy
C 709	55.6	5.6	726	6	BD145399	BD145399 Primer fo	C 782	55	5.6	295150	1	SC0939126	AL939126 Streptomy
C 710	55.6	5.6	726	6	AX865337	AX865337 Sequence	C 783	54.8	5.5	594	6	BD224381	BD224381 Materials
C 711	55.6	5.6	74542	1	EX571965	Continuation (41 o	C 784	54.8	5.5	594	6	AR216431	AR216431 Sequence
C 712	55.6	5.6	110000	1	AP006618	Continuation (44 o	C 785	54.8	5.5	594	6	AR432833	AR432833 Sequence
C 713	55.6	5.6	110000	1	AP006840	Continuation (34 o	C 786	54.8	5.5	607	6	AR074114	AR074114 Sequence
C 714	55.6	5.6	110000	1	AP006840	Continuation (35 o	C 787	54.8	5.5	607	6	BD224299	BD224299 Materials
C 715	55.6	5.6	110000	1	CP00010_30	Continuation (31 o	C 788	54.8	5.5	607	6	BD273001	BD273001 Materials
C 716	55.6	5.6	110000	8	AE016819	Continuation (6 of	C 789	54.8	5.5	607	6	AR216349	AR216349 Sequence
C 717	55.6	5.6	150200	8	AP004459	AP004459 Oryza sat	C 790	54.8	5.5	607	6	AR432751	AR432751 Sequence
C 718	55.6	5.6	155069	8	AP004396	AP004396 Oryza sat	C 791	54.8	5.5	607	6	BD005662	BD005662 Materials
C 719	55.6	5.6	301443	1	AE017239	AE017239 Mycobacte	C 792	54.8	5.5	1795	1	AF118856	AF118856 Streptomy
C 720	55.4	5.6	657	12	AY657485	AY657485 Synthetic	C 793	54.8	5.5	2142	1	CCU42203	U42203 Caulobacter
C 721	55.4	5.6	1251	6	BD180575	BD180575 Highly th	C 794	54.8	5.5	2365	8	AK102809	AK102809 Oryza sat
C 722	55.4	5.6	1726	8	AK064395	AK064395 Oryza sat	C 795	54.8	5.5	2783	1	STMENBT	D13170 Streptomyce
C 723	55.4	5.6	3033	6	AR534432	AR534432 Sequence	C 796	54.8	5.5	2030	8	VCA429230	AJ429230 Volvox ca
C 724	55.4	5.6	3033	6	AX573728	AX573728 Sequence	C 797	54.8	5.5	5500	8	AEGLYRP	AE005785 A.thaliana
C 725	55.4	5.6	11873	1	AE004710	AE004710 Pseudomon	C 798	54.8	5.5	10894	1	AE005785	AE005785 Caulobact
C 726	55.4	5.6	95209	2	AP004323	AP004323 Oryza sat	C 799	54.8	5.5	12528	1	AE005826	AE005826 Caulobact
C 727	55.4	5.6	110000	1	AP006618	Continuation (58 o	C 800	54.8	5.5	58638	7	AY576796	AY576796 Actinopla
C 728	55.4	5.6	110000	1	AP006840	Continuation (15 o	C 801	54.8	5.5	93620	8	AB026636	AB026636 Arabidops
C 729	55.4	5.6	110000	1	AP006840	Continuation (27 o	C 802	54.8	5.5	110000	2	EX255276	Continuation (8 of
C 730	55.4	5.6	128136	1	AF440524	AF440524 Pseudomon	C 803	54.8	5.5	156789	14	AF533768	AF533768 Cercopith
C 731	55.4	5.6	133534	10	AF440524	AF440524 Pseudomon	C 804	54.8	5.5	166182	10	AC084391	AC084391 Mus muscu
C 732	55.4	5.6	158230	1	AF440523	AF440523 Pseudomon	C 805	54.8	5.5	218310	10	AC034265	AC034265 Mus muscu
C 733	55.4	5.6	172081	10	AC137124	AC137124 Mus muscu	C 806	54.8	5.5	231001	2	AC130981	AC130981 Rattus no
C 734	55.4	5.6	197050	1	AL646081	AL646081 Ralstonia	C 807	54.8	5.5	258319	2	AC127770	AC127770 Rattus no
C 735	55.4	5.6	299050	1	SC0939119	AL939119 Streptomy	C 808	54.8	5.5	292100	1	SC0939121	AL939121 Streptomy
C 736	55.4	5.6	299800	1	AP005028	AP005028 Streptomy	C 809	54.6	5.5	955	8	NTU62736	U62736 Nicotiana t
C 737	55.4	5.6	314100	1	SC0939106	AL939106 Streptomy	C 810	54.6	5.5	980	6	AX652989	AX652989 Sequence
C 738	55.2	5.6	986	8	AF377753	AF377753 Zea mays	C 811	54.6	5.5	1261	8	AK112011	AK112011 Oryza sat
C 739	55.2	5.6	1182	8	AK105138	AK105138 Oryza sat	C 812	54.6	5.5	1308	6	BD217906	BD217906 Gene fami
C 740	55.2	5.6	1324	8	OSLIIP19	XS7325 Rice lip19	C 813	54.6	5.5	2830	3	AF027972	AF027972 Nephila c
C 741	55.2	5.6	1344	8	AK061844	AK061844 Oryza sat	C 814	54.6	5.5	3866	1	D31792	D31792 Streptomyce
C 742	55.2	5.6	1375	8	AK065180	AK065180 Oryza sat	C 815	54.6	5.5	4761	1	SCO244019	SCO244019 Streptomy
C 743	55.2	5.6	1679	9	AB001835	AB001835 Homo sapi	C 816	54.6	5.5	4761	3	AC084329	AC084329 Leishmani
C 744	55.2	5.6	2208	1	STMLRWMT	M74717 Streptomyce	C 817	54.6	5.5	5520	3	AC084329	AC084329 Leishmani
C 745	55.2	5.6	9589	1	SC0001205	AJ001205 Streptomy	C 818	54.6	5.5	9811	14	AF449714	AF449714 Cercopith
C 746	55.2	5.6	13508	1	AE005037	AE005037 Halobacte	C 819	54.6	5.5	12277	1	AF340166	AF340166 Streptomy
C 747	55.2	5.6	14219	1	AB0070957	AB0070957 Streptomy	C 820	54.6	5.5	22449	1	SPSNBCDE	Y11548 S.pristinae
C 748	55.2	5.6	21481	2	CR847893	CR847893 Danio rer	C 821	54.6	5.5	22449	1	SPSNBCGN	X98690 S.pristinae
C 749	55.2	5.6	65351	2	AC139773	AC139773 Homo sapi	C 822	54.6	5.5	110086	8	AP003373	AP003373 Oryza sat

823	54.6	5.5	112144	8	AP003758	Oryza sat	896	54	5.5	10274	1	AE005893	Caulobact
824	54.6	5.5	127348	8	AC134769	Genomic s	c 897	54	5.5	18497	9	AF254411	Homo sapi
825	54.6	5.5	142549	2	AP004271	Oryza sat	c 898	54	5.5	110000	8	AF016814	Continuation (4 of
826	54.6	5.5	158405	10	MMHC310M6	AF109906 Mus muscu	c 899	54	5.5	110000	8	AE016820	Continuation (12 c
827	54.6	5.5	161326	9	AC004067	Homo sapi	c 900	54	5.5	143298	8	AC134240	Oryza sat
828	54.6	5.5	163490	8	CNS080CD4	AL954828 Oryza sat	c 901	54	5.5	153431	8	AC134235	Oryza sat
829	54.6	5.5	170666	8	AP003845	AP003845 Oryza sat	902	54	5.5	172876	9	AC114489	Homo sapi
830	54.6	5.5	189050	1	AL646077	RA164607 Ralstonia	903	54	5.5	174992	2	AC025422	Homo sapi
831	54.6	5.5	212050	1	AL646060	AL646060 Ralstonia	904	54	5.5	208936	2	AC010821	Homo sapi
832	54.6	5.5	221899	10	AC087117	AC087117 Mus Muscu	c 905	54	5.5	209844	9	AC011495	Homo sapi
833	54.4	5.5	1443	6	BD180149	BD180149 Highly th	c 906	54	5.5	210614	1	AB088224	Streptomy
834	54.4	5.5	1608	5	LFL308119	LFL308119 Lampetra	c 907	54	5.5	250046	2	AC113592	Mus muscu
835	54.4	5.5	4117	14	AF074337	AF074327 Tupaia he	c 908	54	5.5	298550	1	AP005047	Streptomy
836	54.4	5.5	4120	14	AF074338	AF074328 Tupaia he	909	54	5.5	299425	1	AP005049	Streptomy
837	54.4	5.5	6620	1	AB164631	AB164631 Streptomy	910	54	5.5	303550	1	SC093131	Streptomy
838	54.4	5.5	13461	14	AF084543	AF084543 Tupaia he	911	53.8	5.4	1272	6	CQ801144	Sequence
839	54.4	5.5	13889	10	AF292939	AF292939 Mus muscu	912	53.8	5.4	2007	14	CHV1GC	Caprine her
840	54.4	5.5	54587	2	AC146908_3	Continuation (4 of	913	53.8	5.4	2082	6	AR452220	Sequence
841	54.4	5.5	110000	1	BX571966_10	Continuation (11 o	914	53.8	5.4	2082	6	AX262311	Sequence
842	54.4	5.5	110000	1	CP000011_06	Continuation (7 of	915	53.8	5.4	2199	5	AXJ720743	Gallus ga
843	54.4	5.5	110000	1	CP000011_12	Continuation (13 o	c 916	53.8	5.4	11171	6	CQ801141	Sequence
844	54.4	5.5	110000	1	CP000011_13	Continuation (14 o	917	53.8	5.4	15141	14	SH1PROIE	M34651 Pseudorabie
845	54.4	5.5	110000	8	AE016818_07	Continuation (8 of	c 918	53.8	5.4	24613	1	AV1116644	Streptomy
846	54.4	5.5	112981	8	AC1478002	AC147802 Oryza sat	919	53.8	5.4	64492	1	AB086653	Streptomy
847	54.4	5.5	163732	8	OSJN000033	AL606632 Oryza sat	920	53.8	5.4	85268	2	AC022648	Homo sapi
848	54.4	5.5	195859	14	AF281817	AF281817 Tupaia he	921	53.8	5.4	110000	1	AP006618_12	Continuation (13 o
849	54.4	5.5	213050	1	AL646079	AL646079 Ralstonia	922	53.8	5.4	114793	9	AF217796	Homo sapi
850	54.4	5.5	302007	1	SC09319132	AL939132 Streptomy	923	53.8	5.4	138390	14	AV261359	Bovine he
851	54.4	5.5	322898	1	AE017238	AE017238 Mycobacte	924	53.8	5.4	139544	8	AP004878	Oryza sat
852	54.4	5.5	344321	1	BX640429	BX640429 Bordetell	925	53.8	5.4	145014	8	AP004048	Oryza sat
853	54.4	5.5	348624	1	BX640441	BX640441 Bordetell	926	53.8	5.4	166565	2	AC146324	Canis fam
854	54.4	5.5	349876	1	BX640442	BX640442 Bordetell	c 927	53.8	5.4	299300	1	AP005026	Streptomy
855	54.2	5.5	825	8	AY533122	AY533122 Oryza sat	928	53.8	5.4	300100	1	SC0939123	Streptomy
856	54.2	5.5	1300	8	AK102889	Oryza sat	c 929	53.8	5.4	301457	1	AE016924	Chromobac
857	54.2	5.5	1433	8	AF168779	AF168779 Eucalyptu	c 930	53.8	5.4	321350	1	SC0939111	Streptomy
858	54.2	5.5	1602	1	SLU12007	U12007 Streptomyce	c 931	53.8	5.4	340900	1	SME591791	Shorhizo
859	54.2	5.5	1910	8	AK104793	AK104793 Oryza sat	932	53.6	5.4	6252	8	AY039003	Hordeum v
860	54.2	5.5	1910	8	AK106154	Oryza sat	933	53.6	5.4	10554	1	AE005956	Caulobact
861	54.2	5.5	1934	8	AK098925	Oryza sat	c 934	53.6	5.4	15274	1	AE004994	Halobacte
862	54.2	5.5	1964	8	AK064950	AK064950 Oryza sat	c 935	53.6	5.4	32463	8	CNS080C9W	Oryza sat
863	54.2	5.5	2202	8	AK067226	Oryza sat	936	53.6	5.4	38734	6	BD129566	Polynucle
864	54.2	5.5	3202	1	AF157829	AF157829 Myxococcu	c 937	53.6	5.4	110000	2	BX255276_01	Continuation (2 of
865	54.2	5.5	4858	1	AF162663	AF162663 Myxococcu	c 938	53.6	5.4	146585	8	CNS080CAM	Oryza sat
866	54.2	5.5	8046	1	AF049107	AF049107 Myxococcu	939	53.6	5.4	198873	2	AC022811	Homo sapi
867	54.2	5.5	15141	14	SH1PROIE	M34651 Pseudorabie	940	53.6	5.4	204050	1	AL646073	Ralstonia
868	54.2	5.5	25315	1	AY204472	AY204472 Myxococcu	c 941	53.6	5.4	212050	1	AL646060	Ralstonia
869	54.2	5.5	32748	1	AB070951	AB070951 Streptomy	c 942	53.6	5.4	236054	2	AC114393	Rattus no
870	54.2	5.5	65140	6	AX211705	AX211705 Sequence	c 943	53.6	5.4	270418	1	AE017303	Thermus t
871	54.2	5.5	106562	1	AP004055	AP004055 Oryza sat	c 944	53.6	5.4	302325	1	AE017236	Mycobacte
872	54.2	5.5	110000	1	AP006618_19	Continuation (20 o	945	53.6	5.4	303855	1	AE017230	Mycobacte
873	54.2	5.5	110000	1	AP006840_23	Continuation (24 o	946	53.6	5.4	320150	1	AP005033	Streptomy
874	54.2	5.5	110000	1	BX571966_13	Continuation (14 o	c 947	53.6	5.4	348134	1	BX640420	Bordetell
875	54.2	5.5	110098	8	AP004144	AP004144 Oryza sat	948	53.6	5.4	348642	1	BX640446	Bordetell
876	54.2	5.5	122218	8	AC099399	AC099399 Oryza sat	949	53.4	5.4	1706	8	AK058559	Oryza sat
877	54.2	5.5	123580	1	AF263912	AF263912 Streptomy	950	53.4	5.4	1707	8	AK101900	Oryza sat
878	54.2	5.5	125401	6	AX211739	AX211739 Sequence	951	53.4	5.4	1754	8	AF165181	Zeaa mays
879	54.2	5.5	136150	8	AP002485	AP002485 Oryza sat	c 952	53.4	5.4	2248	6	BD249574	Modificat
880	54.2	5.5	142010	8	AP003928	AP003928 Oryza sat	c 953	53.4	5.4	2248	6	AR340022	Sequence
881	54.2	5.5	189043	8	AP004366	AP004366 Oryza sat	954	53.4	5.4	2336	3	NERDSF	N. Clavipes
882	54.2	5.5	196050	1	AL646058	AL646058 Ralstonia	955	53.4	5.4	2338	6	AR088543	Sequence
883	54.2	5.5	202301	1	AE017286	AE017286 Desulfovi	956	53.4	5.4	2338	6	AR088543	Sequence
884	54.2	5.5	245233	2	AC130123	AC130123 Rattus no	957	53.4	5.4	2798	3	AF448524	Mytilus g
885	54.2	5.5	301443	1	AE017239	AE017239 Mycobacte	958	53.4	5.4	3177	9	AF055989	Homo sapi
886	54.2	5.5	339972	8	OSA307662	AJ307662 Oryza sat	959	53.4	5.4	10091	1	AE011852	Xanthomon
887	54	5.5	885	11	PM7F8G	AL685189 Penicilli	960	53.4	5.4	10256	1	AE004894	Pseudomon
888	54	5.5	1065	6	BD180086	BD180086 Highly th	c 961	53.4	5.4	11626	1	AE011704	Xanthomon
889	54	5.5	1217	1	AF038408	AF038408 Streptococ	c 962	53.4	5.4	11905	1	APU33059	Actinosynn
890	54	5.5	1380	6	E17152	E17152 Micrococcu	c 963	53.4	5.4	12111	1	AE010422	Methanopy
891	54	5.5	1485	6	BD180362	BD180362 Highly th	c 964	53.4	5.4	13750	1	AY260903	Rhodospir
892	54	5.5	2900	1	TTH516007	AU516007 Thermus c	c 965	53.4	5.4	18424	1	AF163841	Myxococcu
893	54	5.5	3444	1	SAU75434	U75434 Streptomyce	c 966	53.4	5.4	39250	1	SV1011500	Streptomy
894	54	5.5	4207	9	BC053992	BC053992 Homo sapi	c 967	53.4	5.4	63082	2	AC022663	Homo sapi
895	54	5.5	4305	9	AK024444	AK024444 Homo sapi	c 968	53.4	5.4	81767	2	AC021929	Homo sapi

969	53.4	5.4	110000	1	AP006618_07	Continuation (8 of	1042	52.8	5.3	3157	1	MSGPOLA	L11920 Mycobacteri
c 970	53.4	5.4	110000	1	CP0006840_22	Continuation (23 of	c1043	52.8	5.3	4423	10	MMUSEF217	X77602 M.musculus
c 971	53.4	5.4	110000	1	CP000011_01	Continuation (2 of	1044	52.8	5.3	11842	1	AE005053	AE005053 Halobac
c 972	53.4	5.4	136254	8	CNS07YP9_	AL713941 Oryza sat	c1045	52.8	5.3	66135	1	AP006840_35	Continuation (36 o
c 973	53.4	5.4	136551	2	AC048354	AC048354 Homo sapi	c1046	52.8	5.3	92509	1	AL646086	AL646086 Ralstonia
c 974	53.4	5.4	141066	8	AP005188	AP005188 Oryza sat	1047	52.8	5.3	110000	1	AE000516_18	Continuation (19 o
c 975	53.4	5.4	151699	8	AP003916	AP003916 Oryza sat	1048	52.8	5.3	110000	1	BX571965	BX571965 Burkholder
c 976	53.4	5.4	155337	2	AC116408	AC116408 Mus muscu	c1049	52.8	5.3	114096	8	AY485643	AY485643 Hordeum v
c 977	53.4	5.4	163778	9	AL391005	AL391005 Human DNA	c1050	52.8	5.3	172647	2	AC130732	AC130732 Oryza sat
c 978	53.4	5.4	181214	2	AC110907	AC110907 Mus muscu	c1051	52.8	5.3	189010	8	AC150509	AC150509 Bos tauru
c 979	53.4	5.4	187410	8	AP005579	AP005579 Oryza sat	c1052	52.8	5.3	299925	1	AP005039	AP005039 Streptomy
c 980	53.4	5.4	233405	2	AC126733	AC126733 Rattus no	1053	52.8	5.3	300050	1	BX248339	BX248339 Mycobac
c 981	53.4	5.4	236502	2	AC098186	AC098186 Rattus no	c1054	52.8	5.3	305584	1	AE016920	AE016920 Chromobac
982	53.4	5.4	272101	1	AE017302	AE017302 Thermus t	1055	52.8	5.3	314100	1	SCO93106	AL939106 Streptomy
983	53.4	5.4	296500	1	SC0939128	AL939128 Streptomy	1056	52.8	5.3	343071	2	AC150933	AC150933 Bos tauru
984	53.4	5.4	308050	1	SC0939124	AL939124 Streptomy	1057	52.8	5.3	347137	1	BX640448	BX640448 Bordetell
985	53.4	5.4	344805	1	BX640434	BX640434 Bordetell	1058	52.8	5.3	347496	1	BX842577	BX842577 Mycobac
986	53.4	5.4	348074	1	BX640449	BX640449 Bordetell	c1059	52.8	5.3	348934	1	BX640417	BX640417 Bordetell
987	53.2	5.4	1183	8	AK109116	AK109116 Oryza sat	c1060	52.8	5.3	349028	1	BX640413	BX640413 Bordetell
988	53.2	5.4	1283	8	AK058442	AK058442 Oryza sat	1061	52.8	5.3	349497	1	BX640440	BX640440 Bordetell
989	53.2	5.4	1341	1	AY337515	AY337515 Myxococcu	1062	52.8	5.3	349726	1	BX640421	BX640421 Bordetell
990	53.2	5.4	1405	8	AK108620	AK108620 Oryza sat	1063	52.6	5.3	948	6	BD180185	BD180185 Highly th
991	53.2	5.4	1509	6	BD180173	BD180173 Highly th	1064	52.6	5.3	1569	5	AY518690	AY518690 Gallus ga
992	53.2	5.4	2672	1	AF159692	AF159692 Myxococcu	1065	52.6	5.3	2466	6	CQ759736	CQ759736 Sequence
993	53.2	5.4	2767	8	SSI224970	AJ224970 Spermatoz	c1066	52.6	5.3	2560	4	AY453841	AY453841 Oryctolag
994	53.2	5.4	10161	1	AF546153	AF546153 Micromono	c1067	52.6	5.3	2561	6	AR409339	AR409339 Sequence
995	53.2	5.4	13325	1	AE005016	AE005016 Halobac	c1068	52.6	5.3	2561	6	AX239605	AX239605 Sequence
996	53.2	5.4	110000	1	AP006618_24	Continuation (25 o	1069	52.6	5.3	2619	6	CQ759734	CQ759734 Sequence
c 997	53.2	5.4	110000	1	AP006618_36	Continuation (37 o	1070	52.6	5.3	2778	6	CQ850770	CQ850770 Sequence
c 998	53.2	5.4	110000	1	AP006618_43	Continuation (44 o	1071	52.6	5.3	2778	9	AK128815	AK128815 Homo sapi
999	53.2	5.4	110000	1	AP006840_28	Continuation (29 o	1072	52.6	5.3	3342	1	AF200819	AF200819 Streptomy
1000	53.2	5.4	110400	8	AP005919	AP005919 Oryza sat	1073	52.6	5.3	3705	6	CQ759732	CQ759732 Sequence
1001	53.2	5.4	116887	10	AL929153	AL929153 Mouse DNA	1074	52.6	5.3	4881	1	AME318385	AJ318385 Amycolato
c1002	53.2	5.4	135838	8	AP484556	AP484556 Streptomy	1075	52.6	5.3	7985	14	AB096202	AB096202 Cercopith
c1003	53.2	5.4	137468	8	AP003269	AP003269 Oryza sat	1076	52.6	5.3	11064	1	D63799	D63799 Thermus the
c1004	53.2	5.4	181676	10	AC124194	AC124194 Mus muscu	1077	52.6	5.3	12162	1	AY034175	AY034175 Streptomy
1005	53.2	5.4	197411	10	AC135961	AC135961 Mus muscu	1078	52.6	5.3	13803	1	AE011784	AE011784 Xanthomon
c1006	53.2	5.4	232605	1	AE017222	AE017222 Thermus t	1079	52.6	5.3	13901	1	AY258009	AY258009 Streptomy
c1007	53.2	5.4	309267	1	AE017235	AE017235 Mycobac	1080	52.6	5.3	29132	1	STH575648	AJ575648 Streptomy
1008	53.2	5.4	348525	1	BX640428	BX640428 Bordetell	1081	52.6	5.3	47090	9	AC092310	AC092310 Homo sapi
1009	53.2	5.4	349354	1	BX640416	BX640416 Bordetell	c1082	52.6	5.3	47090	9	AC093233	AC093233 Homo sapi
1010	53.2	5.4	349672	1	BX640419	BX640419 Bordetell	c1083	52.6	5.3	81767	2	AC021929	AC021929 Homo sapi
c1011	53	5.4	632	6	AR227195	AR227195 Sequence	c1084	52.6	5.3	110000	1	AE000516_27	Continuation (28 o
1012	53	5.4	765	6	BD180096	BD180096 Highly th	1085	52.6	5.3	110000	1	AE016822_21	Continuation (22 o
1013	53	5.4	1929	6	AX811491	AX811491 Sequence	c1086	52.6	5.3	110000	1	AP006618_02	Continuation (3 of
1014	53	5.4	2304	6	BD179527	BD179527 Highly th	c1087	52.6	5.3	110000	1	AP006618_03	Continuation (4 of
1015	53	5.4	2953	10	BC054782	BC054782 Mus muscu	c1088	52.6	5.3	110000	1	AP006618_24	Continuation (25 o
1016	53	5.4	3518	10	MUSHSP7A2	M35021 Mouse heat	c1089	52.6	5.3	110000	1	AP006618_28	Continuation (29 o
1017	53	5.4	3701	1	AF172724	AF172724 Caulobact	c1090	52.6	5.3	110000	2	LMFLCHR34_13	Continuation (14 o
c1018	53	5.4	8113	14	HSBBTICP4A	L14320 Bovine herp	1091	52.6	5.3	135357	8	AP003896	AP003896 Oryza sat
c1019	53	5.4	10029	1	AE012236	AE012236 Xanthomon	c1092	52.6	5.3	138390	14	AY261359	AY261359 Bovine he
c1020	53	5.4	10513	1	AE004792	AE004792 Pseudomon	c1093	52.6	5.3	163328	8	AP004865	AP004865 Oryza sat
c1021	53	5.4	11283	1	AE005710	AE005710 Caulobact	1094	52.6	5.3	183495	8	AP005620	AP005620 Oryza sat
c1022	53	5.4	11923	1	AE005972	AE005972 Caulobact	1095	52.6	5.3	230362	2	AC009942	AC009942 Rattus no
1023	53	5.4	32668	1	MPU575934	AJ575934 Micromono	1096	52.6	5.3	277363	2	AC134745	AC134745 Rattus no
c1024	53	5.4	38146	1	AY524043	AY524043 Micromono	c1097	52.6	5.3	299425	1	AP005049	AP005049 Streptomy
c1025	53	5.4	100773	8	AP466201	AP466201 Sorghum b	1098	52.6	5.3	303550	1	SCO939118	AL939118 Streptomy
c1026	53	5.4	102591	9	AC002978	AC002978 Homo sapi	c1099	52.6	5.3	306550	1	BX248342	BX248342 Mycobac
c1027	53	5.4	110000	1	AP006618_39	Continuation (40 o	c1100	52.6	5.3	346051	1	BX842580	BX842580 Mycobac
c1028	53	5.4	110000	1	AP006618_54	Continuation (55 o	1101	52.4	5.3	1175	5	CMHISH5	X01065 Duck (C. mo
1029	53	5.4	110000	1	AP006840_03	Continuation (4 of	1102	52.4	5.3	1227	6	AX467205	AX467205 Sequence
1030	53	5.4	110000	2	LMFLCHR12_13	Continuation (14 o	1103	52.4	5.3	1485	8	AX337108	AX337108 Oryza sat
1031	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he	1104	52.4	5.3	1891	6	AX337108	AX337108 Sequence
c1032	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he	1105	52.4	5.3	1891	6	AX587764	AX587764 Sequence
c1033	53	5.4	144093	10	AC109193	AC109193 Mus muscu	1106	52.4	5.3	1891	9	HSJUNDR	X56681 Human_jund
1034	53	5.4	178620	10	AC121865	AC121865 Mus muscu	1107	52.4	5.3	2796	3	AF043944	AF043944 Mytilus e
c1035	53	5.4	194387	10	AC105989	AC105989 Mus muscu	1108	52.4	5.3	3139	8	D63955	D63955 Oryza sativ
1036	53	5.4	301925	1	AP005046	AP005046 Streptomy	1109	52.4	5.3	3978	4	BOVADC	B25579 Bovine aden
1037	53	5.4	303842	1	AE016923	AE016923 Chromobac	1110	52.4	5.3	3978	6	AR106654	AR106654 Sequence
c1038	53	5.4	347071	1	BX640415	BX640415 Bordetell	1111	52.4	5.3	3980	1	AF546147	AF546147 Streptomy
1039	53	5.4	348706	1	BX640445	BX640445 Bordetell	1112	52.4	5.3	5117	6	AX818240	AX818240 Sequence
1040	52.8	5.3	1094	11	PM7G11B	AL685196 Penicilli	1113	52.4	5.3	5117	9	AB011105	AB011105 Homo sapi
1041	52.8	5.3	1236	6	AR007558	AR007558 Sequence	1114	52.4	5.3	5204	6	AX512251	AX512251 Sequence

1115	52.4	5.3	5640	6	AR338550	Sequence	1188	52	5.3	2800	1	PSNOSZR	Z13988 P.stutzeri
1116	52.4	5.3	8296	6	AX463772	Sequence	1189	52	5.3	3113	8	SS95BASAL	AJ001438 Spermatoz
1117	52.4	5.3	10911	6	CQ730457	Sequence	1190	52	5.3	3114	12	AX192356	AY192356 Synthetic
1118	52.4	5.3	11238	9	AX697991	Sequence	1191	52	5.3	3135	12	AX192357	AY192357 Synthetic
1119	52.4	5.3	11329	9	AF443072	Homo sapi	1192	52	5.3	3135	12	AX192358	AY192358 Synthetic
1120	52.4	5.3	11350	6	AX463738	Sequence	1193	52	5.3	10352	1	AF546152	AF546152 Streptomy
1121	52.4	5.3	11367	6	AX704754	Sequence	1194	52	5.3	10854	1	AE001886	AE001886 Deinococc
1122	52.4	5.3	16197	1	AE020272	Sequence	1195	52	5.3	11506	1	AE004793	AE004793 Pseudococ
1123	52.4	5.3	60196	6	AX697977	Sequence	1196	52	5.3	49269	8	AC135499	AC135499 Oryza sat
1124	52.4	5.3	79568	2	AC151725	Medicago	1197	52	5.3	110000	1	AE016822_22	Continuation (23 o
1125	52.4	5.3	85434	2	AC066610	Homo sapi	1198	52	5.3	110000	1	AP006840_22	Continuation (23 o
1126	52.4	5.3	85434	2	CNS08CRU	Continuation (14 o	1199	52	5.3	142081	8	AP004572	AP004572 Oryza sat
1127	52.4	5.3	104326	1	AB070940	Streptomy	1200	52	5.3	152974	8	AC135497	AC135497 Oryza sat
1128	52.4	5.3	110000	1	AP006618_13	Continuation (16 o	1201	52	5.3	186090	2	AC097352	AC097352 Canis fam
1129	52.4	5.3	110000	1	AP006618_15	Continuation (3 of	1202	52	5.3	191916	2	AC095027	AC095027 Canis fam
1130	52.4	5.3	110000	1	BS571965_02	Continuation (35 o	1203	52	5.3	191996	9	AC092275	AC092275 Homo sapi
1131	52.4	5.3	110000	1	CP000010_34	Streptomy	1204	52	5.3	193119	8	AC025907	AC025907 Oryza sat
1132	52.4	5.3	138203	8	AY310323	Oryza sat	1205	52	5.3	200968	8	AP005516	AP005516 Oryza sat
1133	52.4	5.3	149098	8	AP003296	Streptomy	1206	52	5.3	211657	10	AL732564	AL732564 Mouse DNA
1134	52.4	5.3	157302	9	AL445209	Human DNA	1207	52	5.3	299925	1	AP005045	AP005045 Streptomy
1135	52.4	5.3	168861	2	AC130786	Papio anu	1208	52	5.3	300029	8	AE017099	AE017099 Oryza sat
1136	52.4	5.3	169162	8	AP004267	Oryza sat	1209	52	5.3	301846	1	AE016913	AE016913 Chromobac
1137	52.4	5.3	176647	8	AC130188	Papio anu	1210	52	5.3	307435	1	AE016914	AE016914 Chromobac
1138	52.4	5.3	196558	10	AC073946	Mus muscu	1211	51.8	5.2	974	8	AF377768	AF377768 Zea mays
1139	52.4	5.3	202270	10	AC102341	Mus muscu	1212	51.8	5.2	975	8	AF377745	AF377745 Zea mays
1140	52.4	5.3	242662	2	AC080020	Mus muscu	1213	51.8	5.2	980	8	AF377759	AF377759 Zea mays
1141	52.4	5.3	247910	1	AE017307	Thermus t	1214	51.8	5.2	980	8	AF377761	AF377761 Zea mays
1142	52.4	5.3	300550	1	AP005030	Streptomy	1215	51.8	5.2	981	8	AY513914	AY513914 Zea luxur
1143	52.4	5.3	320150	1	AP005033	Streptomy	1216	51.8	5.2	981	8	AY513920	AY513920 Zea luxur
1144	52.2	5.3	705	6	BD179549	Highly th	1217	51.8	5.2	981	8	AY513928	AY513928 Zea mays
1145	52.2	5.3	833	8	AY088274	Arabidops	1218	51.8	5.2	982	8	AF377767	AF377767 Zea mays
1146	52.2	5.3	936	6	BD179727	Highly th	1219	51.8	5.2	983	8	AY513929	AY513929 Zea mays
1147	52.2	5.3	996	11	PM12CAG	Penicilli	1220	51.8	5.2	989	8	AY513923	AY513923 Zea mays
1148	52.2	5.3	1140	11	AK071964	Highly th	1221	51.8	5.2	995	8	AY513927	AY513927 Zea mays
1149	52.2	5.3	1611	6	BD180543	Oryza sat	1222	51.8	5.2	1255	10	AF076156	AF076156 Mus muscu
1150	52.2	5.3	1719	6	BD180543	Highly th	1223	51.8	5.2	1262	10	BC010402	BC010402 Mus muscu
1151	52.2	5.3	2085	8	AF325915	Euglena g	1224	51.8	5.2	1673	8	AY600140	AY600140 Broussone
1152	52.2	5.3	2529	1	AY605536	Oryza sat	1225	51.8	5.2	1705	8	AK069785	AK069785 Oryza sat
1153	52.2	5.3	2760	1	SRSENR	Streptomyce	1226	51.8	5.2	1926	6	AR217867	AR217867 Sequence
1154	52.2	5.3	6297	6	AX598629	Sequence	1227	51.8	5.2	1931	6	AR083152	AR083152 Sequence
1155	52.2	5.3	7155	14	RCU64519	Rhodospiril	1228	51.8	5.2	2036	8	AF050631	AF050631 Zea mays
1156	52.2	5.3	9353	14	BHV1UUX	Bovine herp	1229	51.8	5.2	2036	8	AF053206	AF053206 Sequence
1157	52.2	5.3	10460	1	AE011791	Xanthomon	1230	51.8	5.2	2075	6	AR436194	AR436194 Sequence
1158	52.2	5.3	10696	1	AE012103	Xanthomon	1231	51.8	5.2	2075	6	AR433000	AR433000 Sequence
1159	52.2	5.3	14355	3	AF218623S1	Nephila m	1232	51.8	5.2	2075	6	AX482567	AX482567 Sequence
1160	52.2	5.3	31444	14	BVH1LFT31	Bovine herp	1233	51.8	5.2	2075	6	AX565707	AX565707 Sequence
1161	52.2	5.3	66808	1	SAU421825	Stigmatel	1234	51.8	5.2	2075	6	AX597107	AX597107 Sequence
1162	52.2	5.3	76196	1	AY354515	Streptomy	1235	51.8	5.2	2075	9	AF001365	AF001365 Sequence
1163	52.2	5.3	82868	6	CQ792587	Angioccoc	1236	51.8	5.2	2075	9	AF001900	AF001900 Homo sapi
1164	52.2	5.3	82868	6	CQ792587	Sequence	1237	51.8	5.2	2525	6	CQ782831	CQ782831 Sequence
1165	52.2	5.3	82868	6	CQ792604	Sequence	1238	51.8	5.2	2525	6	BD127336	BD127336 Primer fo
1166	52.2	5.3	110000	1	AP006618_58	Continuation (59 o	1239	51.8	5.2	2525	9	AK074866	AK074866 Homo sapi
1167	52.2	5.3	128098	8	AP004309	Oryza sat	1240	51.8	5.2	2597	6	AK0600203	AK0600203 Sequence
1168	52.2	5.3	133887	2	AP004061	Oryza sat	1241	51.8	5.2	2714	9	AF327056	AF327056 Homo sapi
1169	52.2	5.3	143200	8	AP004380	Oryza sat	1242	51.8	5.2	2725	9	BC069227	BC069227 Homo sapi
1170	52.2	5.3	159860	8	AP005647	Oryza sat	1243	51.8	5.2	4469	6	AX236302	AX236302 Sequence
1171	52.2	5.3	190050	1	AL646080	Raistconia	1244	51.8	5.2	4469	6	AX578081	AX578081 Sequence
1172	52.2	5.3	205144	4	AY495827	Oryctolag	1245	51.8	5.2	4469	9	AF056087	AF056087 Homo sapi
1173	52.2	5.3	273285	1	AE017304	Thermus t	1246	51.8	5.2	4612	1	AF317284	AF317284 Burkholde
1174	52.2	5.3	276800	1	SC0939115	Streptomy	1247	51.8	5.2	10732	6	E32986	E32986 Gene encodi
1175	52.2	5.3	300327	1	AE017228	Mycobacte	1248	51.8	5.2	11462	8	AF327876	AF327876 Chlamydom
1176	52.2	5.3	300425	1	AP005038	Streptomy	1249	51.8	5.2	15231	1	AY0166598	AY0166598 Burkholde
1177	52.2	5.3	305584	1	AE016920	Chromobac	1250	51.8	5.2	34600	1	AY028431	AY028431 Burkholde
1178	52.2	5.3	309050	1	SC0939117	Streptomy	1251	51.8	5.2	40343	2	AC099831	AC099831 Homo sapi
1179	52	5.3	991	11	PM12H12B	Penicilli	1252	51.8	5.2	76521	2	AC148294	AC148294 Zea mays
1180	52	5.3	992	8	AF377751	Zea mays	1253	51.8	5.2	104190	8	AP004257	AP004257 Oryza sat
1181	52	5.3	1000	8	AY513932	Zea mays	1254	51.8	5.2	110000	1	AP006618_21	Continuation (22 o
1182	52	5.3	1155	8	AB028182	Oryza sat	1255	51.8	5.2	110000	1	AP006618_28	Continuation (29 o
1183	52	5.3	1255	8	AK073667	Oryza sat	1256	51.8	5.2	110000	1	AP006840_09	Continuation (10 o
1184	52	5.3	1410	1	AME277083	Amycolato	1257	51.8	5.2	110000	1	AP006840_10	Continuation (11 o
1185	52	5.3	1491	6	AX455983	Sequence	1258	51.8	5.2	110000	1	AP006840_26	Continuation (27 o
1186	52	5.3	1703	8	AK120673	Oryza sat	1259	51.8	5.2	110000	2	BX255276_03	Continuation (4 of
1187	52	5.3	1711	1	AF347026	Streptomy	1260	51.8	5.2	110000	2	LMFLCHR36_22	Continuation (23 o

1261	51.8	5.2	113193	1	AF357202	AF357202 Streptomy	1334	51.4	5.2	110000	1	AP006618_44	Continuation (45 o
1262	51.8	5.2	113193	6	AX703543	AX703543 Sequence	1335	51.4	5.2	110000	1	AP006618_45	Continuation (46 o
1263	51.8	5.2	123149	9	AC008655	AC008655 Homo sapi	1336	51.4	5.2	110000	1	AP006840_01	Continuation (2 of
1264	51.8	5.2	185539	2	AC018349	AC018349 Homo sapi	1337	51.4	5.2	110000	1	AY305378_0	AY305378 Ralstonia
1265	51.8	5.2	190590	2	AC135045	AC135045 Homo sapi	1338	51.4	5.2	110000	1	CP000011_04	Continuation (5 of
1266	51.8	5.2	202050	1	AL646065	AL646065 Ralstonia	1339	51.4	5.2	110000	2	LMFLCHR15_5	Continuation (6 of
1267	51.8	5.2	203050	1	AL646071	AL646071 Ralstonia	1340	51.4	5.2	110000	2	LMFLCHR15_6	Continuation (7 of
1268	51.8	5.2	217514	2	AC145779	AC145779 Sus scrofa	1341	51.4	5.2	110000	2	LMFLCHR34_00	AL499623 Leishmani
1269	51.8	5.2	298300	1	AP005025	AP005025 Streptomy	1342	51.4	5.2	130273	8	OSJN00011_	AL606447 Oryza sat
1270	51.8	5.2	298450	1	SC0939107	AP005025 Streptomy	1343	51.4	5.2	152828	8	AC133859	AL133859 Oryza sat
1271	51.8	5.2	298550	1	AP005047	AP005047 Streptomy	1344	51.4	5.2	163945	2	AC116727	AC116727 Mus muscu
1272	51.8	5.2	298900	1	AP005937	AP005937 Bradyrhiz	1345	51.4	5.2	205054	10	AC0169712	AC0169712 Mus muscu
1273	51.8	5.2	299325	1	AP005042	AP005042 Streptomy	1346	51.4	5.2	208524	1	AE016925	AE016925 Chromobac
1274	51.8	5.2	300550	1	AP005030	AP005030 Streptomy	1347	51.4	5.2	301332	1	AE017237	AE017237 Mycobacte
1275	51.8	5.2	301875	1	AP005027	AP005027 Streptomy	1348	51.4	5.2	302300	1	AP005034	AP005034 Streptomy
1276	51.8	5.2	305520	1	AE016780	AE016780 Pseudomon	1349	51.4	5.2	343473	1	BX640451	BX640451 Bordetell
1277	51.8	5.2	349008	1	BX640444	BX640444 Bordetell	1350	51.2	5.2	699	6	AX412281	AX412281 Sequence
1278	51.8	5.2	349841	1	BX572606	BX572606 Rhodosphe	1351	51.2	5.2	699	6	AX412282	AX412282 Sequence
1279	51.6	5.2	486	1	AF071792	AF071792 Micromono	1352	51.2	5.2	699	6	AX507044	AX507044 Sequence
1280	51.6	5.2	730	8	AF060180	AF060180 Nicotiana	1353	51.2	5.2	699	6	AX6511360	AX6511360 Sequence
1281	51.6	5.2	1394	8	AY551433	AY551433 Hordeum v	1354	51.2	5.2	993	6	BD179823	BD179823 Highly th
1282	51.6	5.2	1584	6	BD180289	BD180289 Highly th	1355	51.2	5.2	1182	12	AY659409	AY659409 Synthetic
1283	51.6	5.2	2595	6	BD179554	BD179554 Highly th	1356	51.2	5.2	1220	8	MZETASSELS	L20621 Zea mays al
1284	51.6	5.2	2865	8	AF019296	AF019296 Zea mays	1357	51.2	5.2	1683	6	AX697979	AX697979 Sequence
1285	51.6	5.2	4523	14	MMULGNES	X95710 Pseudorabie	1358	51.2	5.2	2181	8	AK100401	AK100401 Oryza sat
1286	51.6	5.2	4548	8	AY499410	AY499410 Zea mays	1359	51.2	5.2	2277	6	AR004983	AR004983 Sequence
1287	51.6	5.2	29148	14	AY486470S04	AY486473 Human her	1360	51.2	5.2	2815	1	SLCUTRS	X58793 S.lividans
1288	51.6	5.2	39576	3	AC008054	AC008054 Leishmani	1361	51.2	5.2	3480	1	CFICEND	L02544 Cellulomona
1289	51.6	5.2	93821	2	AC021596	AC021596 Homo sapi	1362	51.2	5.2	3993	6	AB0117481	AB0117481 Heterosig
1290	51.6	5.2	110000	1	AE017282_22	Continuation (23 o	1363	51.2	5.2	4467	8	E33370	E33370 NA+-ATPase
1291	51.6	5.2	110000	1	AP006618_30	Continuation (31 o	1364	51.2	5.2	6125	1	PSRSTD	D45195 Pseudomonas
1292	51.6	5.2	110000	1	AP006840_09	Continuation (10 o	1365	51.2	5.2	10375	1	AE004549	AE004549 Pseudomon
1293	51.6	5.2	110000	1	AP006840_32	Continuation (33 o	1366	51.2	5.2	11334	1	AE004948	AE004948 Pseudomon
1294	51.6	5.2	110000	1	BSY71965_05	Continuation (6 of	1367	51.2	5.2	12357	1	AE004471	AE004471 Pseudomon
1295	51.6	5.2	110000	1	CP000010_31	Continuation (32 o	1368	51.2	5.2	13802	1	STE579650	AEJ579650 Streptomy
1296	51.6	5.2	113193	1	AF357202	AF357202 Streptomy	1369	51.2	5.2	22437	1	AF027524	AF027524 Frankia s
1297	51.6	5.2	113193	6	AF703543	AF703543 Sequence	1370	51.2	5.2	77457	1	AF210249	AF210249 Streptomy
1298	51.6	5.2	114051	8	OSJN00036	AL606598 Oryza sat	1371	51.2	5.2	103458	8	AC108502	AC108502 Oryza sat
1299	51.6	5.2	150715	14	AX714813	AY714813 Cercopith	1372	51.2	5.2	110000	1	BX571965_11	Continuation (12 o
1300	51.6	5.2	169003	10	AC115699	AC115699 Mus muscu	1373	51.2	5.2	110000	1	BX571966_07	Continuation (8 of
1301	51.6	5.2	174139	2	AC116700	AC116700 Mus muscu	1374	51.2	5.2	110000	1	CP000010_07	Continuation (8 of
1302	51.6	5.2	192857	8	AP005605	AP005605 Oryza sat	1375	51.2	5.2	118018	8	AP005675	AP005675 Oryza sat
1303	51.6	5.2	213050	1	AL646067	AL646067 Ralstonia	1376	51.2	5.2	137650	8	AC130600	AC130600 Oryza sat
1304	51.6	5.2	226889	14	AC146905	AC146905 Human Her	1377	51.2	5.2	165634	2	CR354375	CR354375 Danio rer
1305	51.6	5.2	229483	14	AC146851	AC146851 Human Her	1378	51.2	5.2	185437	8	AP005422	AP005422 Oryza sat
1306	51.6	5.2	231236	14	AX315197	AY315197 Human her	1379	51.2	5.2	189370	1	AF010496	AF010496 Rhodobact
1307	51.6	5.2	234881	14	AC146906	AC146906 Human Her	1380	51.2	5.2	267320	2	AC106562	AC106562 Rattus no
1308	51.6	5.2	290850	1	SC0939127	AL939127 Streptomy	1381	51.2	5.2	293050	1	SC0939116	AL939116 Streptomy
1309	51.6	5.2	291000	1	SC0939105	AL939105 Streptomy	1382	51.2	5.2	298550	1	AP005029	AP005029 Streptomy
1310	51.6	5.2	299050	1	SC0939104	AL939104 Streptomy	1383	51.2	5.2	300425	1	AP005046	AP005046 Streptomy
1311	51.6	5.2	299425	1	AP005037	AP005037 Streptomy	1384	51.2	5.2	301925	1	AP005046	AP005046 Streptomy
1312	51.6	5.2	299550	1	AP005031	AP005031 Streptomy	1385	51.2	5.2	313200	1	AP005214	AP005214 Corynebac
1313	51.6	5.2	301399	1	AE017233	AE017233 Mycobacte	1386	51.2	5.2	348997	1	BX640427	BX640427 Bordetell
1314	51.6	5.2	348934	1	BX640417	BX640417 Bordetell	1387	51.2	5.2	349028	1	BX640413	BX640413 Bordetell
1315	51.6	5.2	348997	1	BX640427	BX640427 Bordetell	1388	51.2	5.2	349305	1	BX640433	BX640433 Bordetell
1316	51.6	5.2	349008	1	BX640444	BX640444 Bordetell	1389	51.2	5.2	473	1	AB066368	AB066368 Streptomy
1317	51.6	5.2	349016	1	AP003003	AP003003 Mesorhizo	1390	51.2	5.2	473	1	AB066369	AB066369 Streptomy
1318	51.6	5.2	349640	1	BX572600	BX572600 Rhodosphe	1391	51.2	5.2	591	12	AY658503	AY658503 Synthetic
1319	51.4	5.2	985	8	AK058890	AK058890 Oryza sat	1392	51.2	5.2	846	6	BD179798	BD179798 Highly th
1320	51.4	5.2	1746	6	AF425992	AF425992 Streptomy	1393	51.2	5.2	959	8	AY513924	AY513924 Zea mays
1321	51.4	5.2	1926	6	AX811493	AX811493 Sequence	1394	51.2	5.2	1004	8	AY513936	AY513936 Zea mays
1322	51.4	5.2	2454	8	AF022816	AF022816 Chlamydom	1395	51.2	5.2	1007	8	AF377762	AF377762 Zea mays
1323	51.4	5.2	2826	9	HSCBFA	Y11525 H.sapiens m	1396	51.2	5.2	1008	8	AF377752	AF377752 Zea mays
1324	51.4	5.2	3292	10	MUSHBP7A2	M76613 Mouse heat	1397	51.2	5.2	1008	8	AF377755	AF377755 Zea mays
1325	51.4	5.2	3520	5	AY008272	AY008272 Gallus ga	1398	51.2	5.2	1008	8	AF377763	AF377763 Zea mays
1326	51.4	5.2	4725	6	AX697993	AX697993 Sequence	1399	51.2	5.2	1008	8	AF377764	AF377764 Zea mays
1327	51.4	5.2	7916	1	ASY18523	Y18523 Actinoplane	1400	51.2	5.2	1012	8	AF377748	AF377748 Zea mays
1328	51.4	5.2	10968	1	AY204471	AY204471 Myxococcu	1401	51.2	5.2	1012	8	AF377749	AF377749 Zea mays
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1330	51.4	5.2	14999	3	AF218621S1	AF218621 Nephila c	1403	51.2	5.2	1012	8	AF377756	AF377756 Zea mays
1331	51.4	5.2	30000	6	AX250262	AX250262 Sequence	1404	51.2	5.2	1012	8	AF377765	AF377765 Zea mays
1332	51.4	5.2	35138	9	AL353799	AL353799 Human DNA	1405	51.2	5.2	1012	8	AF377766	AF377766 Zea mays
1333	51.4	5.2	103450	1	AF440781	AF440781 Streptomy	1406	51.2	5.2	1014	8	AF377746	AF377746 Zea mays



1407	51	5.2	1015	8	AY5133919	Zea mays	AY5133919	50.8	5.1	1494	8	AK109381	AK109381	Oryza sat
1408	51	5.2	1015	8	AY5133926	Zea mays	AY5133926	50.8	5.1	1502	8	AY187941	AY187941	Oryza sat
1409	51	5.2	1018	8	AF3777747	Zea mays	AF3777747	50.8	5.1	1897	1	MPUFMS14	MPUFMS14	Olivaste
1410	51	5.2	1018	8	AF3777750	Zea mays	AF3777750	50.8	5.1	2018	8	AK071556	AK071556	Oryza sat
1411	51	5.2	1018	8	AF3777757	Zea mays	AF3777757	50.8	5.1	2025	8	AK106761	AK106761	Oryza sat
1412	51	5.2	1018	8	AF3777758	Zea mays	AF3777758	50.8	5.1	2025	5	GGCVP1A4	GGCVP1A4	G.gallus nr
1413	51	5.2	1018	8	AF3777760	Zea mays	AF3777760	50.8	5.1	2025	8	AK121052	AK121052	Oryza sat
1414	51	5.2	1019	8	AY5133915	Zea luxur	AY5133915	50.8	5.1	2358	8	ABU40823	ABU40823	Azospirillum
1415	51	5.2	1019	8	AY5133923	Zea mays	AY5133923	50.8	5.1	2440	8	AK072584	AK072584	Oryza sat
1416	51	5.2	1021	8	AY5133925	Zea mays	AY5133925	50.8	5.1	2440	6	BD179835	BD179835	Highly th
1417	51	5.2	1021	8	AY5133935	Zea mays	AY5133935	50.8	5.1	2616	10	AY706205	AY706205	Mus muscu
1418	51	5.2	1025	8	AY5133922	Zea mays	AY5133922	50.8	5.1	4217	5	AF331669	AF331669	Dromaius
1419	51	5.2	1231	8	AF168778	Eucalyptu	AF168778	50.8	5.1	5760	6	AX616761	AX616761	Sequence
1420	51	5.2	1336	8	AK108802	Oryza sat	AK108802	50.8	5.1	10970	1	AE001869	AE001869	Deinococc
1421	51	5.2	2023	8	AF162938	Streptomy	AF162938	50.8	5.1	12885	1	AE012472	AE012472	Xanthomon
1422	51	5.2	2192	8	AK109617	Oryza sat	AK109617	50.8	5.1	14789	1	AE004916	AE004916	Pseudomon
1423	51	5.2	2560	4	AY453841	Oryctolag	AY453841	50.8	5.1	21953	6	CQ792619	CQ792619	Sequence
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1425	51	5.2	2561	6	AX239605	Sequence	AX239605	50.8	5.1	36270	1	SLLINC	SLLINC	S.lincolney
1426	51	5.2	2687	9	BC066775	Homo sapi	BC066775	50.8	5.1	37000	14	BHTIUL	BHTIUL	Bovine herp
1427	51	5.2	2710	6	AX540750	Sequence	AX540750	50.8	5.1	53951	2	AC148879	AC148879	Chlamydom
1428	51	5.2	2801	9	BC066124	Homo sapi	BC066124	50.8	5.1					
1429	51	5.2	3570	1	STWAFSR	Streptomyce	STWAFSR	50.8	5.1					
1430	51	5.2	3757	1	CFXNCGN	C.fimi xyc	CFXNCGN	50.8	5.1					
1431	51	5.2	5123	14	HEPVIE	Pseudorabie	HEPVIE	50.8	5.1					
1432	51	5.2	6281	14	AF352564	D45382 Streptomyce	AF352564	50.8	5.1					
1433	51	5.2	8199	1	STWAFS1	M57505 Pseudorabie	STWAFS1	50.8	5.1					
1434	51	5.2	8438	14	SHILLT	AE011938 Xanthomon	SHILLT	50.8	5.1					
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1436	51	5.2	11157	1	AE011938	AE001916 Deinococc	AE011938	50.8	5.1					
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1443	51	5.2	110000	1	BS571966_30	CP000010 Burkholde	BS571966_30	50.8	5.1					
1444	51	5.2	135357	8	AP003896	AC130600 Oryza sat	AP003896	50.8	5.1					
1445	51	5.2	137650	8	AC130600	AC130600 Oryza sat	AC130600	50.8	5.1					
1446	51	5.2	14724	8	AC078948	AC162934 Oryza sat	AC078948	50.8	5.1					
1447	51	5.2	150283	8	OSJN00136	AP002093 Oryza sat	OSJN00136	50.8	5.1					
1448	51	5.2	151806	8	AP002093	AL662994 Oryza sat	AP002093	50.8	5.1					
1449	51	5.2	160530	9	AC090330	AC090330 Homo sapi	AC090330	50.8	5.1					
1450	51	5.2	162227	8	OSJN00192	AC101323 Homo sapi	OSJN00192	50.8	5.1					
1451	51	5.2	166618	9	AC010323	AC135429 Oryza sat	AC010323	50.8	5.1					
1452	51	5.2	177374	8	AC135429	AC122509 Mus muscu	AC135429	50.8	5.1					
1453	51	5.2	178757	10	AC122509	AP005620 Oryza sat	AC122509	50.8	5.1					
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1458	51	5.2	248500	1	SC0939120	AP005949 Bradyrhiz	SC0939120	50.8	5.1					
1459	51	5.2	299800	1	AP005040	AE017104 Oryza sat	AP005040	50.8	5.1					
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1469	50.8	5.1	1155	6	AR194833	AX829604 Sequence	AR194833	50.8	5.1					
1470	50.8	5.1	1155	6	AR233105	AX832589 Sequence	AR233105	50.8	5.1					
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## ALIGNMENTS

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LOCUS	AX201342					
DEFINITION	AX201342					
ACCESSION	AX201342					
VERSION	AX201342.1	GI:15391164				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						

Query Match	100.0%	Score 989	DB 6	Length 989	
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Db	1	CGCGGCGCGGAGTCCGAGACCTGTCCAGGAGCTCCAGTCCAGTACCTGCTCTCCGTCGCGCGG	60		
QY	61	TCCCGCGGCTCTCTCGCGCGGATGCCAGCCGCGGTCGCGGCTCTCCGTCGCGCGG	120		
Db	61	TCCCGCGGCTCTCTCGCGCGGATGCCAGCCGCGGTCGCGGCTCTCCGTCGCGCGG	120		
QY	121	CGCTGGCTGGCTGAGCTCAGCGGCGGCGGCTTGGCCACTGGCTCTTCTTCTGGGGA	180		
Db	121	CGCTGGCTGGCTGAGCTCAGCGGCGGCGGCTTGGCCACTGGCTCTTCTTCTGGGGA	180		
QY	181	GGCGGTGCCCCCATGGGAGCGCGGAGAGTGTCTTCCCGGAGGACAGCC	240		
Db	181	GGCGGTGCCCCCATGGGAGCGCGGAGAGTGTCTTCCCGGAGGACAGCC	240		
QY	241	GCCTGTGGCAGTATCTTCTGAGCCGCTCATTCGCGGAGCACCGCGGCTGCGAAGCTGA	300		
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Db	241	GCCTGTGGCAGTATCTTCTGAGCCGCTCCATCGGAGACACCCGGCGCTGCGAAGCCTGA	300
Qy	301	GGCTGCTGACCTGGAGACGCGAGGGGATTTCTATGATGACCTTCGAGAGGCCACG	360
Db	301		
Qy	361	GGCTGCTGACCTGGAGACGCGAGGGGATTTCTATGATGACCTTCGAGAGGCCACG	360
Db	361		
Qy	421	TCTTGGCCAACTGGCGCGCTCATCCAGGCCCAAGAGCGCTGGACCTGGGCACCTTCA	420
Db	361	TCTTGGCCAACTGGCGCGCTCATCCAGGCCCAAGAGCGCTGGACCTGGGCACCTTCA	420
Qy	421	CGGGTACTTCGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT	480
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Qy	481	GGAGGTGACGCGCAGCCCGGAGCTGGGACGGCCCTGTGGAGGAGGCGGAGGGGG	540
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Qy	541	AGCACAAGATCGACCTTCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTTGGCGG	600
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Qy	601	CGGGAGCGCGCACCTTTCGAGCTGGCGCTGGAGTGGGATCGGACCAAGAGAACTTGTCCG	660
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Qy	661	CCTACTACAGCGCTGCTGACGCTGCTGGACCGCGGAGGACCTTCGCGCTTCAGAG	720
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Qy	721	TCTGTGGCGCGGAGGCTGCTGCAACCTTCGAAAGGGGACGCTGGCGCGGAGTGTGC	780
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Qy	781	GAAACTAAACGAAACGATCCGCGGAGCGTCAAGGCTTACATCAGCCTTCCTGCGCCCTGG	840
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Qy	841	GGATGGACTACCTTGGCTTCAAGATCTAGGGCTGGCCCTTAGTGGAGTGGCTCGAGG	900
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AX697237			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1			
Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L.,			
Eaton, D. L., Gao, W. Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,			
Godowski, P. J., Gurney, A. L., Smith, V., Tamas, D., Wood, W. I.,			
Grimaldi, C. J., Hillan, K. J., Paoni, N. F., Roy, M. A., and Watanabe, C. K.			
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the same			
Patent: WO 0078961-A 305 28-DEC-2000;			
Genentech Inc. (US)			
Location/Qualifiers			
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FEATURES			
source			

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ORIGIN					
Query Match		100.0%; Score 989; DB 6; Length 989;			
Best Local Similarity		100.0%; Pred. No. 7.7e-125;			
Matches 989; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	GC	GGGGCCGCGAGTCCGAGACCTGTCCCGAGGAGCTCCAGCTC	ACGTCACGTGACCTGTCACTGCC	60
Qy	61	TCC	CGCGCGCTCTCTGCGCGCGCATGACCCAGCGCGTGC	CGCGCGCTCTCGTGC	120
Db	61	TCC	CGCGCGCTCTCTGCGCGCGCATGACCCAGCGCGTGC	CGCGCGCTCTCGTGC	120
Qy	121	CGT	GGCCCTTGGGCTCAGCGGCACTGGGGCGCGCCCTT	CGCACA	180
Db	121	CGT	GGCCCTTGGGCTCAGCGGCACTGGGGCGCGCCCTT	CGCACA	180
Qy	181	GG	CGGTGCCCCCAATGGCGAGGCGCGGAGAGCAGTGC	CTTGCTTCCCCCGAGGACAGCC	240
Db	181	GG	CGGTGCCCCCAATGGCGAGGCGCGGAGAGCAGTGC	CTTGCTTCCCCCGAGGACAGCC	240
Qy	241	GC	CTGTGGCAGTATCTTCTGAGCGCTTCATGCGGGAGCAC	CCCGCGCTCGAAGCCTGA	300
Db	241	GC	CTGTGGCAGTATCTTCTGAGCGCTTCATGCGGGAGCAC	CCCGCGCTCGAAGCCTGA	300
Qy	301	GG	CTGTGACCTCTGGAGCAGCGCGAGGGGATTTCTAT	GATGACCTGCGAGCAGGCCACG	360
Db	301	GG	CTGTGACCTCTGGAGCAGCGCGAGGGGATTTCTAT	GATGACCTGCGAGCAGGCCACG	360
Qy	361	TC	TGTGGCCAACTGGCGCGGCTCATCCAGGCGCAAGAGCG	CGCTGGACCTGGGGCACTTCA	420
Db	361	TC	TGTGGCCAACTGGCGCGGCTCATCCAGGCCAAGAGCGCG	CTGGACCTGGGGCACTTCA	420
Qy	421	CG	GGCTACTTCGGCCCTGGCGCTTGGCGCTGCGCGGAGCG	GGCGCGTGGTGCACCT	480
Db	421	CG	GGCTACTTCGGCCCTGGCGCTTGGCGCTGCGCGGAGCG	GGCGCGTGGTGCACCT	480
Qy	481	GC	GAGTGGACGCGCGAGCCCGGAGCTGGAGCGGCCCTTG	TGGAGCAGGCCCGAGCGG	540
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Qy	661	CT	TACTACAGCGCTGCTGACGTGCTGCGACCCGGAGGCA	TCCTCGCGCTCCTCAGAG	720
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Qy	781	GAA	ACCTAAACGAAACGATCCGCGGAGCGTCAAGGCTTAC	ATCAGCCTCCTGCCCTGG	840
Db	781	GAA	ACCTAAACGAAACGATCCGCGGAGCGTCAAGGCTTAC	ATCAGCCTCCTGCCCTGG	840
Qy	841	GC	GATGGACTCACTTTGGCTTCAAGATCTAGGGCTGGCC	CTTAGTGGGCTCGAGG	900
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Qy	901	GAG	GGTGTGCTGGGAAACCCAGGAATTGACCTTGAATTTAA	ATTCGAAATTAAGTGGG	960
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QY 961 GCTGGGACACAAAAA 989
Db 961 GCTGGGACACAAAAA 989

RESULT 3
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LOCUS Homo sapiens clone DNA71282 methyltransferase (UNQ766) mRNA, PRI 03-OCT-2003
DEFINITION complete cds.
ACCESSION AY358476
VERSION AY358476.1 GI:37182074
KEYWORDS FLI_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 989)
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Wiedand, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 989).
REFERENCE Clark, H.F.
AUTHORS Direct Submission
TITLE Department of Bioinformatics, Genentech,
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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VERSION AX338454.1 GI:18128893
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Meyers, R.A. and Williamson, M.
TITLE 25692, a novel human o-methyltransferase family member and uses

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JOURNAL	thereof	Db	750	TCCTGTGGCGCGGAAGGTGCTGCAACCTCCGAAAGGGGACGTGGCGCGGAGTGTGTGC	809
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VERSION	BC047774.1				
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JOURNAL					
PUBMED					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					

R. M.

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA q1: 21389376.

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LOCATION/QUALIFIERS
1. 1041

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AUTHORS	Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J., Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C., Reddy, R., Hillman, J.L., and Bandman, O.				
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ACCESSION BC023663
VERSION BC023663.2 GI:40226187
KEYWORDS MGC.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
REFERENCE Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Wang,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Lequellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 913)
Strausberg,R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:23959051.
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgrl.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 39 Row: j Column: 6
This clone was selected for full length sequencing because it
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DEFINITION Sequence 7435 from Patent WO02068579.
ACCESSION CQ721501
VERSION CQ721501.1 GI:42282358
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 7435 06-SEP-2002;
PE Corporation (NY) (US)
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DEFINITION  
AX338456  
ACCESSION  
AX338456.1 GI:18128895  
VERSION  
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ORGANISM  
Homo sapiens  
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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
AUTHORS  
Meyers, R.A. and Williamson, M.  
TITLE  
25692, a novel human O-methyltransferase family member and uses  
thereof  
JOURNAL  
Patent: WO 0183719-A 3 08-NOV-2001;  
Millennium Pharmaceuticals, Inc. (US)  
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BC049670  
ACCESSION  
BC049670.1 GI:29612504  
VERSION  
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Mus musculus  
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Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 946)  
REFERENCE  
AUTHORS  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,  
Schneringer, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
TITLE  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
JOURNAL  
PUBMED  
2 (bases 1 to 946)  
REFERENCE  
AUTHORS  
Strausberg, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (31-MAR-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA



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RESULT 13
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LOCUS Rattus norvegicus clone CH230-34D17, WORKING DRAFT SEQUENCE, 2
DEFINITION AC120475
ACCESSION AC120475
VERSION 7 GI:25137871
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.
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Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguilano,D.,
Anyalebechi,V., Ayodeji,M., Baca,E., Baden,H.,
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Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
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Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geet,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowals,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhera,L., Louisedge,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
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Nwaokemeleh,O., Okwunou,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
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Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sison,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Stroz,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlarczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,J., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 237829)
Worley,K.C.
Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237829)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23267656.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXLH
Center clone name: CH230-34D17
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 218320 bases at least Q40
Consensus quality: 222359 bases at least Q30
Consensus quality: 225092 bases at least Q20
Estimated insert size: 222440; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 236267: contig of 236267 bp in length
* 236268 236367: gap of unknown length
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QY 53 TCACGTCTCCCGCGCTCTCTGCGCGCCGATGACCCAGCGGTGCCCGCTCTCCGT 112
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QY 113 GCCCGCGCGCTGGCGCTGGCTCAGCCACACTGGCGCGCTTGGCCACTGGGCTCTT 172
DB   |||||
DB 81886 CGCACATGGCCAGCGGTGCTGGCTGTCTATTCCACCGCGTGGCCCTTCGCTCTT 81945
QY 173 CTTGGGGAGCGGTGCCCCCATGCGAGCGCGGCGAGAGTGTCTTCCCTCCCGCA 232
DB   |||||
DB 81946 CTTGGGGAATAGTGGCTCTCGTGGGGTTCAGATGGCATGACACTGCTGCCCTTCA 82005
QY 233 GGACAGCCCGCTGTGGCAGTATCTTTGAGCGCTCCATGCGGGAGCACCCGCGCTGGG 292
DB   |||||
DB 82006 GGACAATCCCTGTGGCAGTATCTGTGAGCTGCTCCATGAGGGAACACCCAGCGCTGG 82065
QY 293 AGCCTGAGGCTGTGACCTGAGCAGCGCAGGGGATTTCTATGATGACCTGCGAGCA 352
DB   |||||
DB 82066 GAGCCTGGACTGCTGACCTGGAGCGCGCAGGGGATTCATGATGACCTGTGAACA 82125
QY 353 GGCCCAAGCTCTTGGCCAACTGGCGCGGTCTATCCAGGCAAGAGGCGCTGGACCTGGG 412
DB   |||||
DB 82126 GGCCCAACTTCTGGTCAACCTGGCGCGGTCTATCAAGCCAGAAAGCTCTGGATCTGG 82185
QY 413 CACCTTCAAGGCTA-CTCCGCGCTGGCGCTGGCGCTGGCGTGGCGGACGCGCGCG 471
DB   |||||
DB 82186 TACTTTACGGGTACTCTCGGCGCTGGCGCTAGCCTTGGCGCTTCCGAGGCTGGCGCG 82245
QY 472 TGGTCACTTGGAGGTGAGCGCGACGCCCGGAGCTGGGACGGCCCTTGGAGCGAGG 531
DB   |||||
DB 82246 TGGTCACTTGGAGGTGAGCGAGCGACGCCCGGAGCTGGGAGGGCCCTTGTGGAAGCAGA 82305
QY 532 CGAGCGCGGAGCACAAGATCGACCTCCGCTCAAGCCCGCTTGGAGACCTTGGACGAGC 591
DB   |||||
DB 82306 CAGAGTGGAGCAGAAGATCGAACTTGGCTGCACGCCCGCTTCGAGACTTTGGATGAGT 82365
QY 592 TGCTGGCGCGGCGAGCGCGACCTTTCGACGTGGCGCTGGTGGATGCGGACAGGAGA 651
DB   |||||
DB 82366 TCCTGGCGCGGCGGTGAGCGACATAGCAGTGGTGGAGCGCAGACAAGCCTACTACGAGCA 82425
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DB   |||||
DB 82426 CTGCTGCAACTCTTACGCCCG 82447
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AL390034      38679 bp      DNA      linear      PRI 01-JAN-2002
Human DNA sequence from clone RP11-375G3 on chromosome 10, complete
sequence.
AL390034      AL390034      GI:18041549
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 38679)
Wray, P.
Direct Submission
Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 2, 2002 this sequence version replaced gi:18032099.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em.; EMBL; SW.;
SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-375G3 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-375G3 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-399K21 is at 36680 in this
sequence. The true right end of clone RP11-487I5 is at 2000 in this
sequence.
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terminator reads only."

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terminator reads only."

ORIGIN
  Query Match      26.0%; Score 256.8; DB 9; Length 38679;
  Best Local Similarity 97.4%; Pred. No. 5.3e-26;
  Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 704 CTGCGCGCTCTCAGATCTCTGTGGCGGGAAGGTCTGCAACTCCGAAGGGAGCT 763
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DB 7761 CCCCGCCCTCCCGAGGTCCTGTGGCGGGAAGGTCTGCAACTCCGAAGGGAGCT 7702
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 QY 824 CAGCCTCTCTGCGCCCTGCGGCGATGAGTACCTTGGCTTCAAGATCTTAGGGCTGGCCCT 883  
 Db 7641 CAGCCTCTCTGCGCCCTGCGGCGATGAGTACCTTGGCTTCAAGATCTTAGGGCTGGCCCT 7582  
 QY 884 AGTGAAGTGGCTCGAGGAGGGTGTGCTGGGAACCCAGGAATTGACCTGAGTTTAA 943  
 Db 7581 AGTGAAGTGGCTCGAGGAGGGTGTGCTGGGAACCCAGGAATTGACCTGAGTTTAA 7522  
 QY 944 TTCGAAATAAAGTGGGCTGGGACACA 971  
 Db 7521 TTCGAAATAAAGTGGGCTGGGACACA 7494

## RESULT 15

AC027393/c

LOCUS AC027393 169612 bp DNA linear HTG 24-AUG-2002  
 DEFINITION Homo sapiens chromosome 10, clone RP11-770D23 map 10, WORKING DRAFT  
 SEQUENCES, 28 unordered pieces.

AC027393

VERSION AC027393.3 GI:8076860

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169612)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Unpublished

Homo sapiens chromosome 10, clone RP11-770D23

2 (bases 1 to 169612)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavsky,L., Boukagter,B., Brown,A., Burkett,G.,

Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collamore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 169612)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavsky,L., Boukagter,B., Brown,A., Burkett,G.,

Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collamore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE  
JOURNAL

## COMMENT

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 25, 2000 this sequence version replaced gi:7652066.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L6572  
 Center clone name: 770\_D\_23  
 ----- Summary Statistics  
 Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 155213 bases at least Q40  
 Consensus quality: 162022 bases at least Q30  
 Consensus quality: 164973 bases at least Q20  
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 Insert size: 166912; sum-of-contigs  
 Quality coverage: 4.1 in Q20 bases; agarose-fp  
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1191: contig of 1191 bp in length  
 \* 1192 1291: gap of 100 bp  
 \* 1292 2404: contig of 1113 bp in length  
 \* 2405 2504: gap of 100 bp  
 \* 2505 3705: contig of 1201 bp in length  
 \* 3706 3805: gap of 100 bp  
 \* 3806 4734: contig of 929 bp in length  
 \* 4735 4834: gap of 100 bp  
 \* 4835 6570: contig of 1736 bp in length  
 \* 6571 6670: gap of 100 bp  
 \* 6671 8583: contig of 1913 bp in length  
 \* 8584 8683: gap of 100 bp  
 \* 8684 10290: contig of 1607 bp in length  
 \* 10291 10391: gap of 100 bp  
 \* 10391 11939: contig of 1548 bp in length  
 \* 11939 12038: gap of 100 bp  
 \* 12039 15839: contig of 3801 bp in length  
 \* 15840 19203: contig of 3284 bp in length  
 \* 19204 19303: gap of 100 bp  
 \* 19304 22581: contig of 3278 bp in length  
 \* 22582 22681: gap of 100 bp  
 \* 22682 29487: contig of 2266 bp in length  
 \* 29488 29547: gap of 100 bp  
 \* 29548 28167: contig of 3120 bp in length  
 \* 28168 28267: gap of 100 bp  
 \* 28268 32083: contig of 3816 bp in length  
 \* 32084 32183: gap of 100 bp  
 \* 32184 35533: contig of 3350 bp in length  
 \* 35534 35634: gap of 100 bp  
 \* 41517: contig of 5884 bp in length

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* 41518 41617: gap of 100 bp
* 41618 47143: contig of 5526 bp in length
* 47144 47243: gap of 100 bp
* 47244 51694: contig of 4451 bp in length
* 51695 51794: gap of 100 bp
* 51795 57570: contig of 5776 bp in length
* 57571 57670: gap of 100 bp
* 57671 63190: contig of 5520 bp in length
* 63191 63290: gap of 100 bp
* 63291 70708: contig of 7418 bp in length
* 70709 70808: gap of 100 bp
* 70809 78988: contig of 8180 bp in length
* 78989 79088: gap of 100 bp
* 79089 86527: contig of 7439 bp in length
* 86528 86627: gap of 100 bp
* 86628 99114: contig of 12487 bp in length
* 99115 99214: gap of 100 bp
* 99215 110221: contig of 11007 bp in length
* 110222 110321: gap of 100 bp
* 110322 123287: contig of 12966 bp in length
* 123288 123387: gap of 100 bp
* 123388 147877: contig of 24490 bp in length
* 147878 147977: gap of 100 bp
* 147978 169612: contig of 21635 bp in length.
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Best Local Similarity 97.4%; Pred.No.3.6e-26;
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 704 CCTCGCCGTCCTCAGAGTCCTGTGGCGGGGAAGGTGCTGCAACCTCCGAAAGGGGACGT 763
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    |||||

QY 764 GCGGCGCGAGTGTGTGCGAAACCTAAACGACGCATCCGGCGGGAGCTCAGGGTCTACAT 823
    |||||
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QY 824 CAGCCTCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGATCTAGGGCTGGCCCCCT 883
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QY 884 AGTGAGTGGGCTCGAGGGGAGGGTTGCCTGGGAACCCAGGAATTGACCTTGAGTTTAAA 943
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Db 140231 AGTGAGTGGGCTCGAGGGGAGGGTTGCCTGGGAACCCAGGAATTGACCTTGAGTTTAAA 140172
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QY 944 TTCGAAAATAAAGTGGGCTGGGACACA 971
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Job time : 7565 secs

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